BLAST score

E value

617

2.0e-64



```
4.0e-64
E value
Match length
                  120
                  97
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  146017
Seq. No.
                  LIB3168-068-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
                  554
BLAST score
                  4.0e-57
E value
                  107
Match length
                  95
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146018
                  LIB3168-068-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  619
                  1.0e-64
E value
Match length
                  120
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146019
Seq. ID
                  LIB3168-068-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146020
Seq. ID
                  LIB3168-068-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1628583
```

Match length 120 % identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146021

Seq. ID LIB3168-068-P1-K1-E12

Method BLASTX
NCBI GI g112682
BLAST score 567
E value 1.0e-58
Match length 138
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146022

Seq. ID LIB3168-068-P1-K1-E2

Method BLASTX
NCBI GI g1628583
BLAST score 653
E value 1.0e-68
Match length 126
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146023

Seq. ID LIB3168-068-P1-K1-E3

Method BLASTX
NCBI GI g112681
BLAST score 607
E value 3.0e-63
Match length 141
% identity 84

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146024

Seq. ID LIB3168-068-P1-K1-E5

Method BLASTX
NCBI GI g1628583
BLAST score 597
E value 4.0e-62
Match length 120
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

146025 Seq. No. Seq. ID LIB3168-068-P1-K1-E6 BLASTX Method NCBI GI g112741 728 BLAST score E value 2.0e-77 Match length 137 99 % identity 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868 (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] Seq. No. 146026 Seq. ID LIB3168-068-P1-K1-E7 Method BLASTX NCBI GI g1628583 BLAST score 578 E value 8.0e-60 Match length 119 % identity 94 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146027 LIB3168-068-P1-K1-E8 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 614 E value 5.0e-64 Match length 120 % identity 99 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146028 Seq. ID LIB3168-068-P1-K1-E9 Method BLASTX NCBI GI g1628583 BLAST score 613 E value 6.0e-64 Match length 120 % identity 98 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146029

Seq. ID LIB3168-068-P1-K1-F1

Method BLASTX NCBI GI g112682

```
BLAST score
                   615
                   4.0e-64
E value
Match length
                   143
                   81
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146030
Seq. ID
                   LIB3168-068-P1-K1-F10
Method
                   BLASTX
                   g2129657
NCBI GI
BLAST score
                   293
E value
                   2.0e-26
                   120
Match length
                   57
% identity
NCBI Description
                   oleosin isoform - Arabidopsis thaliana
                   >gi_987014_emb_CAA90877 (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878 (Z54165) oleosin
                   [Arabidopsis thaliana]
Seq. No.
                   146031
Seq. ID
                   LIB3168-068-P1-K1-F11
Method
                   BLASTX
                   q1628583
NCBI GI
BLAST score
                   600
E value
                   2.0e-62
Match length
                   120
                   97
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146032
Seq. No.
Seq. ID
                   LIB3168-068-P1-K1-F12
                   BLASTX
Method
                   g1628583
NCBI GI
BLAST score
                   618
E value
                   2.0e-64
Match length
                   120
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146033
                   LIB3168-068-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112682
BLAST score
                   619
E value
                   1.0e-64
Match length
                   143
% identity
                   82
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
```

cruciferin precursor (CRB) - Arabidopsis thaliana

```
>gi_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

146034
```

 Seq. No.
 146034

 Seq. ID
 LIB3168-068-P1-K1-F3

 Method
 BLASTX

 NCBI GI
 g2129767

 BLAST score
 700

 E value
 4.0e-74

 Match length
 140

 % identity
 94

NCBI Description vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi\_1805364\_dbj\_BAA09615\_ (D61394) beta-VPE [Arabidopsis thaliana]

Seq. No. 146035

Seq. ID LIB3168-068-P1-K1-F4

Method BLASTX
NCBI GI g1628583
BLAST score 402
E value 3.0e-39
Match length 128
% identity 68

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146036

Seq. ID LIB3168-068-P1-K1-F6

Method BLASTX
NCBI GI g1628583
BLAST score 621
E value 7.0e-65
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146037

Seq. ID LIB3168-068-P1-K1-F7

Method BLASTX
NCBI GI g1628583
BLAST score 543
E value 9.0e-56
Match length 118
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146038

Seq. ID LIB3168-068-P1-K1-F8

Method BLASTX
NCBI GI g3834314
BLAST score 560

```
E value
                  2.0e-62
Match length
                  134
% identity
                  87
NCBI Description
                  (AC005679) Similar to gene pi010 glycosyltransferase
                  gi_2257490 from S. pombe clone 1750 gb_AB004534. ESTs
                  gb T46079 and gb AA394466 come from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  146039
Seq. ID
                  LIB3168-068-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  582
                  3.0e-60
E value
Match length
                  140
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  146040
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  587
                  7.0e-61
E value
Match length
                  114
                  97
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana:
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146041
Seq. ID
                  LIB3168-068-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g3242075
BLAST score
                  680
E value
                  8.0e-72
Match length
                  142
% identity
NCBI Description
                  (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis
                  thaliana]
                  146042
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  178
E value
                  2.0e-39
Match length
                  96
% identity
                  86
```

```
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146043
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  306
E value
                  6.0e-28
Match length
                  60
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146044
Seq. No.
                  LIB3168-068-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  400
                  6.0e-39
E value
Match length
                  114
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146045
Seq. No.
                  LIB3168-068-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3256066
BLAST score
                  399
E value
                  8.0e-39
Match length
                  99
% identity
NCBI Description
                  (Y13987) chloroplast NAD-MDH [Arabidopsis thaliana]
                  146046
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  g2264310
BLAST score
                  285
E value
                  1.0e-159
Match length
                  420
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKP11, complete sequence [Arabidopsis thaliana]
                  146047
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  613
E value
                  5.0e-64
Match length
                  120
% identity
                  99
```

```
NCBI Description
                    (U66916) 12S cruciferin seed storage protein [Arabidopsis
                    thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                    cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                    146048
                    LIB3168-068-P1-K1-G9
Seq. ID
Method
                    BLASTX
NCBI GI
                    q112741
BLAST score
                    718
E value
                    3.0e-76
Match length
                    136
                    99
% identity
NCBI Description
                    2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                    PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                    Arabidopsis thaliana > gi_1 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] > gi_3 95201 emb_CAA80868_
                    (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                    >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                    precursor [Arabidopsis thaliana]
Seq. No.
                    146049
Seq. ID
                    LIB3168-068-P1-K1-H10
Method
                    BLASTX
NCBI GI
                    q112741
BLAST score
                    200
E value
                    7.0e-16
Match length
                    65
                    63
% identity
                    2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                    PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                    Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                    (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                    >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                    precursor [Arabidopsis thaliana]
Seq. No.
                    146050
Seq. ID
                    LIB3168-068-P1-K1-H11
Method
                    BLASTX
NCBI GI
                    q112681
BLAST score
                    48
E value
                    1.0e-60
Match length
                    138
% identity
                    12S SEED STORAGE PROTEIN PRECURSOR >gi_81604 pir S08509
NCBI Description
                    cruciferin precursor (CRA1) - Arabidopsis thaliana
                    >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                    tha\overline{\text{liana}} >gi 808936 emb CAA32493 (X14312) 12S seed
                    storage protein [Arabidopsis thaliana]
Seq. No.
                    146051
Seq. ID
                    LIB3168-068-P1-K1-H12
Method
                    BLASTX
NCBI GI
                    g112682
BLAST score
                    616
E value
                    3.0e-64
Match length
                    143
```

Method

BLASTX

```
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] > gi_808937_emb_CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146052
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  573
E value
                  3.0e-59
Match length
                  114
% identity
                  98
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  #thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146053
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  602
E value
                  1.0e-62
Match length
                  120
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146054
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q4455351
BLAST score
                  348
E value
                  7.0e~33
Match length
                  118
% identity
                  60
NCBI Description
                  (AL035524) putative protein [Arabidopsis thaliana]
                  146055
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  q3176701
BLAST score
                  424
E value
                  0.0e + 00
Match length
                  434
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20K24 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146056
                  LIB3168-068-P1-K1-H6
Seq. ID
```

```
g112682
NCBI GI
BLAST score
                  577
E value
                  8.0e-60
Match length
                  124
                  87
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsīs thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146057
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  669
                  2.0e-70
E value
Match length
                  124
% identity
                  99
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  146058
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-H8
Method
                  BLASTN
NCBI GI
                  q725259
BLAST score
                  79
E value
                  4.0e-37
Match length
                  87
% identity
NCBI Description Arabidopsis thaliana oleosin mRNA, complete cds
                  146059
Seq. No.
Seq. ID
                  LIB3168-068-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  608
E value
                  2.0e-63
Match length
                  124
% identity
                  98
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146060
Seq. ID
                  LIB3168-069-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  378
E value
                  1.0e-36
```

```
102
 Match length
 % identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
 NCBI Description
                   PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
 Seq. No.
                   146061
 Seq. ID
                   LIB3168-069-P1-K1-A10
 Method
                   BLASTX
                   g1628583
 NCBI GI
 BLAST score
                   625
 E value
                   2.0e-65
 Match length
                   120
% identity
                   100
 NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146062
 Seq. No.
 Seq. ID
                   LIB3168-069-P1-K1-A11
 Method
                   BLASTX
 NCBI GI
                   q1628583
 BLAST score
                   204
 E value
                   4.0e-16
 Match length
                   54
 % identity
 NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146063
 Seq. No.
 Seq. ID
                   LIB3168-069-P1-K1-A12
 Method
                   BLASTN
 NCBI GI
                   q4539378
 BLAST score
                   426
                   0.0e + 00
 E value
 Match length
                   451
 % identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21
 NCBI Description
                   (ESSA project)
                   146064
 Seq. No.
 Seq. ID
                   LIB3168-069-P1-K1-A5
 Method
                   BLASTX
 NCBI GI
                   q1628583
 BLAST score
                   525
 E value
                   1.0e-53
 Match length
                   105
 % identity
 NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
```

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

```
146065
Seq. No.
Seq. ID
                   LIB3168-069-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g4218963
BLAST score
                   175
                   2.0e-12
E value
Match length
                   30
% identity
                   (AF093672) xyloglucan endotransglycosylase [Arabidopsis
NCBI Description
                   thaliana] >gi_4539300_emb_CAB39603.1_ (AL049480) putative xyloglucan endo-1, 4-beta-D-glucanase [Arabidopsis
                   thaliana]
                   146066
Seq. No.
Seq. ID
                   LIB3168-069-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g112681
                   227
BLAST score
                   1.0e-18
E value
Match length
                   107
                   50
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi_808936 emb_CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   146067
Seq. No.
                   LIB3168-069-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112741
BLAST score
                   498
                   1.0e-50
E value
                   98
Match length
                   96
% identity
NCBI Description
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68855_pir_ NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
                   146068
Seq. No.
Seq. ID
                   LIB3168-069-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   668
E value
                   2.0e-70
Match length
                   141
                   95
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146069
Seq. No.
Seq. ID
                   LIB3168-069-P1-K1-B1
```

```
BLASTN
Method
NCBI GI
                   q4165340
BLAST score
                   328
                   0.0e+00
E value
Match length
                   471
                   93
% identity
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F11M15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   146070
Seq. No.
                   LIB3168-069-P1-K1-B10
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3738257
BLAST score
                   263
E value
                   2.0e-42
Match length
                   107
                   85
% identity
                   (AB018410) cytosolic phosphoglycerate kinase 1 [Populus
NCBI Description
                   nigra]
                   146071
Seq. No.
                   LIB3168-069-P1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4314368
BLAST score
                   316
E value
                   4.0e-29
Match length
                   142
% identity
                   46
                  (ACO06340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   146072
Seq. No.
                   LIB3168-069-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3859606
BLAST score
                   616
E value
                   3.0e-64
Match length
                   140
% identity
                   (AF104919) contains similarity to cysteine proteases (Pfam:
NCBI Description
                   PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]
                   146073
Seq. No.
                   LIB3168-069-P1-K1-B2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q112737
BLAST score
                   341
E value
                   2.0e-32
Match length
                   84
                   81
% identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
```

precursor [Arabidopsis thaliana]

Seq. No.

146079

```
146074
Seq. No.
Seq. ID
                  LIB3168-069-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g2129641
BLAST score
                  582
E value
                  3.0e-60
Match length
                  138
                  86
% identity
NCBI Description
                  major latex protein type 1 - Arabidopsis thaliana
                  >qi 1107493 emb CAA63026 (X91960) major latex protein
                  type1 [Arabidopsis thaliana]
                  146075
Seq. No.
Seq. ID
                  LIB3168-069-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  g3894156
BLAST score
                  155
E value
                  1.0e-81
Match length
                  368
% identity
                  92
                  Arabidopsis thaliana chromosome II BAC T16F16 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146076
                  LIB3168-069-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1592677
BLAST score
                  289
E value
                  6.0e-26
Match length
                  117
% identity
                  56
NCBI Description
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
                  146077
Seq. No.
Seq. ID
                  LIB3168-069-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q4375833
BLAST score
                  383
E value
                  7.0e-37
Match length
                  150
% identity
NCBI Description
                   (AL021713) receptor serine/threonine kinase-like protein
                  [Arabidopsis thaliana]
Seq. No.
                  146078
Seq. ID
                  LIB3168-069-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  558
E value
                  2.0e-57
Match length
                  139
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

```
LIB3168-069-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112737
BLAST score
                   632
                   5.0e-66
E value
                   164
Match length
                   67
% identity
NCBI Description
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
                   146080
Seq. No.
Seq. ID
                   LIB3168-069-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   628
E value
                   1.0e-65
Match length
                   123
                   98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495 emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146081
Seq. ID
                   LIB3168-069-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   g2264311
BLAST score
                   37
E value
                   3.0e-12
Match length
                   63
% identity
                   94
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MLN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146082
Seq. ID
                   LIB3168-069-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   314
E value
                   3.0e-29
Match length
                   84
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146083
Seq. ID
                   LIB3168-069-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   g3928078
BLAST score
                   387
E value
                   2.0e-37
                   121
Match length
```

```
% identity
                   (AC005770) putative protein kinase, calcium dependent
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   146084
                   LIB3168-069-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2651310
BLAST score
                  811
E value
                   4.0e-87
Match length
                   156
                   99
% identity
NCBI Description
                   (AC002336) putative PTR2-B peptide transporter [Arabidopsis
                   thalianal
                   146085
Seq. No.
Seq. ID
                   LIB3168-069-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q3548810
BLAST score
                   195
E value
                   7.0e-15
Match length
                   151
% identity
                   36
NCBI Description
                   (AC005313) putative chloroplast nucleoid DNA binding
                   protein [Arabidopsis thaliana]
                   146086
Seq. No.
Seq. ID
                   LIB3168-069-P1-K1-C9
Method
                   BLASTN
NCBI GI
                   q4757417
BLAST score
                   234
E value
                   1.0e-129
Match length
                   267
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   T30G6, complete sequence
                   146087
Seq. No.
Seq. ID
                   LIB3168-069-P1-K1-D1
Method
                   BLASTN
NCBI GI
                   g3241926
BLAST score
                   53
E value
                   4.0e-21
Match length
                   73
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSG15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146088
Seq. ID
                   LIB3168-069-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   q117238
BLAST score
                   414
E value
                   1.0e-40
Match length
                   124
                   73
% identity
NCBI Description
                  MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (PROTEIN
```

```
CS/CH-42) (MG-PROTOPORPHYRIN IX CHELATASE)
>gi_81656_pir__S12785 protein ch-42 precursor, chloroplast
- Arabidopsis thaliana >gi_1020100_emb_CAA62754_ (X91411)
protoporphyrin-IX Mg-chetalase [Arabidopsis thaliana]
>gi 2832653 emb_CAA16728_ (AL021710) protein ch-42
precursor, chloroplast [Arabidopsis thaliana]
>gi_4490290_emb_CAB38561.1_ (X51799) chloroplast protein
[Arabidopsis thaliana] >gi_228771_prf__1811226A ccsA gene
[Euglena gracilis]
```

Seq. No. 146089 LIB3168-069-P1-K1-D11 Seq. ID Method BLASTX

NCBI GI q112682 BLAST score 44 E value 3.0e - 45Match length 148 % identity 76

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>qi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146090

LIB3168-069-P1-K1-D12 Seq. ID

Method BLASTX NCBI GI q3402711 BLAST score 246 E value 7.0e-21 143 Match length

% identity

(AC004261) putative RNA-binding protein [Arabidopsis NCBI Description

thaliana]

Seq. No. 146091

LIB3168-069-P1-K1-D2 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 501 E value 1.0e-50 Match length 114

% identity 87

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

146092 Seq. No.

LIB3168-069-P1-K1-D4 Seq. ID

Method BLASTX NCBI GI q1628583 259 BLAST score E value 5.0e-23 Match length 55 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S



## cruciferin seed storage protein [Arabidopsis thaliana]

 Seq. No.
 146093

 Seq. ID
 LIB3168-069-P1-K1-D5

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 391

 E value
 4.0e-38

 Match length
 99

 % identity
 76

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

 Seq. No.
 146094

 Seq. ID
 LIB3168-069-P1-K1-D6

 Method
 BLASTX

NCBI GI g1628583 BLAST score 450 E value 7.0e-45 Match length 112 % identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146095

Seq. ID LIB3168-069-P1-K1-D7

Method BLASTX
NCBI GI g3023848
BLAST score 537
E value 4.0e-55
Match length 106
% identity 56

NCBI Description GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE

PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA) >qi 2289095 (U77381) WD-40 repeat protein [Arabidopsis

thaliana]

Seq. No. 146096

Seq. ID LIB3168-069-P1-K1-D8

Method BLASTX
NCBI GI g1628583
BLAST score 604
E value 9.0e-63
Match length 120
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146097

Seq. ID LIB3168-069-P1-K1-D9

Method BLASTN
NCBI GI g4512656
BLAST score 142
E value 6.0e-74

BLAST score

E value

139

6.0e-09

```
398
Match length
% identity
                  90
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
                  146098
Seq. No.
                  LIB3168-069-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2258103
BLAST score
                  252
E value
                  1.0e-139
Match length
                  379
                  91
% identity
                  Arabidopsis thaliana chloroplast genes for trnC and rpoB,
NCBI Description
                  partial cds
                  146099
Seq. No.
                  LIB3168-069-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3047092
                  59
BLAST score
                  8.0e-15
E value
Match length
                  102
                  51
% identity
                  (AF058826) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  146100
                  LIB3168-069-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  773
                  1.0e-82
E value
                  147
Match length
                  100
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed ___
                  storage protein [Arabidopsis thaliana]
                  146101
Seq. No.
Seq. ID
                  LIB3168-069-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  q4512690
BLAST score
                  406
                  0.0e + 00
E value
Match length
                  460
% identity
                  Arabidopsis thaliana chromosome II BAC F11A3 genomic
NCBI Description
                  sequence, complete sequence
                  146102
Seq. No.
Seq. ID
                  LIB3168-069-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g1335862
```

```
Match length
                  41
                  73
% identity
                 (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                  146103
Seq. No.
                  LIB3168-069-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
                  519
BLAST score
                  8.0e-53
E value
                  151
Match length
                  70
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146104
Seq. No.
                  LIB3168-069-P1-K1-E6
Seq. ID
                  BLASTX
Method
                  g1628583
NCBI GI
                  284
BLAST score
                  1.0e-25
E value
                  60
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146105
Seq. No.
                  LIB3168-069-P1-K1-E8
Seq. ID
                  BLASTX
Method
                  g112681
NCBI GI
                  619
BLAST score
                  1.0e-64
E value
                  124
Match length
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__$08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146106
Seq. No.
                  LIB3168-069-P1-K1-E9
Seq. ID
Method
                  BLASTN
                  g2264309
NCBI GI
                  215
BLAST score
                  1.0e-117
E value
                  296
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJJ3, complete sequence [Arabidopsis thaliana]
                  146107
Seq. No.
                  LIB3168-069-P1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16236
```

BLAST score 4.0e-34 E value Match length 94 96 % identity Arabidopsis CRB gene for 12S seed storage protein NCBI Description >gi 166677 gb M37248 ATHCRBAA A.thaliana 12S storage protein CRA1 gene, exons 1-4 Seq. No. 146108 LIB3168-069-P1-K1-F10 Seq. ID Method BLASTX NCBI GI q1628583 BLAST score 634 2.0e-66 E value 123 Match length 99 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 146109 Seq. No. LIB3168-069-P1-K1-F11 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 627 E value 2.0e-65 123 Match length % identity 98 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146110 LIB3168-069-P1-K1-F12 Seq. ID Method BLASTX NCBI GI g2708750 297 BLAST score 6.0e-27 E value Match length 124 % identity 53 NCBI Description (AC003952) putative physical impedence protein [Arabidopsis thaliana] 146111 Seq. No. Seq. ID LIB3168-069-P1-K1-F2 Method BLASTX NCBI GI g3421346 BLAST score 663 E value 1.0e-69 Match length 146 % identity 90 NCBI Description (AJ007723) ribosomal protein S4 [Orobanche minor]

Seq. No. 146112

Seq. ID LIB3168-069-P1-K1-F3

Method BLASTX NCBI GI g2961390

```
BLAST score
                  538
                  3.0e-60
E value
Match length
                  116
% identity
                  96
                   (AL022141) beta-galactosidase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  146113
Seq. ID
                  LIB3168-069-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  536
E value
                  5.0e-55
Match length
                  106
% identity
                  93
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146114
Seq. ID
                  LIB3168-069-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  61
E value
                  2.0e-52
Match length
                  125
% identity
                  91
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146115
Seq. ID
                  LIB3168-069-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  q1946354
BLAST score
                  34
E value
                  7.0e-10
Match length
                  82
% identity
                  94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T06B20 genomic
                  sequence, complete sequence
Seq. No.
                  146116
                  LIB3168-069-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  419
E value
                  2.0e-41
Match length
                  118
% identity
                  75
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
```

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

 Seq. No.
 146117

 Seq. ID
 LIB3168-069-P1-K1-G1

 Method
 BLASTN

NCBI GI g4589439
BLAST score 280
E value 1.0e-156
Match length 448
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MQM1, complete sequence

Seq. No. 146118

Seq. ID LIB3168-069-P1-K1-G10

Method BLASTX
NCBI GI g2129657
BLAST score 428
E value 3.0e-42
Match length 115
% identity 78

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi\_987014\_emb\_CAA90877\_ (Z54164) oleosin [Arabidopsis thaliana] >gi\_987016\_emb\_CAA90878\_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 146119

Seq. ID LIB3168-069-P1-K1-G11

Method BLASTX
NCBI GI g112682
BLAST score 734
E value 5.0e-78
Match length 153
% identity 90

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146120

Seq. ID LIB3168-069-P1-K1-G12

Method BLASTX
NCBI GI g2130159
BLAST score 162
E value 6.0e-11
Match length 78
% identity 54

NCBI Description hypothetical protein 85 - maize chloroplast

>gi\_902275\_emb\_CAA60340\_ (X86563) ORF85 [Zea mays]
>gi\_902296\_emb\_CAA60360\_ (X86563) ORF85 [Zea mays]

Seq. No. 146121

Seq. ID LIB3168-069-P1-K1-G2

Method BLASTX NCBI GI g1628583

```
191
BLAST score
                   1.0e-14
E value
Match length
                   48
                   77
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146122
Seq. No.
                  LIB3168-069-P1-K1-G3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4512656
BLAST score
                   136
                   1.0e-70
E value
                   228
Match length
                   89
% identity
                   Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                   sequence, complete sequence
                   146123
Seq. No.
                   LIB3168-069-P1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   334
E value
                   2.0e-31
                   94
Match length
% identity
                   71
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146124
                   LIB3168-069-P1-K1-G6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q16472
BLAST score
                   273
E value
                   1.0e-152
Match length
                   309
                   97
% identity
                  A.thaliana rRNA repeat unit, most frequent IGR type
NCBI Description
                   146125
Seq. No.
                   LIB3168-069-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   625
                   2.0e-65
E value
Match length
                   120
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146126
                   LIB3168-069-P1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2500376
```

```
BLAST score
                  509
                  1.0e-51
E value
Match length
                  111
                  91
% identity
                  60S RIBOSOMAL PROTEIN L34 >gi 4262177_gb_AAD14494_
NCBI Description
                  (AC005508) 23552 [Arabidopsis thaliana]
Seq. No.
                  146127
Seq. ID
                  LIB3168-069-P1-K1-H10
                  BLASTX
Method
                  q112739
NCBI GI
BLAST score
                  66
E value
                  1.0e-45
                  137
Match length
                  74
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205 emb_CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  146128
Seq. No.
Seq. ID
                  LIB3168-069-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  348
E value
                  3.0e-43
Match length
                  122
                  72
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146129
                  LIB3168-069-P1-K1-H12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  49
E value
                  4.0e-60
Match length
                  120
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146130
Seq. No.
                  LIB3168-069-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  638
                  9.0e-67
E value
                  172
Match length
                  72
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__$08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
```

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed
storage protein [Arabidopsis thaliana]

Seq. No. 146131

Seq. ID LIB3168-069-P1-K1-H3

Method BLASTX
NCBI GI g1628583
BLAST score 156
E value 2.0e-15
Match length 83
% identity 61

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146132

Seq. ID LIB3168-069-P1-K1-H4

Method BLASTX
NCBI GI g1628583
BLAST score 561
E value 1.0e-57
Match length 157
% identity 73

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146133

Seq. ID LIB3168-069-P1-K1-H6

Method BLASTX
NCBI GI g1628583
BLAST score 495
E value 4.0e-50
Match length 111
% identity 83

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146134

Seq. ID LIB3168-069-P1-K1-H8

Method BLASTX
NCBI GI g4115943
BLAST score 770
E value 3.0e-82
Match length 148
% identity 98

NCBI Description (AF118223) contains similarity to eukaryotic protein kinase

domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4)

[Arabidopsis thaliana]

Seq. No. 146135

Seq. ID LIB3168-069-P1-K1-H9

Method BLASTX NCBI GI g112741

```
748
BLAST score
E value
                  1.0e-79
Match length
                  142
                  99
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201 emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146136
Seq. ID
                  LIB3168-070-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g3281847
BLAST score
                  246
E value
                  1.0e-136
Match length
                  378
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20
                  (ESSAII project)
Seq. No.
                  146137
Seq. ID
                  LIB3168-070-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  q2058295
BLAST score
                  57
E value
                  3.0e-23
Match length
                  253
% identity
                  93
NCBI Description A.thaliana chloroplast ndhG gene
                  146138
Seq. No.
Seq. ID
                  LIB3168-070-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q2961377
BLAST score
                  573
E value
                  3.0e-59
Match length
                  110
% identity
NCBI Description
                  (AL022141) putative receptor protein kinase [Arabidopsis
                  thaliana]
Seq. No.
                  146139
Seq. ID
                  LIB3168-070-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  67
E value
                  3.0e-50
Match length
                  140
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
```

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

Seq. No.

Seq. ID

Method

NCBI GI BLAST score

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

BLAST score

Match length

% identity

BLAST score

Match length

% identity

Match length % identity

```
>gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  146140
                  LIB3168-070-P1-K1-A5
                  BLASTN
                  q2264307
                  98
                  7.0e-48
                  198
                  87
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MED24, complete sequence [Arabidopsis thaliana]
                  146141
                  LIB3168-070-P1-K1-B2
                  BLASTX
                  g1628583
                  102
                  1.0e-37
                  86
                  96
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146142
                  LIB3168-070-P1-K1-B3
                  BLASTX
                  q1628583
                  178
                  1.0e-13
                  57
                  68
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146143
                  LIB3168-070-P1-K1-B4
                  BLASTN
                  q4512656
                  75
                  6.0e - 34
                  349
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
                  146144
```

Seq. ID Method NCBI GI BLAST score

E value Match length % identity

NCBI Description

Seq. No.

LIB3168-070-P1-K1-B5 Seq. ID

Method BLASTX NCBI GI a3831459 BLAST score 314 7.0e-29 E value Match length 64 98 % identity

Seq. ID Method

```
NCBI Description (AC005700) putative homeobox protein [Arabidopsis thaliana]
                  146145
Seq. No.
                  LIB3168-070-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3776578
BLAST score
                  507
E value
                  2.0e-51
Match length
                  139
                  78
% identity
NCBI Description
                  (AC005388) ESTs gb F13915 and gb F13916 come from this
                  gene. [Arabidopsis thaliana]
                  146146
Seq. No.
Seq. ID
                  LIB3168-070-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  93
                  3.0e-14
E value
Match length
                  52
                  87
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146147
Seq. No.
                  LIB3168-070-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3608126
BLAST score
                  256
E value
                  1.0e-142
Match length
                  290
                  97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146148
                  LIB3168-070-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  92
                  5.0e-56
E value
Match length
                  141
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146149
```

18279

LIB3168-070-P1-K1-C12

BLASTX

```
NCBI GI
                   q112741
BLAST score
                   561
E value
                   7.0e-58
Match length
                   103
% identity
                   100
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
                   146150
Seq. No.
Seq. ID
                   LIB3168-070-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   q2618602
BLAST score
                   382
                   0.0e + 00
E value
Match length
                   436
                   96
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146151
Seq. ID
                   LIB3168-070-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   a1628583
                   494
BLAST score
E value
                   6.0e-50
Match length
                   129
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146152
                   LIB3168-070-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129657
                   427
BLAST score
E value
                   4.0e-42
                   115
Match length
% identity
NCBI Description
                   oleosin isoform - Arabidopsis thaliana
                   >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                   [Arabidopsis thaliana]
Seq. No.
                   146153
                   LIB3168-070-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112681
                   77
BLAST score
                   4.0e-35
E value
                   89
Match length
                   98
% identity
```

Seq. No.

146158

```
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146154
Seq. No.
Seq. ID
                  LIB3168-070-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  632
                  4.0e-66
E value
Match length
                  142
                  87
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146155
Seq. ID
                  LIB3168-070-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  a1628583
BLAST score
                  43
                  3.0e-22
E value
Match length
                  92
                  75
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146156
Seq. ID
                  LIB3168-070-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  394
                  3.0e-38
E value
Match length
                  97
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146157
Seq. ID
                  LIB3168-070-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q1072480
BLAST score
                  71
                  3.0e-58
E value
Match length
                  143
% identity
NCBI Description
                  cruciferin 1 precursor - rape
```

```
LIB3168-070-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  186
                  4.0e-14
E value
Match length
                  97
                  73
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 (Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146159
Seq. No.
Seq. ID
                  LIB3168-070-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  105
E value
                  2.0e-49
Match length
                  139
% identity
                  76
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  146160
Seq. No.
Seq. ID
                  LIB3168-070-P1-K1-D9
Method
                  BLASTN
                  g3510340
NCBI GI
BLAST score
                  82
E value
                  9.0e-39
Match length
                  113
% identity
                  94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDN11, complete sequence [Arabidopsis thaliana]
                  146161
Seq. No.
Seq. ID
                  LIB3168-070-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  56
E value
                  7.0e-39
Match length
                  122
% identity
                  73
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146162
Seq. No.
                  LIB3168-070-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  251
```

Method

BLASTX

```
4.0e-22
E value
Match length
                  55
% identity
                  89
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146163
                  LIB3168-070-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3152940
BLAST score
                  201
E value
                  1.0e-15
Match length
                  88
                  49
% identity
NCBI Description
                  (AF065483) sorting nexin 1 [Homo sapiens]
                  146164
Seq. No.
Seq. ID
                  LIB3168-070-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q2564114
BLAST score
                  246
E value
                  5.0e-21
Match length
                  79
% identity
                  63
                  (AF000372) UDP glucose:flavonoid 3-o-glucosyltransferase
NCBI Description
                  [Vitis vinifera]
Seq. No.
                  146165
Seq. ID
                  LIB3168-070-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                  655
E value
                  7.0e-69
Match length
                  148
% identity
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  146166
Seq. ID
                  LIB3168-070-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  283
E value
                  2.0e-25
Match length
                  117
% identity
                  52
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  146167
                  LIB3168-070-P1-K1-E5
Seq. ID
```

```
q1628583
NCBI GI
                   651
BLAST score
                   2.0e-68
E value
Match length
                   138
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146168
                   LIB3168-070-P1-K1-E7
Seq. ID
Method
                   BLASTX
                   g3834319
NCBI GI
BLAST score
                   262
                   7.0e-23
E value
Match length
                   129
                   48
% identity
NCBI Description
                   (AC005679) Similar to gi 2244754 heat shock transcription
                   factor HSF30 homolog from Arabidopsis thaliana chromosome 4
                   contig gb Z97335. [Arabidopsis thaliana]
                   146169
Seq. No.
                   LIB3168-070-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204299
BLAST score
                   442
E value
                   2.0e-46
                   146
Match length
                   76
% identity
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                   146170
Seq. No.
                   LIB3168-070-P1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112682
BLAST score
                   82
E value
                   2.0e-63
                   145
Match length
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
                   146171
Seq. No.
Seq. ID
                   LIB3168-070-P1-K1-F10
                   BLASTN
Method
NCBI GI
                   q3766106
                   282
BLAST score
                   1.0e-157
E value
                   442
Match length
```

18284

```
Seq. No.
                   146172
                   LIB3168-070-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   83
E value
                   2.0e-58
Match length
                   146
% identity
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146173
                   LIB3168-070-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g119350
BLAST score
                   56
E value
                   1.0e-28
Match length
                   76
% identity
NCBI Description
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                   thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                   [Arabidopsis thaliana]
                   >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
                   (2-phospho-D-glycerate hydroylase); identical to P25696
                   [Arabidopsis thaliana]
                   146174
Seq. No.
Seq. ID
                   LIB3168-070-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   q1490554
BLAST score
                   231
E value
                   1.0e-19
Match length
                   71
% identity
NCBI Description
                   (U63633) S-adenosylmethionine decarboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   146175
Seq. ID
                   LIB3168-070-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   q4262250
BLAST score
                   460
E value
                   5.0e-46
Match length
                   96
% identity
NCBI Description
                   (AC006200) putative aldolase [Arabidopsis thaliana]
Seq. No.
                   146176
                   LIB3168-070-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204299
BLAST score
                   95
```

```
2.0e-27
E value
Match length
                  74
% identity
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  146177
Seq. ID
                  LIB3168-070-P1-K1-G10
Method
                  BLASTX
NCBI GÍ
                  g112739
BLAST score
                  227
E value
                  2.0e-21
Match length
                  95
% identity
                  63
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146178
Seq. ID
                  LIB3168-070-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  a112681
BLAST score
                  504
E value
                  4.0e-51
Match length
                  149
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146179
Seq. ID
                  LIB3168-070-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  102
E value
                  6.0e-38
Match length
                  89
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146180
Seq. ID
                  LIB3168-070-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  q2842474
BLAST score
                  35
E value
                  1.0e-10
Match length
                  106
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
```

```
(ESSAII project)
Seq. No.
                  146181
                  LIB3168-070-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  92
E value
                  1.0e-64
Match length
                  144
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  146182
Seq. No.
Seq. ID
                  LIB3168-070-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  49
                  3.0e-59
E value
                  121
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146183
                  LIB3168-070-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1531762
BLAST score
                  189
E value
                  3.0e-14
Match length
                  51
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thalianal
Seq. No.
                  146184
Seq. ID
                  LIB3168-070-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  113
E value
                  8.0e-60
Match length
                  119
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

146185

Seq. ID LIB3168-071-P1-K1-A1

Method BLASTX NCBI GI q461838

Seq. No.

```
BLAST score
                    1.0e-01
E value
Match length
                    69
% identity
                    84
                   CRUCIFERIN PGCRURSE5 PRECURSOR (11S GLOBULIN) (12S STORAGE
NCBI Description
                    PROTEIN) >gi 282895 pir_S26223 cruciferin - radish
                    >gi 21118 emb CAA42478 (X59808) cruciferin [Raphanus
                    sativus]
                    146186
Seq. No.
                    LIB3168-071-P1-K1-A10
Seq. ID
Method
                    BLASTX
NCBI GI
                    q1628583
BLAST score
                    151
E value
                    2.0e-10
Match length
                    59
% identity
                    (U66916) 12S cruciferin seed storage protein (Arabidopsis
NCBI Description
                    thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                    cruciferin seed storage protein [Arabidopsis thaliana]
                    146187
Seq. No.
Seq. ID
                    LIB3168-071-P1-K1-A11
Method
                    BLASTN
NCBI GI
                    q4589440
BLAST score
                    189
                    1.0e-102
E value
Match length
                    351
                    96
% identity
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                    MSD21, complete sequence
                    146188
Seq. No.
Seq. ID
                    LIB3168-071-P1-K1-A12
Method
                    BLASTX
NCBI GI
                    q114654
BLAST score
                    145
                    8.0e-13
E value
Match length
                    81
% identity
NCBI Description
                    ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
                    >gi_67898_pir__LWNTA H+-transporting ATP synthase (EC
3.6.1.34) lipid-binding protein - common tobacco
                    chloroplast >gi 11812 emb CAA77343 (Z00044) ATPase III
                    subunit [Nicotiana tabacum] >gi_343484 (M10124) ATPase
subunit III [Nicotiana tabacum] >gi_224347_prf__1102209A
                    ATPase III, H translocating [Nicotiana sp.]
                    >gi 225272 prf 1211235G ATPase III [Nicotiana tabacum]
Seq. No.
                    146189
Seq. ID
                    LIB3168-071-P1-K1-A3
Method
                    BLASTN
NCBI GI
                    q2191157
BLAST score
                    325
                    0.0e + 00
E value
Match length
                    426
                    94
% identity
```

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score

% identity

Seq. No. Seq. ID

Method

NCBI GI

E value

BLAST score

% identity

Seq. No.

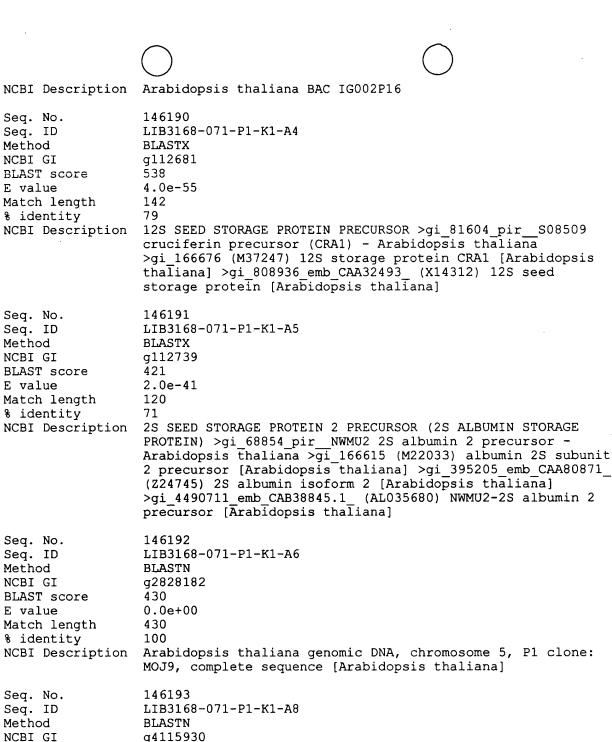
Seq. ID

Method

NCBI GI

E value

% identity



Seq. No.

Seq. ID

Method NCBI GI g4115930 BLAST score 226 E value 1.0e-124 Match length 302 93 % identity

NCBI Description Arabidopsis thaliana BAC T4B21

146194 Seq. No.

Seq. ID LIB3168-071-P1-K1-A9

BLASTN Method NCBI GI g2842474

BLAST score

```
BLAST score
                  102
                  2.0e-50
E value
Match length
                  214
                  87
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                   (ESSAII project)
Seq. No.
                  146195
Seq. ID
                  LIB3168-071-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  432
E value
                  6.0e-43
Match length
                  92
% identity
                  91
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146196
Seq. ID
                  LIB3168-071-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q4678291
BLAST score
                  142
E value
                  5.0e-74
Match length
                  182
% identity
                  95
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10
                   (ESSA project)
Seq. No.
                  146197
Seq. ID
                  LIB3168-071-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  q4519183
BLAST score
                  67
E value
                  1.0e-29
Match length
                  175
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15C23, complete sequence
Seq. No.
                  146198
Seq. ID
                  LIB3168-071-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  q4589969
BLAST score
                  286
E value
                  1.0e-160
Match length
                  347
% identity
                  95
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F1P15 genomic
                  sequence, complete sequence
Seq. No.
                  146199
                  LIB3168-071-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
```



E value 2.0e-59 Match length 134 % identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146200

Seq. ID LIB3168-071-P1-K1-B6

Method BLASTX
NCBI GI g1628583
BLAST score 421
E value 2.0e-41
Match length 103
% identity 82

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146201

Seq. ID LIB3168-071-P1-K1-B7

Method BLASTX
NCBI GI g4263825
BLAST score 347
E value 5.0e-33
Match length 96
% identity 67

NCBI Description (AC006067) hypothetical protein [Arabidopsis thaliana]

Seq. No. 146202

Seq. ID LIB3168-071-P1-K1-B8

Method BLASTX
NCBI GI g1628583
BLAST score 210
E value 6.0e-17
Match length 96
% identity 53

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146203

Seq. ID LIB3168-071-P1-K1-C1

Method BLASTX
NCBI GI g4204299
BLAST score 277
E value 4.0e-25
Match length 57
% identity 95

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 146204

Seq. ID LIB3168-071-P1-K1-C10

Method BLASTX

```
NCBI GI
                  g112682
BLAST score
                  553
                   6.0e-57
E value
                  138
Match length
                  78
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146205
Seq. No.
Seq. ID
                  LIB3168-071-P1-K1-C11
                  BLASTN
Method
NCBI GI
                  g2465922
BLAST score
                  345
                  0.0e+00
E value
                  420
Match length
                  95
% identity
                  Arabidopsis thaliana receptor-like serine/threonine kinase
NCBI Description
                   (RKF1) mRNA, complete cds
                  146206
Seq. No.
Seq. ID
                  LIB3168-071-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  386
                  2.0e-37
E value
                  78
Match length
% identity
                  100
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146207
Seq. ID
                  LIB3168-071-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  q3449334
                  390
BLAST score
                  0.0e+00
E value
Match length
                  424
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146208
                  LIB3168-071-P1-K1-C3
Seq. ID
                  BLASTX
Method
NCBI GI
                  q119143
BLAST score
                  605
E value
                  5.0e-63
Match length
                  120
```

ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

97

% identity

NCBI Description

>gi\_81606\_pir\_\_S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi\_295788\_emb\_CAA34453\_
(X16430) elongation factor 1-alpha [Arabidopsis thaliana]

Seq. No.

Seq. ID

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value Match length

Seq. No.

Seq. ID

Method

NCBI GI

E value Match length

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

529

111

4.0e-54

BLAST score

% identity

BLAST score

% identity

BLAST score

Match length

% identity

Method NCBI GI

```
>gi_1369927_emb_CAA34454_ (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                  >qi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
                  146209
                  LIB3168-071-P1-K1-C4
                  BLASTX
                  g119143
                  276
                  4.0e-29
                  82
                  83
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_81606_pir__S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453
                  (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1369927 emb CAA34454 (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                  >qi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
                  146210
                  LIB3168-071-P1-K1-C5
                  BLASTX
                  g267073
                  656
                  5.0e-69
                  122
                  99
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
                  146211
                  LIB3168-071-P1-K1-C6
                  BLASTX
                  g3482929
                  245
                  8.0e-21
                  66
NCBI Description
                  (AC003970) Putative transcription factor [Arabidopsis
                  thaliana]
                  146212
                  LIB3168-071-P1-K1-C7
                  BLASTX
                  g4033349
```

```
% identity
NCBI Description
                   (AJ223496) phosphoenolpyrovate carboxylase [Brassica
                   juncea]
                   146213
 Seq. No.
                   LIB3168-071-P1-K1-C8
 Seq. ID
                   BLASTX
Method
NCBI GI
                   g112682
BLAST score
                   563
 E value
                   4.0e-58
                   128
Match length
                   84
 % identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir__S08510
NCBI Description
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
 Seq. No.
                   146214
                   LIB3168-071-P1-K1-D1
 Seq. ID
Method
                   BLASTN
 NCBI GI
                   g4079614
 BLAST score
                   138
                   1.0e-71
 E value
Match length
                   194
                   93
 % identity
                   Arabidopsis thaliana chromosome I BAC F21M11 genomic
 NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
 Seq. No.
                   146215
                   LIB3168-071-P1-K1-D10
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g1246823
 BLAST score
                   412
 E value
                   1.0e-40
Match length
                   89
 % identity
                    (X89865) unknown [Phoenix dactylifera]
. NCBI Description
                   146216
 Seq. No.
                   LIB3168-071-P1-K1-D11
 Seq. ID
 Method -
                   BLASTX
 NCBI GI
                   g1076401
 BLAST score
                   314
                   7.0e-29
 E value
 Match length
                   121
 % identity
                   57
                   DNA-directed RNA polymerase (EC 2.7.7.6) beta chain -
 NCBI Description
                   Arabidopsis thaliana chloroplast (fragment)
                   >gi 664896 emb_CAA58965_ (X84159) RNA polymerase subunit
                   beta [Arabidopsis thaliana]
 Seq. No.
                   146217
                   LIB3168-071-P1-K1-D12
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g112682
 BLAST score
                   556
```

.18294

E value 3.0e-57

Match length 131
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510
cruciferin precursor (CRB) - Arabidopsis thaliana
>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis

Seq. No. 146218

Seq. ID LIB3168-071-P1-K1-D2

Method BLASTX
NCBI GI g1628583
BLAST score 681
E value 6.0e-72
Match length 142
% identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

storage protein [Arabidopsis thaliana]

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

Seq. No. 146219

Seq. ID LIB3168-071-P1-K1-D3

Method BLASTN
NCBI GI g4582411
BLAST score 341
E value 0.0e+00
Match length 428
% identity 99

NCBI Description Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,

complete sequence

Seq. No. 146220

Seq. ID LIB3168-071-P1-K1-D4

Method BLASTX
NCBI GI g112681
BLAST score 590
E value 3.0e-61
Match length 138
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146221

Seq. ID LIB3168-071-P1-K1-D5

Method BLASTX
NCBI GI g1628583
BLAST score 617
E value 2.0e-64
Match length 119
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                  146222
Seq. ID
                  LIB3168-071-P1-K1-D6
                  BLASTX
Method
                  g1628583
NCBI GI
                  658
BLAST score
E value
                  3.0e-69
Match length
                  128
                  98
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146223
                  LIB3168-071-P1-K1-D7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4586241
BLAST score
                  215
E value
                  1.0e-117
                  368
Match length
                  52
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
NCBI Description
                  (ESSA project)
Seq. No.
                  146224
                  LIB3168-071-P1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g119150
BLAST score
                  719
E value
                  2.0e-76
                  137
Match length
                  100
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_82081_pir__S10507 translation elongation factor eEF-1
                  alpha chain - tomato >gi_19273_emb_CAA32618_ (X14449) EF
                  1-alpha (AA 1-448) [Lycopersicon esculentum]
                  >gi 295810 emb CAA37212 (X53043) elongation factor 1-alpha
                  [Lycopersicon esculentum]
                  146225
Seq. No.
                  LIB3168-071-P1-K1-D9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3600062
BLAST score
                  318
E value
                  1.0e-179
Match length
                  408
% identity
                  100
NCBI Description Arabidopsis thaliana BAC T25C13
                  146226
Seq. No.
Seq. ID
                  LIB3168-071-P1-K1-E1
Method
                  BLASTN
NCBI GI
                  g2244870
BLAST score
                  116
                  9.0e-59
E value
                  214
Match length
                  87
% identity
```

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   146227
Seq. No.
Seq. ID
                   LIB3168-071-P1-K1-E10
Method
                   BLASTN
NCBI GI
                   g4585952
BLAST score
                   368
                   0.0e+00
E value
                   400
Match length
                  98
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F26F24,
NCBI Description
                   complete sequence
                   146228
Seq. No.
Seq. ID
                   LIB3168-071-P1-K1-E12
Method
                   BLASTN
NCBI GI
                   g441490
                   100
BLAST score
E value
                   4.0e-49
Match length
                  141
% identity
                   93
NCBI Description S.alba chloroplast trnR gene
Seq. No.
                   146229
Seq. ID
                   LIB3168-071-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   g2880057
BLAST score
                   657
E value
                   4.0e-69
                   140
Match length
                   89
% identity
                   (AC002340) putative RNA helicase A, 5' partial [Arabidopsis
NCBI Description
                   thaliana]
                   146230
Seq. No.
                   LIB3168-071-P1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                   q3184281
BLAST score
                   493
E value
                   6.0e-50
                   122
Match length
% identity
                   80
                   (AC004136) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   146231
                  LIB3168-071-P1-K1-E4
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1346754
BLAST score
                   473
```

E value 1.0e-47 Match length 100 90 % identity

NCBI Description

SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 2 >gi\_421851\_pir\_\_S31086 phosphoprotein phosphatase (EC 3.1.3.16) 1 catalytic chain (clone TOPP2) - Arabidopsis thaliana >gi 166797 (M93409) catalytic subunit [Arabidopsis

```
thaliana]
```

```
Seq. No.
Seq. ID
                  LIB3168-071-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  69
                  3.0e-40
E value
                  89
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146233
                  LIB3168-071-P1-K1-E8
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2618603
BLAST score
                  122
E value
                  5.0e-62
Match length
                  278
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSL3, complete sequence [Arabidopsis thaliana]
                  146234
Seq. No.
                  LIB3168-071-P1-K1-E9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3150036
BLAST score
                  89
E value
                  2.0e-42
Match length
                  130
                  93
% identity
NCBI Description
                  Arabidopsis thaliana Myb transcription factor homolog
                   (ATR1) gene, complete cds, receptor-like protein kinase
                  (RLK1) gene, partial cds
                  146235
Seq. No.
                  LIB3168-071-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  618
E value
                  1.0e-64
Match length
                  120
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146236
Seq. ID
                  LIB3168-071-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g112743
```

Method BLASTX
NCBI GI g112743
BLAST score 681
E value 6.0e-72
Match length 137
% identity 93

```
2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >qi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146237
                  LIB3168-071-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1592677
BLAST score
                  249
E value
                  3.0e-21
                  121
Match length
```

% identity 46
NCBI Description (X91912) LEA76 homologue type2 [Arabidopsis thaliana]

 Seq. No.
 146238

 Seq. ID
 LIB3168-071-P1-K1-F2

 Method
 BLASTX

 NCBI GI
 q4204298

NCBI GI g420429
BLAST score 642
E value 2.0e-67
Match length 139
% identity 89

NCBI Description (AC003027) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

Seq. No. 146239

Seq. ID LIB3168-071-P1-K1-F3

Method BLASTN
NCBI GI g4199934
BLAST score 290
E value 1.0e-162
Match length 294
% identity 100

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18,

complete sequence [Arabidopsis thaliana]

Seq. No. 146240

Seq. ID LIB3168-071-P1-K1-F4

Method BLASTN
NCBI GI g4371278
BLAST score 81
E value 1.0e-37
Match length 193
% identity 85

NCBI Description Arabidopsis thaliana chromosome II BAC T2N18 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 146241

Seq. ID LIB3168-071-P1-K1-F5

Method BLASTX
NCBI GI g1628583
BLAST score 564
E value 3.0e-58

Seq. ID

```
140
Match length
                  79
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146242
Seq. No.
                  LIB3168-071-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129653
BLAST score
                  721
                  1.0e-76
E value
Match length
                  138
% identity
                  100
                  myosin heavy chain MYA2 - Arabidopsis thaliana
NCBI Description
                  >gi_499047_emb_CAA84066_ (Z34293) myosin [Arabidopsis
                  thaliana]
Seq. No.
                  146243
                  LIB3168-071-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129642
                  682
BLAST score
                  5.0e-72
E value
Match length
                  130
% identity
                  96
                  major latex protein type 3 - Arabidopsis thaliana
NCBI Description
                  >qi 1107495 emb CAA63027 (X91961) major latex protein
                  type3 [Arabidopsis thaliana]
Seq. No.
                  146244
                  LIB3168-071-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  563
E value
                  4.0e-58
Match length
                  133
% identity
                  83
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146245
Seq. ID
                  LIB3168-071-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3894171
BLAST score
                  520
E value
                  1.0e-56
Match length
                  126
% identity
                   (AC005312) putative glutathione s-transferase [Arabidopsis
NCBI Description
                  thaliana]
                  146246
Seq. No.
```

18300

LIB3168-071-P1-K1-G4

```
Method
                  BLASTN
NCBI GI
                  q4691223
BLAST score
                  234
E value
                  1.0e-129
Match length
                  426
% identity
                  97
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                  (ESSA project)
                  146247
Seq. No.
Seq. ID
                  LIB3168-071-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  565
E value
                  3.0e-58
                  142
Match length
                  80
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146248
Seq. No.
Seq. ID
                  LIB3168-071-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g2501064
BLAST score
                  644
E value
                  1.0e-67
Match length
                  122
% identity
                  96
                  PROBABLE THREONYL-TRNA SYNTHETASE, CYTOPLASMIC
NCBI Description
                  (THREONINE--TRNA LIGASE) (THRRS) >gi 2191162 (AF007270)
                  Similar to threonyl-tRNA synthetase; coded for by A.
                  thaliana cDNA R65376 [Arabidopsis thaliana]
Seq. No.
                  146249
Seq. ID
                  LIB3168-071-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  q4455095
BLAST score
                  106
                  2.0e-52
E value
Match length
                  268
                  91
% identity
                  Draba stylaris tRNA-Leu (trnL) and tRNA-Phe (trnF) genes,
NCBI Description
                  chloroplast genes for chloroplast RNAs, partial sequence
Seq. No.
                  146250
Seq. ID
                  LIB3168-071-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  344
E value
                  2.0e-32
Match length
                  105
% identity
                  67
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
```

Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

\*

146251 Seq. No.

Seq. ID LIB3168-071-P1-K1-G9

Method BLASTN NCBI GI q2264316 BLAST score 67 3.0e-29 E value 423 Match length 45 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MRO11, complete sequence [Arabidopsis thaliana]

Seq. No. 146252

Seq. ID LIB3168-071-P1-K1-H1

Method BLASTN NCBI GI g3449331 35 BLAST score E value 4.0e-10 422 Match length 32 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MNC17, complete sequence [Arabidopsis thaliana]

146253 Seq. No.

Seq. ID LIB3168-071-P1-K1-H10

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 2.0e-65 120 Match length 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

146254 Seq. No.

Seq. ID LIB3168-071-P1-K1-H12

Method BLASTX NCBI GI g112737 BLAST score 539 E value 3.0e-55 Match length 135 77 % identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 146255

Seq. ID LIB3168-071-P1-K1-H2

Method BLASTX

% identity

64

```
NCBI GI
                  g1628583
BLAST score
                  653
E value
                  1.0e-68
Match length
                  138
                  92
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146256
Seq. ID
                  LIB3168-071-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  641
E value
                  3.0e-67
                  135
Match length
                  90
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  146257
Seq. No.
Seq. ID
                  LIB3168-071-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  524
E value
                  1.0e-53
Match length
                  134
% identity
                  78
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495 emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146258
Seq. ID
                  LIB3168-071-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g4406776
BLAST score
                  394
E value
                  0.0e + 00
Match length
                  413
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14H2O genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146259
Seq. ID
                  LIB3168-071-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  347
                  7.0e-33
E value
Match length
                  116
```

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 146260

Seq. ID LIB3168-071-P1-K1-H8

Method BLASTX
NCBI GI g3608135
BLAST score 290
E value 4.0e-26
Match length 82
% identity 66

NCBI Description (AC005314) putative DNA binding factor [Arabidopsis

thaliana]

146261

Seq. No.

Seq. ID LIB3168-071-P1-K1-H9

Method BLASTN
NCBI GI g3242970
BLAST score 290
E value 1.0e-162
Match length 351
% identity 95

NCBI Description Arabidopsis thaliana BAC T419, chromosome IV, near 17 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 146262

Seq. ID LIB3168-072-P1-K1-A1

Method BLASTX
NCBI GI g112737
BLAST score 650
E value 3.0e-68
Match length 151
% identity 83

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_ NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204\_emb\_CAA80870\_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710 emb\_CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 146263

Seq. ID LIB3168-072-P1-K1-A12

Method BLASTX
NCBI GI g112681
BLAST score 664
E value 5.0e-70
Match length 125
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed



storage protein [Arabidopsis thaliana] 146264 Seq. No. LIB3168-072-P1-K1-A2 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 250 5.0e-22 E value 62 Match length % identity 84 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 146265 Seq. No. Seq. ID LIB3168-072-P1-K1-A3 Method BLASTX NCBI GI g2129538 BLAST score 241 2.0e-20 E value 50 Match length 94 % identity NCBI Description AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232) AT103 [Arabidopsis thaliana] Seq. No. 146266 Seq. ID LIB3168-072-P1-K1-A6 Method BLASTX NCBI GI g4204299 BLAST score 537 5.0e-55 E value Match length 105 % identity 100 NCBI Description (AC003027) lcl\_prt\_seq No definition line found [Arabidopsis thaliana] Seq. No. 146267 Seq. ID LIB3168-072-P1-K1-A7 Method BLASTN NCBI GI g1906825 BLAST score 143 E value 7.0e-75 175 Match length 96 % identity NCBI Description A.thaliana hsp81.2 gene Seq. No. 146268 LIB3168-072-P1-K1-A9 Seq. ID Method

Method BLASTX
NCBI GI g112743
BLAST score 481
E value 2.0e-48
Match length 148
% identity 65

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68856\_pir\_\_NWMU4 2S albumin 4 precursor -

Arabidopsis thaliana >gi\_166617 (M22033) albumin 2S subunit

4 precursor [Arabidopsis thaliana] >gi\_395202\_emb CAA80869\_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

146269 Seq. No. Seq. ID LIB3168-072-P1-K1-B1 Method BLASTN NCBI GI g3449321 BLAST score 160

E value 1.0e-84 308 Match length 99 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MTG10, complete sequence [Arabidopsis thaliana]

Seq. No. 146270

Seq. ID LIB3168-072-P1-K1-B11

Method BLASTX NCBI GI q112682 BLAST score 618 E value 2.0e-64 Match length 144 % identity 82

12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>qi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146271

Seq. ID LIB3168-072-P1-K1-B12

Method BLASTX NCBI GI q112737 BLAST score 554 E value 5.0e-57 Match length 124 % identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >qi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204 emb\_CAA80870\_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 146272

LIB3168-072-P1-K1-B3 Seq. ID

Method BLASTX NCBI GI g417383 397 BLAST score E value 6.0e-39 Match length 89 % identity

NITRILASE 2 >gi 322548 pir S31969 nitrilase (EC 3.5.5.1) -NCBI Description

Arabidopsis tha  $\overline{1}$ iana  $\overline{9}$ i  $2\overline{26}$ 56 emb CAA48377 (X68305) nitrilase II [Arabidopsis thaliana] >gi 508733 (U09958)



nitrilase [Arabidopsis thaliana] Seq. No. 146273 Seq. ID LIB3168-072-P1-K1-B4 Method BLASTX NCBI GI g119143 BLAST score 721 1.0e-76 E value Match length 138 100 % identity ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) NCBI Description >gi\_81606\_pir\_\_S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453 (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi 1369927 emb CAA34454 (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455 (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana] >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana] >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana] 146274 Seq. No. Seq. ID LIB3168-072-P1-K1-B5 BLASTX Method NCBI GI g3335171 BLAST score 595 E value 7.0e-62 125 Match length % identity 91 (AF067858) embryo-specific protein 3 [Arabidopsis thaliana] NCBI Description Seq. No. 146275 Seq. ID LIB3168-072-P1-K1-B6 Method  ${\tt BLASTX}$ NCBI GI g112743 BLAST score 667 E value 4.0e-70 166 Match length 78 % identity NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi\_68856\_pir\_\_NWMU4 2S albumin 4 precursor -Arabidopsis thaliana >gi\_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi\_395202\_emb\_CAA80869\_ (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]

>gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 146276

Seq. ID LIB3168-072-P1-K1-B7

Method BLASTX
NCBI GI g1628583
BLAST score 410
E value 2.0e-40
Match length 105
% identity 79

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S



## cruciferin seed storage protein [Arabidopsis thaliana]

146277 Seq. No. Seq. ID LIB3168-072-P1-K1-B8 Method BLASTX NCBI GI q1628583 BLAST score 302 2.0e-27 E value 91 Match length 67 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146278

Seq. ID LIB3168-072-P1-K1-B9

Method BLASTX NCBI GI g4490704 BLAST score 764 E value 2.0e-81 Match length 155 99 % identity

NCBI Description (AL035680) putative protein [Arabidopsis thaliana]

Seq. No.

LIB3168-072-P1-K1-C1 Seq. ID

146279

Method BLASTX NCBI GI g112737 BLAST score 724 E value 8.0e-77 Match length 164 84 % identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 146280

Seq. ID LIB3168-072-P1-K1-C11

Method BLASTN NCBI GI q2341023 BLAST score 56 E value 1.0e-22 Match length 228 92 % identity

Sequence of BAC F19P19 from Arabidopsis thaliana chromosome NCBI Description

1, complete sequence [Arabidopsis thaliana]

Seq. No. 146281

LIB3168-072-P1-K1-C12 Seq. ID

BLASTX Method NCBI GI q4204298 BLAST score 492 E value 9.0e-50

```
Match length
                  116
% identity
                  83
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
                  146282
Seq. No.
                  LIB3168-072-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4734009
BLAST score
                  348
E value
                  9.0e-33
                  140
Match length
                  50
% identity
                  (AC007178) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  146283
                  LIB3168-072-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432860
BLAST score
                  322
                  4.0e-34
E value
Match length
                  78
% identity
                  100
                   (AC006300) putative glucose-induced repressor protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  146284
                  LIB3168-072-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935167
BLAST score
                  544
E value
                  1.0e-55
Match length
                  123
% identity
NCBI Description
                  (AC004557) F17L21.10 [Arabidopsis thaliana]
Seq. No.
                  146285
                  LIB3168-072-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                  827
E value
                  7.0e-89
Match length
                  176
% identity
                  90
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  146286
                  LIB3168-072-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  660
E value
                  2.0e-69
Match length
                  157
% identity
                  82
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

cruciferin seed storage protein [Arabidopsis thaliana] 146287 Seq. No. Seq. ID LIB3168-072-P1-K1-C8 Method BLASTX NCBI GI q3850584 BLAST score 167 E value 6.0e-26 Match length 67 94 % identity (AC005278) ESTs gb H37641 and gb AA651422 come from this NCBI Description gene. [Arabidopsis thaliana] 146288 Seq. No. Seq. ID LIB3168-072-P1-K1-C9 Method BLASTX NCBI GI g1628583 BLAST score 467 4.0e-47 E value Match length 96 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 146289 Seq. No. Seq. ID LIB3168-072-P1-K1-D1 Method BLASTN NCBI GI g4512656 396 BLAST score 0.0e+00E value Match length 400 100 % identity Arabidopsis thaliana chromosome II BAC F7D19 genomic NCBI Description sequence, complete sequence

Seq. No. 146290

Seq. ID LIB3168-072-P1-K1-D10

Method BLASTX NCBI GI g112737 BLAST score 596 6.0e-62 E value 144 Match length 80 % identity

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 146291

Seq. ID LIB3168-072-P1-K1-D11

Method BLASTX NCBI GI g112739 BLAST score 398

E value 5.0e-49
Match length 143
% identity 70
NCBI Description 2S SEED

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi\_4490711\_emb\_CAB38845.1\_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 146292

Seq. ID LIB3168-072-P1-K1-D12

Method BLASTX
NCBI GI g3983125
BLAST score 49
E value 7.0e-40
Match length 106
% identity 78

NCBI Description (AF097648) phosphate/triose-phosphate translocator

precursor [Arabidopsis thaliana]

Seq. No. 146293

Seq. ID LIB3168-072-P1-K1-D4

Method BLASTX
NCBI GI g1628583
BLAST score 606
E value 5.0e-63
Match length 148
% identity 80

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146294

Seq. ID LIB3168-072-P1-K1-D5

Method BLASTN
NCBI GI g4585952
BLAST score 256
E value 1.0e-142
Match length 371
% identity 92

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F26F24,

complete sequence

Seq. No. 146295

Seq. ID LIB3168-072-P1-K1-D6

Method BLASTN
NCBI GI g2842474
BLAST score 71
E value 7.0e-32
Match length 175

Match length 175 8 identity 86

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No. 146296

Method

BLASTX

```
LIB3168-072-P1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  203
E value
                  8.0e-33
Match length
                  95
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146297
Seq. ID
                  LIB3168-072-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  812
E value
                  4.0e-87
Match length
                  166
                  91
% identity
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146298
Seq. ID
                  LIB3168-072-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  181
E value
                  2.0e-13
Match length
                  101
% identity
                  42
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146299
Seq. ID
                  LIB3168-072-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4204298
                  607
BLAST score
E value
                  3.0e-63
Match length
                  151
% identity
                  79
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  146300
Seq. ID
                  LIB3168-072-P1-K1-E11
```

```
NCBI GI
                  g3242706
BLAST score
                  275
E value
                  3.0e-24
Match length
                  114
                  55
% identity
NCBI Description
                  (AC003040) cyclin-dependent kinase inhibitor protein
                  [Arabidopsis thaliana] >gi 3550262 (AF079587)
                  cyclin-dependent kinase inhibitor; ICK1 [Arabidopsis
                  thaliana]
                  146301
Seq. No.
Seq. ID
                  LIB3168-072-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  541
E value
                  1.0e-55
Match length
                  115
% identity
                  88
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937 emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146302
Seq. No.
Seq. ID
                  LIB3168-072-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g3695386
BLAST score
                  198
E value
                  1.0e-107
Match length
                  251
                  94
% identity
NCBI Description Arabidopsis thaliana BAC T2L5
Seq. No.
                  146303
                  LIB3168-072-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  810
E value
                  6.0e-87
                  173
Match length
                  89
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB (Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146304
Seq. No.
Seq. ID
                  LIB3168-072-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  515
E value
                  2.0e-52
Match length
                  117
% identity
                  84
NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
```

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

 Seq. No.
 146305

 Seq. ID
 LIB3168-072-P1-K1-E6

 Method
 BLASTX

 NCBI GI
 g112681

NCBI GI g112681
BLAST score 199
E value 5.0e-16
Match length 45
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146306

Seq. ID LIB3168-072-P1-K1-E7

Method BLASTX
NCBI GI g82051
BLAST score 290
E value 3.0e-26
Match length 113
% identity 53

NCBI Description lipid body-associated membrane protein - carrot

>gi 259453 bbs 117620 (S47635) lipid body membrane

protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,

180 aa] [Daucus carota]

Seq. No. 146307

Seq. ID LIB3168-072-P1-K1-E8

Method BLASTX
NCBI GI g1628583
BLAST score 424
E value 5.0e-42
Match length 103
% identity 82

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146308

Seq. ID LIB3168-072-P1-K1-E9

Method BLASTX
NCBI GI g1899188
BLAST score 494
E value 7.0e-50
Match length 171
% identity 28

NCBI Description (U90212) DNA binding protein ACBF [Nicotiana tabacum]

Seq. No. 146309

```
Seq. ID
                   LIB3168-072-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   g4581084
BLAST score
                   338
E value
                   0.0e + 00
Match length
                   394
                   97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
                   sequence, complete sequence
Seq. No.
                   146310
                   LIB3168-072-P1-K1-F10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2182287
BLAST score
                   403
E value
                   0.0e + 00
Match length
                   462
% identity
                   97
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T7N9,
                   complete sequence [Arabidopsis thaliana]
                   146311
Seq. No.
Seq. ID
                  LIB3168-072-P1-K1-F11
Method
                  BLASTN
NCBI GI
                   q3236234
BLAST score
                   164
E value
                   2.0e-87
Match length
                   176
                   98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146312
Seq. ID
                  LIB3168-072-P1-K1-F12
Method
                  BLASTX
NCBI GI
                   q1628583
BLAST score
                   646
E value
                   9.0e-68
Match length
                  152
                   84
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146313
Seq. ID
                  LIB3168-072-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  638
E value
                  7.0e-67
Match length
                  145
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
```

Seq. No. 146314

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

```
LIB3168-072-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  594
E value
                  1.0e-61
Match length
                  146
% identity
                  79
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146315
Seq. ID
                  LIB3168-072-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  55
E value
                  2.0e-38
                  86
Match length
                  98
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146316
Seq. ID
                  LIB3168-072-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  545
E value
                  5.0e-56
Match length
                  113
                  90
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146317
Seq. No.
Seq. ID
                  LIB3168-072-P1-K1-F7
                  BLASTX
Method
NCBI GI
                  g3193331
BLAST score
                  298
E value
                  6.0e-27
Match length
                  55
% identity
NCBI Description (AF069299) No definition line found [Arabidopsis thaliana]
                  146318
Seq. No.
Seq. ID
                  LIB3168-072-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  253
E value
                  2.0e-22
                  65
Match length
% identity
NCBI Description
                 (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
```



## cruciferin seed storage protein [Arabidopsis thaliana]

 Seq. No.
 146319

 Seq. ID
 LIB3168-072-P1-K1-F9

 Method
 BLASTX

 NCBI GI
 g1628583

BLAST score 117 E value 2.0e-65 Match length 167 % identity 80

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146320

Seq. ID LIB3168-072-P1-K1-G10

Method BLASTX
NCBI GI g1628583
BLAST score 168
E value 2.0e-12
Match length 36
% identity 83

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3168-072-P1-K1-G11

146321

Method BLASTX
NCBI GI g112681
BLAST score 428
E value 2.0e-42
Match length 124
% identity 74

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146322

Seq. ID LIB3168-072-P1-K1-G12

Method BLASTX
NCBI GI g112681
BLAST score 644
E value 2.0e-67
Match length 128
% identity 98

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146323

Seq. ID LIB3168-072-P1-K1-G2

Method BLASTX

```
NCBI GI
                  g3426041
BLAST score
                  271
                  9.0e-24
E value
                  70
Match length
% identity
NCBI Description
                  (AC005168) unknown protein [Arabidopsis thaliana]
Seq. No.
                  146324
Seq. ID
                  LIB3168-072-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  760
E value
                  1.0e-81
                  155
Match length
                  94
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146325
Seq. ID
                  LIB3168-072-P1-K1-G5
                  BLASTN
Method
NCBI GI
                  q1628582
BLAST score
                  64
                  2.0e-27
E value
Match length
                  183
                  85
% identity
                  Arabidopsis thaliana 12S cruciferin seed storage protein
NCBI Description
                  (ATCRU3) gene, complete cds
                  146326
Seq. No.
                  LIB3168-072-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  606
E value
                  4.0e-63
Match length
                  145
                  81
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  146327
Seq. No.
Seq. ID
                  LIB3168-072-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g82232
                  399
BLAST score
                  6.0e-39
E value
Match length
                  121
                  65
% identity
NCBI Description rpoC protein homolog - common tobacco chloroplast
```

```
Seq. No.
                  146328
Seq. ID
                  LIB3168-072-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  q1877523
BLAST score
                  207
E value
                   1.0e-112
Match length
                   423
                   99
% identity
NCBI Description
                  Arabidopsis thaliana BAC T7I23, complete sequence
                   [Arabidopsis thaliana]
                  146329
Seq. No.
Seq. ID
                  LIB3168-072-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                   571
E value
                   5.0e-59
                  137
Match length
% identity
                   81
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                   (224745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146330
Seq. ID
                  LIB3168-072-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q2246456
BLAST score
                   753
E value
                   3.0e-80
                  149
Match length
% identity
                   95
NCBI Description
                   (U71400) S-adenosyl-methionine-sterol-C-methyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                  146331
                  LIB3168-072-P1-K1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3659491
BLAST score
                  322
E value
                   0.0e + 00
Match length
                   400
                   94
% identity
NCBI Description
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146332
                  LIB3168-072-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  696
E value
                  1.0e-73
Match length
                  154
```

```
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__ $08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146333
                  LIB3168-072-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  49
E value
                  5.0e-21
Match length
                  59
                  93
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146334
Seq. ID
                  LIB3168-073-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  q4115370
BLAST score
                  365
E value
                  0.0e + 00
Match length
                  368
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F27D4 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146335
Seq. ID
                  LIB3168-073-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q3618320
BLAST score
                  345
E value
                  2.0e-32
Match length
                  93
% identity
NCBI Description (AB001888) zinc finger protein [Oryza sativa]
Seq. No.
                  146336
Seq. ID
                  LIB3168-073-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q267069
BLAST score
                  441
                  6.0e-44
E value
Match length
                  81
                  100
% identity
NCBI Description TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >qi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
```

146337 Seq. No.

Seq. ID LIB3168-073-P1-K1-A3

Method BLASTX NCBI GI g1628583

```
BLAST score
E value
                   1.0e-69
Match length
                   126
% identity
                   99
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146338
Seq. No.
Seq. ID
                   LIB3168-073-P1-K1-A4
Method
                   BLASTN
NCBI GI
                   q4678340
BLAST score
                   433
                   0.0e+00
E value
Match length
                   437
% identity
                   100
NCBI Description
                   Arabidopsis thaliana DNA chromosome 3, BAC clone
                   (ESSA project)
                   146339
Seq. No.
                   LIB3168-073-P1-K1-A5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2351066
BLAST score
                   339
E value
                   0.0e + 00
Match length
                   428
                   95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOP9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146340
                   LIB3168-073-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2388582
BLAST score
                   361
E value
                   2.0e-34
Match length
                   71
                   100
% identity
NCBI Description
                   (AC000098) Contains similarity to Rattus O-GlcNAc
                   transferase (gb_U76557). [Arabidopsis thaliana]
                   146341
Seq. No.
Seq. ID
                   LIB3168-073-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g398963
                   172
BLAST score
E value
                   3.0e-12
Match length
                   82
                   48
% identity
NCBI Description
                   4-COUMARATE--COA LIGASE 1 (4CL) >gi 100413 pir A39827
                   4-coumarate--CoA ligase (EC 6.2.1.1\overline{2}) 1 - potato >gi 169574
                   (M62755) 4-coumarate--CoA ligase [Solanum tuberosum]
                   146342
Seq. No.
Seq. ID
                   LIB3168-073-P1-K1-A8
Method
                   BLASTX
NCBI GI
                  g112681
```

```
BLAST score
E value
                  3.0e-66
                  120
Match length
                  98
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  tha\overline{l}iana] >gi_808936_emb_CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146343
Seq. No.
Seq. ID
                  LIB3168-073-P1-K1-A9
Method
                  BLASTX
                  g112682
NCBI GI
                  555
BLAST score
                  9.0e-58
E value
                  127
Match length
                  89
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146344
                  LIB3168-073-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  117
E value
                  4.0e-59
                  303
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  146345
                  LIB3168-073-P1-K1-B11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4193388
BLAST score
                  437
E value
                  3.0e-43
Match length
                  116
% identity
                  (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                  brasiliensis]
Seq. No.
                  146346
                  LIB3168-073-P1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q112682
BLAST score
                  550
E value
                  1.0e-56
Match length
                  117
                  88
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
```

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 146347

Seq. ID LIB3168-073-P1-K1-B3

Method BLASTN
NCBI GI g2828185
BLAST score 142
E value 5.0e-74
Match length 363
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MUD21, complete sequence [Arabidopsis thaliana]

Seq. No. 146348

Seq. ID LIB3168-073-P1-K1-B4

Method BLASTX
NCBI GI g1628583
BLAST score 616
E value 3.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146349

Seq. ID LIB3168-073-P1-K1-B6

Method BLASTX
NCBI GI g1174846
BLAST score 379
E value 2.0e-36
Match length 72
% identity 93

NCBI Description UBIQUITIN-CONJUGATING ENZYME E2-17 KD 3 (UBIQUITIN-PROTEIN

LIGASE 3) (UBIQUITIN CARRIER PROTEIN 3)

>gi\_1076425\_pir\_\_S43782 ubiquitin-conjugating enzyme UBC3 -

Arabidopsis thaliana >gi\_431262 (L19352) ubiquitin

conjugating enzyme [Arabidopsis thaliana]

Seq. No. 146350

Seq. ID LIB3168-073-P1-K1-B7

Method BLASTX
NCBI GI g112743
BLAST score 639
E value 5.0e-67
Match length 118
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68856\_pir\_\_NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi\_166617 (M22033) albumin 2S subunit

4 precursor [Arabidopsis thaliana] >gi\_395202\_emb\_CAA80869\_(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]

>gi\_4490713\_emb\_CAB38847.1\_ (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 146351

```
Seq. ID
                  LIB3168-073-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  549
                  1.0e-56
E value
Match length
                  106
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146352
Seq. ID
                  LIB3168-073-P1-K1-B9
                  BLASTX
Method
NCBI GI
                  g3421102
BLAST score
                  437
E value
                  2.0e-43
Match length
                  83
% identity
NCBI Description
                  (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
                  thaliana]
                  146353
Seq. No.
Seq. ID
                  LIB3168-073-P1-K1-C1
                  BLASTX
Method
NCBI GI
                  g112737
BLAST score
                  351
E value
                  3.0e-33
                  96
Match length
                  73
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146354
Seq. ID
                  LIB3168-073-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g2191126
BLAST score
                  267
E value
                  1.0e-148
Match length
                  322
% identity
                  97
NCBI Description Arabidopsis thaliana BAC IG002N01
                  146355
Seq. No.
Seq. ID
                  LIB3168-073-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  118
E value
                  7.0e-06
                  77
Match length
% identity
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis
```

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146356

Seq. ID LIB3168-073-P1-K1-C12

Method BLASTX
NCBI GI g2924509
BLAST score 174
E value 2.0e-12
Match length 77
% identity 44

NCBI Description (AL022023) subtilisin proteinase-like [Arabidopsis

thaliana]

146357

Seq. No.

Seq. ID LIB3168-073-P1-K1-C5

Method BLASTX
NCBI GI g4512675
BLAST score 347
E value 9.0e-33
Match length 104
% identity 68

NCBI Description (AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No. 146358

Seq. ID LIB3168-073-P1-K1-C6

Method BLASTX
NCBI GI g1628583
BLAST score 737
E value 2.0e-78
Match length 145
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146359

Seq. ID LIB3168-073-P1-K1-C7

Method BLASTN
NCBI GI g3252804
BLAST score 254
E value 1.0e-141
Match length 352
% identity 97

NCBI Description Arabidopsis thaliana chromosome II BAC F26C24 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 146360

Seq. ID LIB3168-073-P1-K1-C9

Method BLASTX
NCBI GI g1628583
BLAST score 634
E value 2.0e-66
Match length 121
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S



cruciferin seed storage protein [Arabidopsis thaliana] 146361 Seq. No. Seq. ID LIB3168-073-P1-K1-D1 Method BLASTX NCBI GI g4469003 BLAST score 413 E value 1.0e-40 Match length 102 77 % identity NCBI Description (AL035602) putative protein [Arabidopsis thaliana] 146362 Seq. No. Seq. ID LIB3168-073-P1-K1-D10 BLASTX Method NCBI GI g2252866 BLAST score 201 E value 1.0e-15 Match length 52 73 % identity (AF013294) contains region of similarity to SYT NCBI Description [Arabidopsis thaliana] 146363 Seq. No. LIB3168-073-P1-K1-D11 Seq. ID BLASTX Method NCBI GI g4115918 222 BLAST score E value 4.0e-18 Match length 50 % identity 86 (AF118222) similar to nascent polypeptide associated NCBI Description complex alpha chain [Arabidopsis thaliana] Seq. No. 146364 LIB3168-073-P1-K1-D12 Seq. ID Method BLASTX NCBI GI g224293 BLAST score 410 E value 4.0e-40 Match length 82 100 % identity NCBI Description histone H4 [Triticum aestivum] 146365 Seq. No. Seq. ID LIB3168-073-P1-K1-D2 Method BLASTX NCBI GI g2129767 BLAST score 670 E value 1.0e-70 140 Match length 91 % identity vacuolar processing enzyme (EC 3.4.22.-) isozyme beta NCBI Description

precursor - Arabidopsis thaliana >gi\_1805364\_dbj\_BAA09615\_

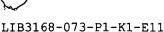
(D61394) beta-VPE [Arabidopsis thaliana]

Seq. No. 146366

```
LIB3168-073-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3193297
BLAST score
                  535
E value
                  8.0e-55
Match length
                  120
% identity
NCBI Description
                   (AF069298) similar to epoxide hydrolases [Arabidopsis
                  thaliana]
                  146367
Seq. No.
Seq. ID
                  LIB3168-073-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  748
E value
                  9.0e-80
Match length
                  143
% identity
                  100
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146368
                  LIB3168-073-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  635
                  1.0e-66
E value
                  120
Match length
% identity
                  98
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146369
                  LIB3168-073-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2232354
BLAST score
                  201
                  1.0e-15
E value
                  77
Match length
                  49
% identity
                  (AF006081) UDPG glucosyltransferase [Solanum berthaultii]
NCBI Description
Seq. No.
                  146370
                  LIB3168-073-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363484
BLAST score
                  374
E value
                  6.0e-36
Match length
                  110
                  73
% identity
                  IAA13 protein - Arabidopsis thaliana >gi 972929 (U18415)
NCBI Description
                  IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin
                  inducible protein, IAA13 [Arabidopsis thaliana]
Seq. No.
                  146371
```

18327





Method BLASTX NCBI GI g4063751 BLAST score 260 E value 1.0e-22

Match length 143 % identity

Seq. ID

NCBI Description (AC005851) putative white protein [Arabidopsis thaliana]

>gi 4510409 gb AAD21495.1 (AC006929) putative white

protein [Arabidopsis thaliana]

Seq. No. 146372

Seq. ID LIB3168-073-P1-K1-E12

Method BLASTN g4589430 NCBI GI BLAST score 330 E value 0.0e + 00Match length 426 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MLD14, complete sequence

Seq. No.

Seq. ID LIB3168-073-P1-K1-E2

146373

Method BLASTX NCBI GI g2119846 BLAST score 601 E value 2.0e-62 130 Match length % identity

chlorophyll a/b-binding protein type I precursor Lhb1B2 -NCBI Description

Arabidopsis thaliana >gi\_16364\_emb\_CAA45790\_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi\_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi 3337371 (AC004481) photosystem II type I

chlorophyll a/b binding protein [Arabidopsis thaliana]

146374 Seq. No.

Seq. ID LIB3168-073-P1-K1-E3

Method BLASTX NCBI GI g4115943 BLAST score 513 E value 2.0e-52 Match length 109 % identity

(AF118223) contains similarity to eukaryotic protein kinase NCBI Description

domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF

hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4)

[Arabidopsis thaliana]

146375 Seq. No.

Seq. ID LIB3168-073-P1-K1-E4

BLASTX Method NCBI GI g1628583 BLAST score 109 E value 7.0e-52

```
Match length
                  113
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146376
Seq. No.
                  LIB3168-073-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4581138
                  77
BLAST score
E value
                  4.0e-35
                  169
Match length
% identity
                  86
                  Arabidopsis thaliana chromosome II BAC F1011 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  146377
                  LIB3168-073-P1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2264321
BLAST score
                  324
E value
                  0.0e + 00
Match length
                  434
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146378
                  LIB3168-073-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  525
E value
                  9.0e-54
Match length
                  113
                  86
% identity
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869_
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
                  146379
Seq. No.
Seq. ID
                  LIB3168-073-P1-K1-E9
Method
                  BLASTX
                  q3413700
NCBI GI
                  433
BLAST score
                  5.0e-43
E value
                  85
Match length
% identity
                  (AC004747) putative YME1 protein [Arabidopsis thaliana]
```

NCBI Description

Seq. No. 146380

Seq. ID LIB3168-073-P1-K1-F1

Method BLASTN

Method

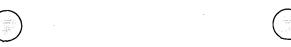
**BLASTX** 

```
q3449330
NCBI GI
                   198
BLAST score
                   1.0e-107
E value
                   367
Match length
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MDJ14, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146381
                   LIB3168-073-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g120675
BLAST score
                   469
E value
                   5.0e-47
Match length
                   107
                   84
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                   >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                   alba]
Seq. No.
                   146382
Seq. ID
                   LIB3168-073-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q4510397
BLAST score
                   736
                   2.0e-78
E value
                   143
Match length
% identity
NCBI Description
                   (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
                   146383
Seq. No.
Seq. ID
                   LIB3168-073-P1-K1-F12
Method
                   BLASTN
NCBI GI
                   g4371278
BLAST score
                   212
                   1.0e-115
E value
Match length
                   424
                   99
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T2N18 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   146384
Seq. No.
Seq. ID
                   LIB3168-073-P1-K1-F3
Method
                   BLASTN
NCBI GI
                   q2264307
BLAST score
                   126
E value
                   2.0e-64
Match length
                   316
                   91
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MED24, complete sequence [Arabidopsis thaliana]
                   146385
Seq. No.
                   LIB3168-073-P1-K1-F4
Seq. ID
```

```
q1628583
NCBI GI
BLAST score
                  49
                  6.0e-23
E value
Match length
                  58
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146386
Seq. ID
                  LIB3168-073-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  583
                  2.0e-60
E value
                  136
Match length
% identity
                  82
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146387
Seq. ID
                  LIB3168-073-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  617
                  2.0e-64
E value
                  124
Match length
                  93
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146388
Seq. ID
                  LIB3168-073-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g730129
BLAST score
                  707
E value
                  6.0e-75
Match length
                  140
% identity
                  99
                  NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I)
NCBI Description
                  >gi 3169310 (AF017641) nucleoside diphosphate kinase type 1
                  [Arabidopsis thaliana]
Seq. No.
                  146389
Seq. ID
                  LIB3168-073-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g3170525
BLAST score
                  400
E value
                  5.0e-39
Match length
                  99
% identity
                  79
```

18331 -

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NCBI Description (AF054615) cellulase [Fragaria x ananassa]

Seq. No.

146390

Seq. ID

LIB3168-073-P1-K1-F9

Method NCBI GI BLASTX q112681

BLAST score

504

E value Match length 3.0e-51121

82

% identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.

146391 Seq. ID

LIB3168-073-P1-K1-G1

Method NCBI GI BLASTX g1169598

BLAST score E value

571

Match length

4.0e-59 103 99

% identity NCBI Description

OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

(DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12

desaturase [Arabidopsis thaliana]

Seq. No.

146392

Seq. ID

LIB3168-073-P1-K1-G10

Method NCBI GI BLASTX g112682

BLAST score E value

686 2.0e-72

Match length

141

92

% identity NCBI Description

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir \$08510

cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.

146393

Seq. ID

LIB3168-073-P1-K1-G12

Method NCBI GI BLASTN

BLAST score

q511598 338

E value

0.0e+00

Match length

374 28

% identity

NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene,

complete cds

Seq. No.

146394

Seq. ID

LIB3168-073-P1-K1-G3

Method

BLASTN

NCBI GI

g4757414

18332

```
BLAST score
                  412
E value
                  0.0e + 00
Match length
                  420
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
                  146395
Seq. No.
                  LIB3168-073-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  775
E value
                  6.0e-83
Match length
                  146
                  100
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146396
                  LIB3168-073-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  369
```

E value 2.0e-35 Match length 116 % identity 66 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor ~ Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870 (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 146397 Seq. ID LIB3168-073-P1-K1-G6 BLASTX Method NCBI GI g131143 BLAST score 690 E value 5.0e-73 Match length 133

95

PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 NCBI Description

> >gi 72670 pir AlNTP7 photosystem I P700 apoprotein Al common tobacco chloroplast >gi 11830 emb CAA77352 (Z00044)

PSI P700 apoprotein Al [Nicotiana tabacum]

>gi 225198 prf 1211235AC photosystem I P700 apoprotein Al

[Nicotiana tabacum]

146398 Seq. No.

% identity

Seq. ID LIB3168-073-P1-K1-G7

Method BLASTN NCBI GI g4585896 BLAST score 343

```
0.0e + 00
E value
                   423
Match length
                   94
% identity
                  Arabidopsis thaliana chromosome II BAC F13I13 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  146399
Seq. ID
                  LIB3168-073-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1628583
                  257
BLAST score
E value
                  3.0e-22
                  51
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146400
Seq. No.
                  LIB3168-073-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
                  573
BLAST score
E value
                  3.0e-59
                  109
Match length
                   98
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146401
Seq. No.
                  LIB3168-073-P1-K1-H12
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4519189
                  193
BLAST score
E value
                  1.0e-104
                  326
Match length
                   49
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5A21, complete sequence
                  146402
Seq. No.
                  LIB3168-073-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112681
                  585
BLAST score
E value
                  1.0e-60
```

139 Match length 82 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

146403

Seq. No. LIB3168-073-P1-K1-H3 Seq. ID

```
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  608
E value
                  2.0e-63
Match length
                  120
% identity
                  97
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146404
Seq. No.
Seq. ID
                  LIB3168-073-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  48
E value
                  4.0e-68
Match length
                  131
% identity
                  98
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146405
Seq. ID
                  LIB3168-073-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  541
E value
                  1.0e-55
                  106
Match length
% identity
                  96
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146406
Seq. ID
                  LIB3168-073-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g595413
BLAST score
                  163
                  3.0e-11
E value
Match length
                  104
% identity
                  38
NCBI Description (U11236) beta COP [Saccharomyces cerevisiae]
Seq. No.
                  146407
Seq. ID
                  LIB3168-073-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2660672
BLAST score
                  337
E value
                  2.0e-31
Match length
```

% identity 89
NCBI Description (AC002342) similar to pMS10 protein [Arabidopsis thaliana]

•

Seq. No. 146408

Seq. ID LIB3168-074-P1-K1-A11 Method BLASTX NCBI GI g112681

BLAST score 629
E value 9.0e-66
Match length 158
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146409

Seq. ID LIB3168-074-P1-K1-A3

Method BLASTX
NCBI GI g1107501
BLAST score 420
E value 3.0e-41
Match length 139
% identity 63

NCBI Description (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)

Match to gb X91954 orf gene product from A. thaliana. ESTs gb Z17604, gb H76594, gb AA597972 and gb AA394824 come from

this gene. [Arabidopsis thaliana]

Seq. No. 146410

Seq. ID LIB3168-074-P1-K1-A4

Method BLASTX
NCBI GI g1628583
BLAST score 639
E value 7.0e-67
Match length 123
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146411

Seq. ID LIB3168-074-P1-K1-A5

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146412

Seq. ID LIB3168-074-P1-K1-A6

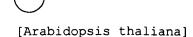
Method BLASTX

```
NCBI GI
                  g1628583
BLAST score
                  393
E value
                  1.0e-38
Match length
                  78
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146413
Seq. ID
                  LIB3168-074-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  55
E value
                  1.0e-67
Match length
                  138
                  96
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146414
Seq. ID
                  LIB3168-074-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  542
E value
                  1.0e-55
                  144
Match length
% identity
                  76
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146415
Seq. ID
                  LIB3168-074-P1-K1-B10
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  711
E value
                  2.0e-75
                  158
Match length
% identity
                  84
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146416
Seq. ID
                  LIB3168-074-P1-K1-B11
```

BLASTX Method NCBI GI g1113941 BLAST score 96 E value 3.0e-03

```
Match length
                   100
% identity
                   66
                   (U40713) Pv42p [Phaseolus vulgaris]
NCBI Description
Seq. No.
                   146417
Seq. ID
                   LIB3168-074-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g112741
BLAST score
                   592
E value
                   2.0e-61
Match length
                   142
% identity
                   81
NCBI Description
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
Seq. No.
                   146418
Seq. ID
                   LIB3168-074-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   q4159712
BLAST score
                   195
E value
                   1.0e-106
Match length
                   263
% identity
                   94
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MWI23, complete sequence
Seq. No.
                   146419
Seq. ID
                   LIB3168-074-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   381
E value
                   1.0e-36
Match length
                   101
                   97
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146420
Seq. ID
                   LIB3168-074-P1-K1-B6
Method
                   BLASTN
NCBI GI
                   q3080430
BLAST score
                   272
E value
                   1.0e-151
Match length
                   496
                   100
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
                   (ESSAII project)
Seq. No.
                   146421
Seq. ID
                   LIB3168-074-P1-K1-B7
Method
                   BLASTX
```

```
NCBI GI
                  q4204299
                  783
BLAST score
E value
                  1.0e-83
                  169
Match length
                  90
% identity
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  146422
Seq. ID
                  LIB3168-074-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  q16231
BLAST score
                  55
E value
                  6.0e-23
Match length
                  67
% identity
                  96
                  Arabidopsis CRA1 gene for 12S seed storage protein
NCBI Description
                  >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage
                                                                 TOTAL STATE
                  protein CRA1 gene, exons 1-4
                  146423
Seq. No.
                  LIB3168-074-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  625
                  3.0e-65
E value
                  120
Match length
                  100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146424
                  LIB3168-074-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112737
                  322
BLAST score
                  1.0e-29
E value
                  153
Match length
% identity
                  49
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  146425
Seq. No.
                  LIB3168-074-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  603
E value
                  1.0e-62
                  149
Match length
% identity
NCBI Description
                  (AC003027) lcl prt_seq No definition line found
```



146426 Seq. No. Seq. ID LIB3168-074-P1-K1-C2 Method BLASTX NCBI GI q4582468 BLAST score 722 E value 1.0e-76

Match length 146 100 % identity

(AC007071) putative 40S ribosomal protein; contains NCBI Description

C-terminal domain [Arabidopsis thaliana]

Seq. No. 146427

LIB3168-074-P1-K1-C4 Seq. ID

Method BLASTN NCBI GI q4220645 BLAST score 165 E value 1.0e-87 Match length 380 95 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MYA6, complete sequence [Arabidopsis thaliana]

Seq. No. 146428

Seq. ID LIB3168-074-P1-K1-C5

Method BLASTX NCBI GI g112737 BLAST score 549 E value 2.0e-56 Match length 137 78 % identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 146429

Seq. ID LIB3168-074-P1-K1-C6

Method BLASTX NCBI GI g112682 BLAST score 679 E value 1.0e-72 Match length 165 % identity 84

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir \$08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>qi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

146430 Seq. No.

Seq. ID LIB3168-074-P1-K1-C8

Method BLASTX NCBI GI g1628583 BLAST score 625 E value 3.0e-65 Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146431

Seq. ID LIB3168-074-P1-K1-C9

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146432

Seq. ID LIB3168-074-P1-K1-D1

Method BLASTN
NCBI GI g4581161
BLAST score 147
E value 6.0e-77
Match length 458
% identity 27

NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No. 146433

Seq. ID LIB3168-074-P1-K1-D10

Method BLASTX
NCBI GI g112681
BLAST score 729
E value 2.0e-77
Match length 162
% identity 86

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146434

Seq. ID LIB3168-074-P1-K1-D11

Method BLASTX
NCBI GI g112741
BLAST score 785
E value 5.0e-84
Match length 162
% identity 91

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi\_4490712 emb\_CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 146435

Seq. ID LIB3168-074-P1-K1-D12

Method BLASTX
NCBI GI g112739
BLAST score 673
E value 8.0e-71
Match length 168
% identity 79

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi\_4490711\_emb\_CAB38845.1\_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 146436

Seq. ID LIB3168-074-P1-K1-D2

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146437

Seq. ID LIB3168-074-P1-K1-D3

Method BLASTX
NCBI GI g4204299
BLAST score 640
E value 6.0e-67
Match length 124
% identity 100

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 146438

Seq. ID LIB3168-074-P1-K1-D5

Method BLASTN
NCBI GI g3869069
BLAST score 445
E value 0.0e+00
Match length 449
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MEB5, complete sequence [Arabidopsis thaliana]

Seq. No. 146439

Seq. ID LIB3168-074-P1-K1-D6

```
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  862
E value
                  5.0e-93
Match length
                  160
% identity
                  99
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  146440
Seq. No.
Seq. ID
                  LIB3168-074-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  - 611
E value
                  1.0e-63
Match length
                  117
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146441
                  LIB3168-074-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  719
E value
                  3.0e-76
Match length
                  173
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146442
                  LIB3168-074-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  626
E value
                  2.0e-65
Match length
                  167
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146443
Seq. No.
                  LIB3168-074-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  642
E value
                  3.0e-67
Match length
                  123
```

E value

6.0e-30

```
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146444
                  LIB3168-074-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2088638 ·
BLAST score
                  468
E value
                  0.0e + 00
Match length
                  484
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  146445
Seq. No.
                  LIB3168-074-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  642
E value
                  3.0e-67
Match length
                  123
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146446
                  LIB3168-074-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  904
E value
                  7.0e-98
                  184
Match length
                  94
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146447
Seq. ID
                  LIB3168-074-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  q4220638
BLAST score
                  508
                  0.0e + 00
E value
Match length
                  527
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                  146448
Seq. No.
Seq. ID
                  LIB3168-074-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  321
```

18344

بريقي.

BLAST score

Match length

E value

323

62

6.0e-30

```
Match length
                  83
% identity
                  77
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146449
Seq. ID
                  LIB3168-074-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  223
E value
                  5.0e-18
Match length
                  98
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146450
                  LIB3168-074-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  739
                  2.0e-84
E value
Match length
                  170
                  93
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146451
Seq. ID
                  LIB3168-074-P1-K1-E7
Method
                  BLASTX
                  g112681
NCBI GI
BLAST score
                  745
E value
                  3.0e-79
Match length
                  178
% identity
                  85
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146452
Seq. ID
                  LIB3168-074-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q1628583
```

18345



% identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

146453 Seq. No.

Seq. ID LIB3168-074-P1-K1-E9

BLASTX Method q1628583 NCBI GI BLAST score 804 3.0e-86 E value Match length 165 % identity 94

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146454

Seq. ID LIB3168-074-P1-K1-F1

Method BLASTX NCBI GI g112737 320 BLAST score 2.0e-29 E value Match length 151 49 % identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 146455

LIB3168-074-P1-K1-F11 Seq. ID

Method BLASTN NCBI GI q4691223 BLAST score 143 2.0e-74 E value Match length 391 92 % identity

Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15 NCBI Description

(ESSA project)

Seq. No. 146456

LIB3168-074-P1-K1-F12 Seq. ID

Method BLASTX NCBI GI g112682 BLAST score 696 1.0e-73 E value 159 Match length 82 % identity

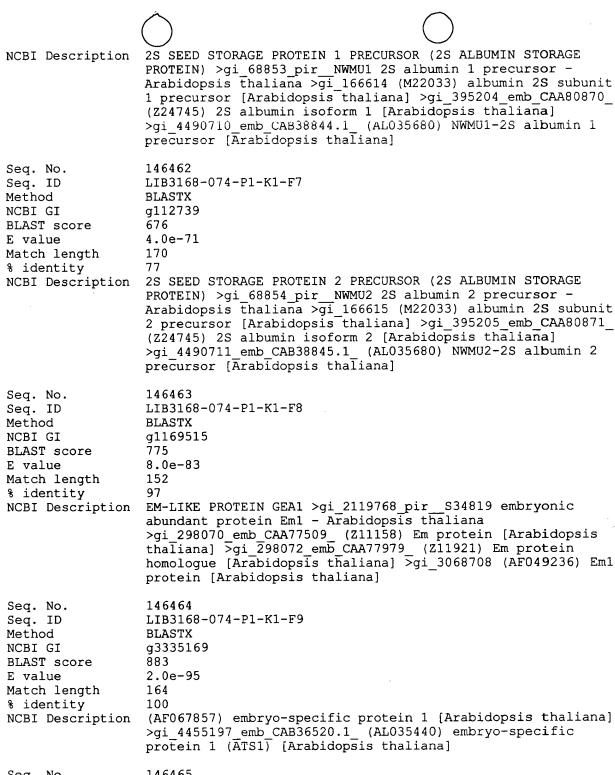
12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir\_\_S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

```
146457
Seq. No.
Seq. ID
                  LIB3168-074-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  642
E value
                  3.0e-67
Match length
                  123
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146458
Seq. No.
Seq. ID
                  LIB3168-074-P1-K1-F3
                  BLASTX
Method
NCBI GI
                  g4531444
BLAST score
                  247
E value
                  6.0e-21
Match length
                  71
% identity
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
NCBI Description
                  146459
Seq. No.
                  LIB3168-074-P1-K1-F4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  637
E value
                  1.0e-66
                  122
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146460
Seq. No.
Seq. ID
                  LIB3168-074-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g112681
BLAST score
                  673
E value
                  6.0e-71
                  154
Match length
                  85
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__ $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146461
Seq. No.
Seq. ID
                  LIB3168-074-P1-K1-F6
                  BLASTX
Method
                  g112737
NCBI GI
BLAST score
                  549
E value
                  3.0e-71
Match length
                  163
% identity
                  76
```



146465 Seq. No.

Seq. ID LIB3168-074-P1-K1-G1

BLASTX Method NCBI GI q112681 BLAST score 675 E value 4.0e-71

158 Match length % identity 84 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir 508509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] 146466 Seq. No. LIB3168-074-P1-K1-G10 Seq. ID Method BLASTX NCBI GI g131289 BLAST score 69 1.0e-75 E value 171 Match length 77 % identity PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) NCBI Description (CP43) >gi 72709 pir F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast >gi 225285 prf 1211235W photosystem II 44kD protein [Nicotiana tabacum] 146467 Seq. No. LIB3168-074-P1-K1-G11 Seq. ID Method BLASTX NCBI GI g119350 BLAST score 515 E value 2.0e-52 Match length 102 98 % identity ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) NCBI Description (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 81608 pir JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis thaliana >gi\_16271\_emb\_CAA41114\_ (X58107) enolase [Arabidopsis thaliana] >gi 4581151 gb AAD24635.1 AC006919 13 (AC006919) enolase (2-phospho-D-glycerate hydroylase); identical to P25696 [Arabidopsis thaliana] Seq. No. 146468 Seq. ID LIB3168-074-P1-K1-G12 Method BLASTX NCBI GI g1628583 BLAST score 820 E value 4.0e-88 Match length 156 % identity 100 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146469 LIB3168-074-P1-K1-G2 Seq. ID Method BLASTX

Method BLASTX
NCBI GI g1628583
BLAST score 617
E value 2.0e-64

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

Match length 129 % identity 98 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146470 Seq. ID LIB3168-074-P1-K1-G3 Method BLASTX NCBI GI g112739 BLAST score 557 E value 3.0e-57 Match length 148 76 % identity 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb\_CAA80871\_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana] 146471 Seq. No. Seq. ID LIB3168-074-P1-K1-G4 Method BLASTX NCBI GI q1628583 BLAST score 634 E value 3.0e-66 Match length 123 % identity 99 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146472 Seq. ID LIB3168-074-P1-K1-G6 Method BLASTX NCBI GI q118926 BLAST score 303 E value 1.0e-27 Match length 120 52 % identity DESSICATION-RELATED PROTEIN CLONE PCC13-62 PRECURSOR NCBI Description >gi 320600 pir E45509 desiccation-related protein (clone PCC13-62) - Craterostigma plantagineum >gi 167479 (M62991) dessication-related protein [Craterostigma plantagineum] >gi 227781 prf 1710351E abscisic acid responsive protein E [Craterostigma plantagineum] Seq. No. 146473

18350

LIB3168-074-P1-K1-G7

BLASTX

638

138

90

g4204298

8.0e-67

Match length

102

```
NCBI Description (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
                  146474
Seq. No.
Seq. ID
                  LIB3168-074-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g3402678
BLAST score
                  628
E value
                  1.0e-65
Match length
                  160
                  79
% identity
NCBI Description (AC004697) putative adenylate kinase [Arabidopsis thaliana]
                  146475
Seq. No.
                  LIB3168-074-P1-K1-G9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1363488
                                                    3.X
BLAST score
                  643
E value
                  2.0e-67
Match length
                  125
                  99
% identity
                  IAA8 protein - Arabidopsis thaliana >gi 972919 (U18410)
NCBI Description
                  IAA8 [Arabidopsis thaliana] >gi 4314364 gb AAD15575
                  (AC006340) auxin-induced IAA8 protein [Arabidopsis
                  thalianal
                  146476
Seq. No.
Seq. ID
                  LIB3168-074-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  882
E value
                  2.0e-95
                  180
Match length
                  94
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146477
Seq. No.
                  LIB3168-074-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  3.0e-65
Match length
                  120
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146478
                  LIB3168-074-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  530
E value
                  2.0e-54
```

18351

% identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis tha $\overline{\text{liana}}$  >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3168-074-P1-K1-H2

146479

Method BLASTX NCBI GI q1628583 BLAST score 631 E value 6.0e-66 123 Match length 98 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3168-074-P1-K1-H3

146480

Method BLASTX NCBI GI q1628583 BLAST score 642 E value 3.0e-67 123 Match length 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146481

Seq. ID LIB3168-074-P1-K1-H4

**BLASTX** Method NCBI GI g1628583 BLAST score 255 6.0e-22 E value Match length 136 75 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146482

Seq. ID LIB3168-074-P1-K1-H8

Method BLASTX NCBI GI q2129657 BLAST score 489 E value 3.0e-49 Match length 130 79 % identity

oleosin isoform - Arabidopsis thaliana NCBI Description

>gi\_987014\_emb\_CAA90877\_ (Z54164) oleosin [Arabidopsis
thaliana] >gi\_987016\_emb\_CAA90878\_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 146483

```
LIB3168-074-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q137465
BLAST score
                  778
E value
                  4.0e-83
Match length
                  157
% identity
                  98
NCBI Description
                  VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)
                   (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886
                  H+-transporting ATPase (EC 3.6.1.35) 57K chain -
                  Arabidopsis thaliana >qi 166627 (J04185) nucleotide-binding
                  subunit of vacuolar ATPase [Arabidopsis thaliana]
Seq. No.
                  146484
Seq. ID
                  LIB3168-075-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  617
E value
                  3.0e-64
Match length
                  158
% identity
                  77
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146485
Seq. ID
                  LIB3168-075-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  174
E value
                  5.0e-86
Match length
                  183
% identity
                  87
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146486
Seq. ID
                  LIB3168-075-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  q3763915
BLAST score
                  479
```

Method BLASTN
NCBI GI g3763915
BLAST score 479
E value 0.0e+00
Match length 503
% identity 99

NCBI Description Arabidopsis thaliana chromosome II BAC F14B2 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 146487

Seq. ID LIB3168-075-P1-K1-A2

Method BLASTX

```
NCBI GI
                  q2129767
BLAST score
                  697
E value
                  1.0e-73
Match length
                  140
                  94
% identity
                  vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
NCBI Description
                  precursor - Arabidopsis thaliana >gi_1805364_dbj_BAA09615
                  (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
                  146488
                  LIB3168-075-P1-K1-A3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4159704
BLAST score
                  99
E value
                  6.0e-49
Match length
                  99
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MCB17, complete sequence
                  146489
Seq. No.
                  LIB3168-075-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                  560
E value
                  1.0e-57
Match length
                  113
% identity
                  96
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  146490
                  LIB3168-075-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267073
BLAST score
                  746
E value
                  2.0e-79
Match length
                  137
% identity
                  99
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
                  146491
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  713
E value
                  1.0e-75
Match length
                  148
% ideratity
                  90
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
```

>qi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana] Seq. No. 146492 Seq. ID LIB3168-075-P1-K1-A7 Method BLASTX NCBI GI g112739 BLAST score 563 5.0e-58 E value Match length 149 75 % identity 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871 (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi\_4490711\_emb\_CAB38845.1\_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana] 146493 Seq. No. Seq. ID LIB3168-075-P1-K1-A9 Method BLASTX NCBI GI q1082359 BLAST score 174 E value 2.0e-12 Match length 68 % identity 49 excision repair protein ERCC5 - human >qi 306742 (L20046) NCBI Description excision repair protein [Homo sapiens] Seq. No. 146494 LIB3168-075-P1-K1-B1 Seq. ID Method BLASTX NCBI GI q112681 BLAST score 659 E value 3.0e-69 Match length 129 % identity 99 NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 146495 Seq. ID LIB3168-075-P1-K1-B10 Method BLASTN NCBI GI g1628582 BLAST score 124

E value 3.0e-63 319 Match length % identity

NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein

(ATCRU3) gene, complete cds

Seq. No. 146496

Seq. ID LIB3168-075-P1-K1-B11

```
Method
                  BLASTX
NCBI GI
                  q129817
BLAST score
                  610
E value
                  1.0e-63
Match length
                  131
% identity
                  90
NCBI Description
                  BASIC PEROXIDASE E PRECURSOR >gi 81653 pir JU0458
                  peroxidase (EC 1.11.1.7) E - Arabidopsis thaliana
                  >gi 166807 (M58381) peroxidase [Arabidopsis thaliana]
                  146497
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2828281
BLAST score
                  482
E value
                  2.0e-48
Match length
                  171
% identity
                  58
NCBI Description
                  (ALO21687) hypothetical protein [Arabidopsis thaliana]
                  >gi 2832635_emb_CAA16764_ (AL021711) hypothetical protein
                  [Arabidopsis thaliana]
                  146498
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g1176671
BLAST score
                  325
E value
                  5.0e-30
Match length
                  123
                  49
% identity
                  PUTATIVE GLUCOSYLTRANSFERASE CO8B11.8
NCBI Description
                  >gi_3874174_emb_CAA86666_ (Z46676) C08B11.8 [Caenorhabditis
                  elegans]
                  146499
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g3860277
BLAST score
                  624
E value
                  4.0e-65
Match length
                  152
% identity
NCBI Description
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
                  146500
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g1109699
BLAST score
                  702
                  3.0e-74
E value
Match length
                  138
% identity
                  98
NCBI Description (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
Seq. No.
                  146501
```

```
LIB3168-075-P1-K1-B8
Seq. ID
                  BLASTX
Method
                  q2980641
NCBI GI
BLAST score
                  444
                  4.0e-44
E value
                  152
Match length
                  62
% identity
NCBI Description
                  (Y11250) multi resistance protein [Arabidopsis thaliana]
Seq. No.
                  146502
                  LIB3168-075-P1-K1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4091806
BLAST score
                  188
                  3.0e-14
E value
                  86
Match length
% identity
                  48
                  (AF052585) CONSTANS-like protein 2 [Malus domestica]
NCBI Description
Seq. No.
                  146503
                  LIB3168-075-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  759
E value
                  6.0e-81
Match length
                  166
                  87
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146504
Seq. ID
                  LIB3168-075-P1-K1-C12
Method
                  BLASTX
                  q4204299
NCBI GI
BLAST score
                  802
                  5.0e-86
E value
                  173
Match length
% identity
                  90
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
                  146505
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q133916
                  605
BLAST score
                  7.0e-63
E value
Match length
                  124
                  91
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 >gi 70857 pir__R3SP2
NCBI Description
                  ribosomal protein S2 - spinach chloroplast
                  >gi 12256 emb CAA29343 (X05916) rps2 protein (AA 1-236)
                  [Spinacia oleracea]
```

```
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-C5
Method
                  BLASTN
NCBI GI
                  q2264310
BLAST score
                  419
E value
                  0.0e + 00
Match length
                  460
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKP11, complete sequence [Arabidopsis thaliana]
                  146507
Seq. No.
                  LIB3168-075-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  766
E value
                  8.0e-82
Match length
                  160
% identity
                  91
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146508
Seq. ID
                  LIB3168-075-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g3449315
BLAST score
                  473
E value
                  0.0e + 00
Match length
                  558
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K23L20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146509
Seq. ID
                  LIB3168-075-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  642
E value
                  3.0e-67
Match length
                  123
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146510
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g82223
BLAST score
                  55
E value
                  5.0e-11
Match length
                  60
% identity
                  72
NCBI Description hypothetical protein 70B - common tobacco chloroplast
```

>gi\_11878\_emb\_CAA77391\_ (Z00044) hypothetical protein
[Nicotiana tabacum] >gi\_1223681\_emb\_CAA77402\_ (Z00044)
hypothetical protein [Nicotiana tabacum]
>gi\_225250\_prf\_\_1211235CJ ORF 70B [Nicotiana tabacum]

Seq. No. 146511

Seq. ID LIB3168-075-P1-K1-D1

Method BLASTX
NCBI GI g2435518
BLAST score 343
E value 3.0e-32
Match length 112
% identity 68

NCBI Description (AF024504) contains similarity to C3HC4-type zinc fingers

[Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3168-075-P1-1-D11

146512

Method BLASTX
NCBI GI g2129657
BLAST score 255
E value 4.0e-30
Match length 107
% identity 74

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi\_987014\_emb\_CAA90877\_ (Z54164) oleosin [Arabidopsis
thaliana] >gi\_987016\_emb\_CAA90878\_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 146513

Seq. ID LIB3168-075-P1-K1-D12

Method BLASTN
NCBI GI g2104523
BLAST score 363
E value 0.0e+00
Match length 382
% identity 99

NCBI Description Arabidopsis thaliana BAC T10M13 from chromosome IV, from

10.8 cM to 11.6 cM, complete sequence

Seq. No. 146514

Seq. ID LIB3168-075-P1-K1-D3

Method BLASTX
NCBI GI g1628583
BLAST score 343
E value 1.0e-32
Match length 104
% identity 71

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146515

Seq. ID LIB3168-075-P1-K1-D4

Method BLASTX
NCBI GI g4507311
BLAST score 215

E value 4.0e-17 Match length 103 % identity NCBI Description suppressor of Ty (S.cerevisiae) 4 homolog 1 >gi 3122873 sp Q16550 SPT4 HUMAN TRANSCRIPTION INITIATION PROTEIN SPT4 HOMOLOG 1 >gi 1209779 (U43923) similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] >gi 1401053 (U38818) SUPT4H [Homo sapiens] >gi 1401055 (U38817) SUPT4H [Homo sapiens] >gi 1401066 (U43154) Supt4h [Mus musculus] >qi 3779194 (U96809) chromatin structural protein homolog [Mus musculus] 146516 Seq. No. Seq. ID LIB3168-075-P1-K1-D5 Method BLASTX NCBI GI g112737 BLAST score 445 E value 2.0e-44 Match length 115 74 % identity 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68853 pir\_NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870 (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana] Seq. No. 146517 Seq. ID LIB3168-075-P1-K1-D6 BLASTX Method NCBI GI g112739 BLAST score 654 E value 1.0e-68 Match length 169 76 % identity 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871 (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 146518

Seq. ID LIB3168-075-P1-K1-D9

Method BLASTX NCBI GI g1903357 BLAST score 306 E value 7.0e-28 Match length 95 % identity

(AC000104) Strong similarity to Arabidopsis 2A6 NCBI Description

(gb X83096). [Arabidopsis thaliana]

Seq. No. 146519

```
LIB3168-075-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
                  455
BLAST score
E value
                  2.0e-45
Match length
                  140
% identity
                  71
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146520
Seq. ID
                  LIB3168-075-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  668
E value
                  3.0e-70
                  135
Match length
% identity
                  95
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495 emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146521
Seq. ID
                  LIB3168-075-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  747
E value
                  1.0e-79
Match length
                  149
% identity
                  95
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  146522
                                                            25.
Seq. ID
                  LIB3168-075-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g2160132
BLAST score
                  36
                  2.0e-11
E value
Match length
                  43
                  95
% identity
                  Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146523
Seq. ID
                  LIB3168-075-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  q3482964
BLAST score
                  365
E value
                  0.0e+00
Match length
                  420
% identity
                  96
                  Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
NCBI Description
                   (ESSAII project)
```

```
146524
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2529672
BLAST score
                  230
E value
                  5.0e-19
                  59
Match length
% identity
NCBI Description (AC002535) putative pectinesterase [Arabidopsis thaliana]
                  146525
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-E6
                  BLASTX
Method
NCBI GI
                  g1170939
BLAST score
                  565
                  3.0e-58
E value
Match length
                  118
                  90
% identity
NCBI Description S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1084408_pir_S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi 429108 emb CAA80867 (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
                  146526
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g132863
BLAST score
                  637
                  8.0e-67
E value
                  123
Match length
                  97
% identity
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L2
NCBI Description
                  >gi 12214 emb CAA46568 (X65615) ribosomal protein L2
                  [Sinapis alba]
Seq. No.
                  146527
Seq. ID
                  LIB3168-075-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2154720
BLAST score
                  244
E value
                  1.0e-20
Match length
                  49
% identity
                  100
NCBI Description (Y07648) nitrilase 1 [Arabidopsis thaliana]
                  146528
Seq. No.
                  LIB3168-075-P1-K1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16181
BLAST score
                  40
E value
                  4.0e-13
Match length
                  279
% identity
                  79
NCBI Description A.thaliana gene for tonoplast intrinsic protein
```

Seq. No.

BLAST score

Match length

% identity

Seq. ID

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

BLAST score

Match length % identity

Method NCBI GI

```
alpha-TIP(Ara) >gi_166622_gb_M84343_ATHATIP Arabidopsis
                  thaliana tonoplast intrinsic protein (alpha-TIP) gene,
                  complete cds
                  146529
                  LIB3168-075-P1-K1-F11
                  BLASTX
                  g112741
                  854
                  5.0e-92
                  161
                  98
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >qi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  146530
                  LIB3168-075-P1-K1-F2
                  BLASTN
                  q3869064
                  424
                  0.0e + 00
                  498
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1013, complete sequence [Arabidopsis thaliana]
                  146531
                  LIB3168-075-P1-K1-F3
                  BLASTX
                  q1628583
                  461
                  2.0e-46
                  91
                  98
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146532
                  LIB3168-075-P1-K1-F4
                  BLASTX
                  q1628583
                  642
                  3.0e-67
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Seq. No.

Seq. ID

Method NCBI GI BLAST score E value Match length 123 100 % identity

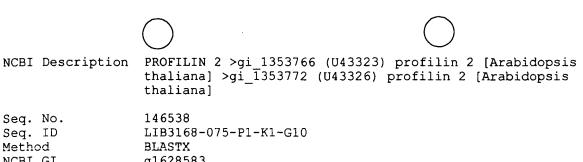
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146533

LIB3168-075-P1-K1-F5 Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  604
                  6.0e-63
E value
                  137
Match length
% identity
                  85
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146534
Seq. ID
                  LIB3168-075-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g2351374
BLAST score
                  384
E value
                  4.0e-37
                  93
Match length
% identity
NCBI Description
                  (U54560) putative 26S proteasome subunit athMOV34
                  [Arabidopsis thaliana]
Seq. No.
                  146535
                  LIB3168-075-P1-K1-F7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4337109
BLAST score
                  193
E value
                  1.0e-14
Match length
                  103
                  47
% identity
NCBI Description (AF129756) BAT3 [Homo sapiens]
Seq. No.
                  146536
Seq. ID
                  LIB3168-075-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  702
E value
                  3.0e-74
Match length
                  164
                  82
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  146537
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-G1
                  BLASTX
Method
NCBI GI
                  g2499811
BLAST score
                  624
E value
                  3.0e-65
Match length
                  122
% identity
                  98
```



Method NCBI GI q1628583 BLAST score 452 E value 6.0e-49 Match length 129 % identity 77

Seq. No. Seq. ID

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

146539 Seq. No.

LIB3168-075-P1-K1-G11 Seq. ID

Method BLASTX g4678226 NCBI GI BLAST score 581 E value 7.0e-61 Match length 137 % identity 93

(AC007135) putative 40S ribosomal protein S14 [Arabidopsis NCBI Description

thaliana]

146540 Seq. No.

LIB3168-075-P1-K1-G12 Seq. ID

BLASTX Method NCBI GI g112682 BLAST score 52 E value 6.0e-53 Match length 143 % identity 78

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB (Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

146541 Seq. No.

LIB3168-075-P1-K1-G2 Seq. ID

Method **BLASTX** NCBI GI g1628583 BLAST score 667 E value 4.0e-70 Match length 161 % identity 81

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

146542 Seq. No.

Seq. ID LIB3168-075-P1-K1-G4

Method BLASTX NCBI GI g112739

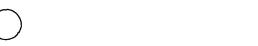
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435
BLAST score
E value
                  3.0e-55
                  141
Match length
                  79
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  146543
Seq. No.
                  LIB3168-075-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3292827
BLAST score
                  504
E value
                  4.0e-51
Match length
                  118
                  79
% identity
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  146544
                  LIB3168-075-P1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2342673
                  274
BLAST score
E value
                  1.0e-153
Match length
                  290
                  99
% identity
                  Sequence of BAC F7G19 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q3924615
BLAST score
                  139
E value
                  2.0e-08
Match length
                  55
% identity
                  (AF069442) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  146546
Seq. No.
                  LIB3168-075-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  560
E value
                  2.0e-63
Match length
                  160
                  77
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >qi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
```

18366

2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

.....



precursor [Arabidopsis thaliana] Seq. No. 146547 LIB3168-075-P1-K1-G9 Seq. ID BLASTN Method NCBI GI g4159704 BLAST score 320 E value 1.0e-180 Match length 407 % identity 95 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description MCB17, complete sequence 146548 Seq. No. Seq. ID LIB3168-075-P1-K1-H10 Method BLASTX NCBI GI g2245085 BLAST score 284 E value 1.0e-25 Match length 68 % identity NCBI Description (Z97343) lactate dehydrogenase [Arabidopsis thaliana] Seq. No. 146549 LIB3168-075-P1-K1-H12 Seq. ID Method BLASTX NCBI GI q112737 BLAST score 567 E value 2.0e-58 Match length 141 % identity 79 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana] 146550 Seq. No. Seq. ID LIB3168-075-P1-K1-H3 Method BLASTN NCBI GI q3892698 BLAST score 36 2.0e-11 E value Match length 48 % identity 94 NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (ESSAII project)

Seq. No. 146551

Seq. ID LIB3168-075-P1-K1-H4

Method BLASTX
NCBI GI g112682
BLAST score 655
E value 8.0e-69
Match length 153

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% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
                   146552
Seq. No.
Seq. ID
                  LIB3168-075-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  q16559
                   174
BLAST score
                   4.0e-93
E value
                   232
Match length
% identity
                   95
                  A.thaliana gene for tRNA-Ala (P-2-L)
NCBI Description
                   146553
Seq. No.
                  LIB3168-075-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g112681
BLAST score
                   567
E value
                   2.0e-58
Match length
                   124
% identity
                   93
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146554
                   LIB3168-075-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   651
E value
                   3.0e-68
                   134
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146555
Seq. ID
                   LIB3168-075-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q112737
BLAST score
                   86
E value
                   1.0e-63
                   163
Match length
                   78
% identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
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18368

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1



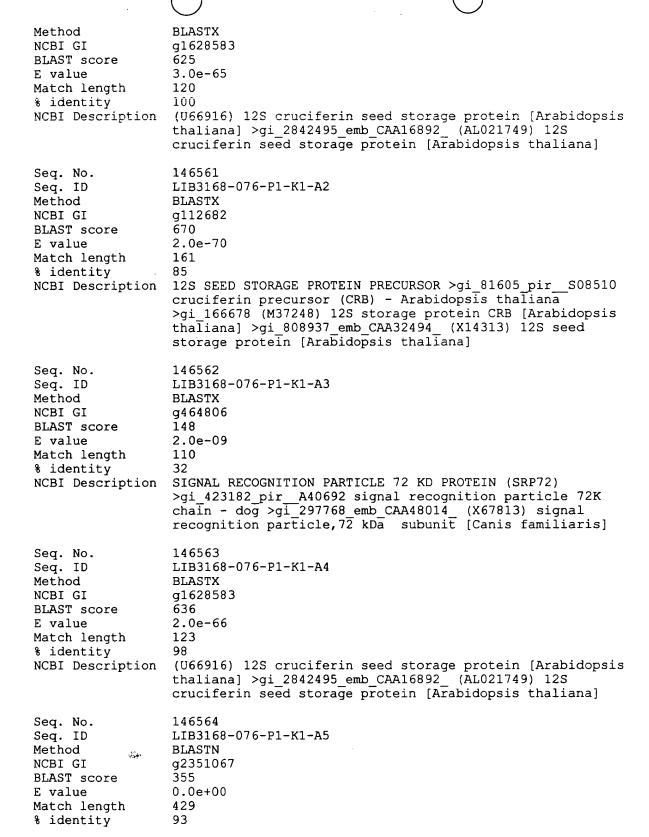
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precursor [Arabidopsis thaliana]
Seq. No.
                  146556
Seq. ID
                  LIB3168-075-P1-K1-H9
                  BLASTX
Method
NCBI GI
                  g112739
BLAST score
                  48
E value
                  3.0e-49
Match length
                  148
                  78
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146557
                  LIB3168-076-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4335744
BLAST score
                  161
E value
                  3.0e-85
Match length
                  420
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC T4M8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  LIB3168-076-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2500347
BLAST score
                  441
E value
                  1.0e-43
Match length
                  128
                  71
% identity
                  NHP2/RS6 FAMILY PROTEIN YEL026W HOMOLOG
NCBI Description
                  >gi 3878691 emb CAA90127 (Z49911) similar to ribosomal
                  protein (L7AE family); cDNA EST EMBL: D73957 comes from this
                  gene; cDNA EST EMBL:D71298 comes from this gene; cDNA EST
                  EMBL: D74077 comes from this gene; cDNA EST EMBL: D71393
                  comes from this gene; cD
Seq. No.
                  146559
Seq. ID
                  LIB3168-076-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  q4589428
BLAST score
                  433
E value
                  0.0e + 00
Match length
                  491
% identity
                  97
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MFH8, complete sequence

Seq. No. 146560

Seq. ID LIB3168-076-P1-K1-A12



Method

NCBI GI

E value

BLAST score

Match length

BLASTX

163

145

q3478700

8.0e-67

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MPO12, complete sequence [Arabidopsis thaliana]
                   146565
Seq. No.
                   LIB3168-076-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   625
E value
                   2.0e-65
Match length
                   120
                   100
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146566
Seq. ID
                   LIB3168-076-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   q2160151
BLAST score
                   747
E value
                   2.0e-79
Match length
                   176
% identity
                   85
NCBI Description
                   (AC000375) Strong similarity to Brassica aspartic protease
                   (gb X77260). [Arabidopsis thaliana]
Seq. No.
                   146567
Seq. ID
                   LIB3168-076-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g112681
BLAST score
                   810
E value
                   6.0e-87
Match length
                   174
% identity
                   92
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir $08509
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146568
Seq. ID
                  LIB3168-076-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g1402904
BLAST score
                  724
E value
                   7.0e-77
Match length
                  139
                   99
% identity
NCBI Description
                   (X98313) peroxidase [Arabidopsis thaliana]
Seq. No.
                  146569
Seq. ID
                  LIB3168-076-P1-K1-B10
```

Method

BLASTX

```
% identity
NCBI Description (AF034387) AFT protein [Arabidopsis thaliana]
                  146570
Seq. No.
Seq. ID
                  LIB3168-076-P1-K1-B11
                  BLASTX
Method
NCBI GI
                  q418854
                  768
BLAST score
                  4.0e-82
E value
                  154
Match length
                  18
% identity
                  ubiquitin precursor - parsley >gi_288112_emb_CAA45621
NCBI Description
                  (X64344) polyubiquitin [Petroselinum crispum]
                  >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                  [Petroselinum crispum]
                  146571
Seq. No.
                  LIB3168-076-P1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129532
BLAST score
                  396
                  2.0e-38
E value
                  105
Match length
                  73
% identity
                  acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -
NCBI Description
                  Arabidopsis thaliana >gi 1107507 emb CAA63746 (X93461)
                  acyl-[acyl-carrier protein] desaturase [Arabidopsis
                  thaliana]
Seq. No.
                  146572
                  LIB3168-076-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q112682
BLAST score
                  717
                  4.0e-76
E value
                  159
Match length
                  84
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146573
Seq. No.
                  LIB3168-076-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4512690
BLAST score
                  455
                  0.0e + 00
E value
Match length
                  490
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F11A3 genomic
NCBI Description
                  sequence, complete sequence
                  146574
Seq. No.
Seq. ID
                  LIB3168-076-P1-K1-B4
```

```
NCBI GI
                   g3367515
BLAST score
                   709
E value
                   5.0e-75
Match length
                   141
                   96
% identity
                   (AC004392) Similar to
NCBI Description
                   glucose-6-phosphate/phosphate-translocator (GPT)
                  gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
Seq. No.
                   146575
Seq. ID
                  LIB3168-076-P1-K1-B5
Method
                  BLASTN
NCBI GI
                   q3449323
BLAST score
                   51
                   8.0e-20
E value
Match length
                   71
                   93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MZA15, complete sequence [Arabidopsis thaliana]
                   146576
Seq. No.
Seq. ID
                  LIB3168-076-P1-K1-B6
Method
                  BLASTX
NCBI GI
                   q112681
BLAST score
                   749
                   9.0e-80
E value
                   174
Match length
% identity
                   84
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir __S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146577
                   LIB3168-076-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4218121
BLAST score
                   588
                   7.0e-61
E value
Match length
                   172
% identity
                   67
                   (AL035353) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   146578
Seq. ID
                   LIB3168-076-P1-K1-B8
Method
                   BLASTN
NCBI GI
                   g3046847
BLAST score
                   296
E value
                   1.0e-165
Match length
                   556
% identity
                  Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
NCBI Description
                   K11J9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146579
Seq. ID
                  LIB3168-076-P1-K1-B9
```

```
Method
                  BLASTX
NCBI GI
                  q2129657
BLAST score
                  534
                  2.0e-54
E value
Match length
                  137
% identity
                  81
NCBI Description
                  oleosin isoform - Arabidopsis thaliana
                  >gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                  [Arabidopsis thaliana]
Seq. No.
                  146580
Seq. ID
                  LIB3168-076-P1-K1-C1
                  BLASTX
Method
NCBI GI
                  g1817546
BLAST score
                  175
E value
                  4.0e-13
Match length
                  64
                  55
% identity
NCBI Description
                 (D83997) mabinlin [Capparis masaikai]
Seq. No.
                  146581
Seq. ID
                  LIB3168-076-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  588
E value
                  6.0e-61
Match length
                  141
% identity
                  81
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  146582
Seq. No.
Seq. ID
                  LIB3168-076-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  613
                  8.0e-64
E value
Match length
                  149
% identity
                  79
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146583
Seq. ID
                  LIB3168-076-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g112682
```

18374.

```
BLAST score
                  697
E value
                  1.0e-73
Match length
                  169
                  79
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146584
Seq. No.
Seq. ID
                  LIB3168-076-P1-K1-C3
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  760
                  5.0e-81
E value
                  159
Match length
% identity
                  92
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146585
Seq. ID
                  LIB3168-076-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  744
                  4.0e-79
E value
Match length
                  155
% identity
                  92
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146586
                  LIB3168-076-P1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  577
E value
                  1.0e-59
Match length
                  145
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146587
                  LIB3168-076-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2622714
BLAST score
                  329
E value
                  2.0e-30
```

(AE000918) phosphonopyruvate decarboxylase

[Methanobacterium thermoautotrophicum]

136

Match length % identity

NCBI Description

```
146588
Seq. No.
Seq. ID
                   LIB3168-076-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g112681
BLAST score
                   609
                   1.0e-63
E value
Match length
                   121
% identity
                   99
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   tha\overline{liana} >gi_808936_emb_CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146589
                   LIB3168-076-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112737
BLAST score
                   331
                   3.0e - 31
E value
Match length
                   84
% identity
                   77
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
Seq. No.
                   146590
Seq. ID
                   LIB3168-076-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g114661
BLAST score
                   621
E value
                   1.0e-64
Match length
                   129
% identity
                   ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV)
NCBI Description
                   >gi 67924 pir LWNT6 H+-transporting ATP synthase (EC
                   3.6.1.34) chain a - common tobacco chloroplast
                   >gi_11813_emb_CAA77344_ (Z00044) ATPase sunthase IV subunit
[Nicotiana tabacum] >gi_225273_prf__1211235H ATPase a
                   [Nicotiana tabacum]
Seq. No.
                   146591
Seq. ID
                   LIB3168-076-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g112737
BLAST score
                   280
E value
                   7.0e-25
Match length
                   124
% identity
                   52
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
```

Match length

152

```
precursor [Arabidopsis thaliana]
                   146592
Seq. No.
                   LIB3168-076-P1-K1-D10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4096078
BLAST score
                   38
E value
                    4.0e-12
Match length
                    38
% identity
                    100
                   Arabidopsis thaliana chromosome I BAC T5A14 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   LIB3168-076-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                    g2129657
BLAST score
                    337
E value
                    5.0e-35
Match length
                    109
% identity
                    73
NCBI Description
                   oleosin isoform - Arabidopsis thaliana
                   >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                    [Arabidopsis thaliana]
Seq. No. :
                    146594
Seq. ID
                   LIB3168-076-P1-K1-D12
Method
                   BLASTN
NCBI GI
                    q336275
BLAST score
                    222
E value
                    1.0e-122
Match length
                    330
% identity
                    91
NCBI Description
                   Alnus incana chloroplast tRNA-Ala-tgc (trnA) and
                    tRNA-Ile-gta (trnI) genes, complete cds
Seq. No.
                    146595
Seq. ID
                    LIB3168-076-P1-K1-D4
Method
                    BLASTN
NCBI GI
                    g2828182
BLAST score
                    533
E value
                    0.0e+00
Match length
                    552
% identity
                    99
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOJ9, complete sequence [Arabidopsis thaliana]
Seq. No.
                    146596
                   LIB3168-076-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                    g112739
                   588
BLAST score
E value
                    6.0e-61
```

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

% identity NCBI Description

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi\_68854\_pir\_\_ NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi\_4490711\_emb\_CAB38845.1\_(AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana]

Seq. No. 146597

Seq. ID LIB3168-076-P1-K1-D6

Method BLASTX
NCBI GI g1345973
BLAST score 638
E value 9.0e-67
Match length 137
% identity 84

NCBI Description

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi\_541882\_pir\_\_JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi\_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi\_471091\_dbj\_BAA04505\_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi\_1197795\_dbj\_BAA05514\_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi\_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 146598

Seq. ID LIB3168-076-P1-K1-D7

Method BLASTX
NCBI GI g1628583
BLAST score 485
E value 6.0e-49
Match length 117
% identity 82

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146599

Seq. ID LIB3168-076-P1-K1-D8

Method BLASTX
NCBI GI g112739
BLAST score 440
E value 1.0e-64
Match length 168
% identity 75

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 146600

Seq. ID LIB3168-076-P1-K1-D9

```
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  648
E value
                  6.0e-68
Match length
                  165
                  81
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146601
                  LIB3168-076-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                   642
E value
                   3.0e-67
Match length
                  123
% identity
                   100
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146602
                  LIB3168-076-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2618601
BLAST score
                   68
E value
                   7.0e-30
Match length
                   100
                   92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146603
                  LIB3168-076-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q112681
BLAST score
                   639
E value
                   5.0e-67
Match length
                   125
% identity
                   99
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   tha\overline{\text{liana}} >gi 808936 emb CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146604
                  LIB3168-076-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1351272
BLAST score
                   512
E value
                   4.0e-52
Match length
                  124
% identity
                   84
```

NCBI Description TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >qi 414550

(U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi\_742408\_prf\_\_2009415A triose phosphate

isomerase [Arabidopsis thaliana]

Seq. No. 146605

Seq. ID LIB3168-076-P1-K1-E2

Method BLASTX NCBI GI q4584535 BLAST score 252 E value 2.0e-21 Match length 48 % identity

NCBI Description (ALO49608) putative protein [Arabidopsis thaliana]

146606 Seq. No.

LIB3168-076-P1-K1-E3 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 625 E value 3.0e-65 Match length 120 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146607

Seq. ID LIB3168-076-P1-K1-E4

Method BLASTX NCBI GI g4204299 BLAST score 736 E value 3.0e-78 Match length 165 % identity 88

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 146608

LIB3168-076-P1-K1-E5 Seq. ID

Method BLASTX NCBI GI g112681 BLAST score 687 E value 2.0e-72 146 Match length % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146609

LIB3168-076-P1-K1-E6 Seq. ID

Method BLASTX NCBI GI g3176714 BLAST score 871

```
4.0e-94
E value
Match length
                  170
% identity
                  99
                  (AC002392) putative tRNA-splicing endonuclease positive
NCBI Description
                  effector [Arabidopsis thaliana]
Seq. No.
                  146610
Seq. ID
                  LIB3168-076-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  646
E value
                  5.0e-68
Match length
                  154
% identity
                  84
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146611
Seq. ID
                  LIB3168-076-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q2182286
BLAST score
                  167
E value
                  5.0e-89
Match length
                  259
                  91
% identity
                  Sequence of BAC F20P5 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146612
Seq. ID
                  LIB3168-076-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  500
E value
                  1.0e-50
Match length
                  142
                  71
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146613
Seq. ID
                  LIB3168-076-P1-K1-F12
Method
                  BLASTX
NCBÌ GI
                  q1628583
BLAST score
                  642
E value
                  3.0e-67
```

100 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

123

Match length

% identity

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

Method

NCBI GI

BLASTX

g112681



## cruciferin seed storage protein [Arabidopsis thaliana]

146614 Seq. No. LIB3168-076-P1-K1-F2 Seq. ID Method BLASTN NCBI GI g1707006 BLAST score 434 0.0e + 00E value Match length 466 99 % identity Arabidopsis thaliana chromosome II BAC T1B8 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana] 146615 Seq. No. Seq. ID LIB3168-076-P1-K1-F3 Method BLASTX NCBI GI g112681 BLAST score 525 E value 3.0e-65Match length 176 79 % identity 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir \$08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis  $tha\overline{liana}$  >gi\_808936\_emb\_CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] 146616 Seq. No. LIB3168-076-P1-K1-F4 Seq. ID Method BLASTX NCBI GI q1628583 BLAST score 519 7.0e-53 E value Match length 146 72 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 146617 Seq. No. Seq. ID LIB3168-076-P1-K1-F6 Method BLASTX NCBI GI g112682 BLAST score 524 9.0e-75 E value Match length 169 83 % identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir \_\_S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi\_808937\_emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 146618 LIB3168-076-P1-K1-F7 Seq. ID

```
BLAST score
                    506
                    4.0e-52
E value
Match length
                   147
                   74
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir_S08509
NCBI Description
                    cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146619
                   LIB3168-076-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1617268
BLAST score
                   437
E value
                    5.0e-60
Match length
                   140
% identity
                    82
NCBI Description (Z72153) acyl CoA synthetase [Brassica napus]
Seq. No.
                   146620
Seq. ID
                   LIB3168-076-P1-K1-F9
Method
                   BLASTX
NCBI GI
                    g4469003
BLAST score
                    601
E value
                    8.0e-68
Match length
                   152
% identity
                    87
                    (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    146621
Seq. ID
                    LIB3168-076-P1-K1-G1
Method
                   BLASTX
NCBI GI
                    g2129657
BLAST score
                    458
E value
                    1.0e-45
Match length
                    121
                    79
% identity
NCBI Description
                   oleosin isoform - Arabidopsis thaliana
                   >gi_987014\_emb\_CAA90877\_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016\_emb\_CAA90878\_ (Z54165) oleosin
                    [Arabidopsis thaliana]
Seq. No.
                   146622
Seq. ID
                   LIB3168-076-P1-K1-G10
Method
                   BLASTX
NCBI GI
                    g1628583
BLAST score
                    625
E value
                    3.0e-65
Match length
                   120
                    100
% identity
```

NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146623

Seq. ID LIB3168-076-P1-K1-G2

Method BLASTX NCBI GI g112681 BLAST score 596 E value 6.0e-62 Match length 138 % identity 84

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146624

Seq. ID LIB3168-076-P1-K1-G3

Method BLASTX NCBI GI q112682 BLAST score 607 3.0e-63 E value Match length 142 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

146625 Seq. No.

Seq. ID LIB3168-076-P1-K1-G4

Method BLASTX NCBI GI q112682 BLAST score 737 2.0e-78 E value Match length 163

% identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis tha $\overline{\text{liana}}$  >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

146626 Seq. No.

Seq. ID LIB3168-076-P1-K1-G5

Method BLASTX NCBI GI q112739 BLAST score 516 2.0e-52 E value Match length 139 % identity

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit

2 precursor [Arabidopsis thaliana] >gi 395205\_emb\_CAA80871\_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

146627 Seq. No.

```
LIB3168-076-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  583
                  7.0e-69
E value
Match length
                  162
                  83
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146628
                  LIB3168-076-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  767
E value
                  5.0e-82
Match length
                  148
                  100
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146629
Seq. ID
                  LIB3168-076-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g1742961
BLAST score
                  236
E value
                  4.0e-20
Match length
                  87
% identity
NCBI Description
                   (X94756) cystathionine gamma-synthase [Arabidopsis
                  thaliana]
Seq. No.
                  146630
Seq. ID
                  LIB3168-076-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                  688
E value
                  1.0e-72
Match length
                  135
                  99
% identity
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  146631
Seq. ID
                  LIB3168-076-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  545
E value
                  4.0e-56
Match length
                  101
                  100
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
```

18385

æ.

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

BLAST score E value

Match length

% identity

BLAST score

Match length

% identity

```
Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  146632
                  LIB3168-076-P1-K1-H10
                  BLASTX
                  q418854
                  654
                  1.0e-68
                  136
                  17
                  ubiquitin precursor - parsley >gi 288112 emb CAA45621
NCBI Description
                  (X64344) polyubiquitin [Petroselinum crispum]
                  >gi_288114_emb_CAA45622_ (X64345) polyubiquitin
                  [Petroselinum crispum]
                  146633
                  LIB3168-076-P1-K1-H11
                  BLASTN
                  g3869062
                  46
                  1.0e-16
                  115
                  90
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K11I1, complete sequence [Arabidopsis thaliana]
                  146634
                  LIB3168-076-P1-K1-H12
                  BLASTX
                  g3335169
                  656
                  2.0e-74
                  144
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
```

Seq. No. Seq. ID Method NCBI GI BLAST score E value Match length % identity

NCBI Description >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

146635 Seq. No.

Seq. ID LIB3168-076-P1-K1-H2

Method BLASTN NCBI GI g4206762 BLAST score 243 1.0e-134 E value 363 Match length

% identity

NCBI Description Arabidopsis thaliana cell wall-plasma membrane linker

protein homolog (CWLP) mRNA, complete cds

Seq. No. 146636

Seq. ID LIB3168-076-P1-K1-H4

Method BLASTN NCBI GI g2443899

Match length

```
BLAST score
                  298
                  1.0e-167
E value
Match length
                  475
                  100
% identity
                  Arabidopsis thaliana BAC T3F12 from chromosome IV near 24
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146637
Seq. ID
                  LIB3168-076-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  572
E value
                  4.0e-59
Match length
                  140
                  79
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146638
Seq. ID
                  LIB3168-076-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  399
E value
                  5.0e-39
Match length
                  105
% identity
                  75
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146639
Seq. ID
                  LIB3168-076-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  g4159707
BLAST score
                  223
E value
                  1.0e-122
Match length
                  404
% identity
                  91
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJK13, complete sequence
Seq. No.
                  146640
Seq. ID
                  LIB3168-076-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  448
                  2.0e-44
E value
```

```
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146641
                  LIB3168-076-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1497986
BLAST score
                  347
E value
                  0.0e+00
Match length
                  434
% identity
                  99
NCBI Description
                  Arabidopsis thaliana SCARECROW (SCARECROW1) gene, complete
                  146642
Seq. No.
                  LIB3168-077-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                  574
E value
                  2.0e-59
Match length
                  129
% identity
                   (AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  146643
Seq. No.
                  LIB3168-077-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3142289
BLAST score
                  420
E value
                  3.0e-41
Match length
                  123
                   67
% identity
NCBI Description
                   (AC002411) Strong similarity to beta-keto-Coa synthase
                  gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
                  146644
Seq. No.
                  LIB3168-077-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  618
                  2.0e-64
E value
Match length
                  120
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146645
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g2129639
BLAST score
                  697
E value
                  9.0e-74
Match length
                  136
```

100 NCBI Description luminal binding protein (BiP) - Arabidopsis thaliana >gi 1303695 dbj BAA12348 (D84414) luminal binding protein (BiP) [Arabidopsis thaliana] 146646 LIB3168-077-P1-K1-A2 BLASTX g1628583 757 8.0e-81

NCBI GI BLAST score E value Match length 147 100 % identity

% identity

Seq. No. Seq. ID

Method

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146647

Seq. ID LIB3168-077-P1-K1-A3

Method BLASTX NCBI GI g1107501 BLAST score 404 E value 2.0e-39 Match length 127 % identity 65

NCBI Description (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392) Match to gb X91954 orf gene product from A. thaliana. ESTs gb\_Z17604, gb\_H76594, gb\_AA597972 and gb\_AA394824 come from this gene. [Arabidopsis thaliana]

Seq. No. 146648

LIB3168-077-P1-K1-A7 Seq. ID

Method BLASTN NCBI GI g4468103 BLAST score 240 E value 1.0e-132 Match length 385 % identity 99

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9

(ESSA project)

Seq. No. 146649

Seq. ID LIB3168-077-P1-K1-A9

Method BLASTX NCBI GI g1628583 BLAST score 385 E value 3.0e-37 Match length 72 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146650

Seq. ID LIB3168-077-P1-K1-B10

Method BLASTN NCBI GI g2864607

```
BLAST score
                  463
                  0.0e + 00
E value
                  463
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
NCBI Description
                  (ESSAII project)
Seq. No.
                  146651
Seq. ID
                  LIB3168-077-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g881615
BLAST score
                  797
E value
                  2.0e-85
Match length
                  153
                  100
% identity
                  (U29142) fatty acid elongase 1 [Arabidopsis thaliana]
NCBI Description
                  >gi 3096921_emb_CAA18831.1_ (AL023094) fatty acid elongase
                  1 [Arabidopsis thaliana]
                  146652
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  593
E value
                  2.0e-61
Match length
                  113
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146653
Seq. ID
                  LIB3168-077-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q112741
                  691
BLAST score
                  5.0e-73
E value
                  132
Match length
                  98
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  146654
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2492952
BLAST score
                  215
E value
                  3.0e-17
Match length
                  55
                  67
% identity
                  CHORISMATE SYNTHASE 1 PRECURSOR
NCBI Description
                  (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE PHOSPHOLYASE 1)
```

>gi\_542026\_pir\_\_S40410 chorismate synthase (EC 4.6.1.4) 1 precursor - tomato >gi\_410482\_emb\_CAA79859\_ (Z21796) chorismate synthase 1 [Lycopersicon esculentum]

 Seq. No.
 146655

 Seq. ID
 LIB3168-077-P1-K1-B8

 Method
 BLASTX

 NCBI GI
 q115783

 NCBI GI
 g115783

 BLAST score
 676

 E value
 3.0e-71

 Match length
 128

 % identity
 99

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 146656

Seq. ID LIB3168-077-P1-K1-C10

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146657

Seq. ID LIB3168-077-P1-K1-C11

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146658

Seq. ID LIB3168-077-P1-K1-C12

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 3.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146659

Seq. ID LIB3168-077-P1-K1-C2

Method BLASTX NCBI GI g4204260



BLAST score 257 E value 3.0e-22 Match length 59 % identity 86

NCBI Description (AC005223) 25568 [Arabidopsis thaliana]

Seq. No.

146660

Seq. ID LIB3168-077-P1-K1-C3

Method BLASTX
NCBI GI g112681
BLAST score 655
E value 8.0e-69
Match length 150
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. Seq. ID

146661

LIB3168-077-P1-K1-C4

Method BLASTN
NCBI GI g4191760
BLAST score 221
E value 1.0e-121
Match length 425
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17F8,

complete sequence [Arabidopsis thaliana]

Seq. No. 146662

Seq. ID LIB3168-077-P1-K1-C6

Method BLASTN
NCBI GI g3133272
BLAST score 35
E value 4.0e-10
Match length 43
% identity 95

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T17H7,

complete sequence [Arabidopsis thaliana]

Seq. No. 146663

Seq. ID LIB3168-077-P1-K1-D10

Method BLASTX
NCBI GI g112681
BLAST score 668
E value 2.0e-70
Match length 150
% identity 86

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi\_808936\_emb\_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146664

```
LIB3168-077-P1-K1-D11
Seq. ID
                  BLASTN
Method
NCBI GI
                   g3540210
BLAST score
                   350
                   0.0e + 00
E value
                   389
Match length
                   98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F5A8 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146665
                  LIB3168-077-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3335171
BLAST score
                   605
E value
                   6.0e-63
Match length
                  141
% identity
NCBI Description
                   (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
                   146666
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-D2
Method
                  BLASTX
NCBI GI
                   q1628583
BLAST score
                   625
E value
                   3.0e-65
Match length
                   120
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146667
Seq. ID
                  LIB3168-077-P1-K1-D3
Method
                  BLASTX
NCBI GI
                   q112682
BLAST score
                  650
E value
                   3.0e-68
Match length
                  148
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
                   cruciferin precursor (CRB) - Arabidopsīs thalīanā
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                  146668
Seq. ID
                  LIB3168-077-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  816
E value
                  1.0e-87
Match length
                  155
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

cruciferin seed storage protein [Arabidopsis thaliana]

```
146669
Seq. No.
                  LIB3168-077-P1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
                  739
BLAST score
                  1.0e-78
E value
Match length
                  154
                  93
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146670
                  LIB3168-077-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  624
E value
                  3.0e-65
Match length
                  146
% identity
                  82
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146671
Seq. ID
                  LIB3168-077-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2894562
BLAST score
                  216
E value
                  2.0e-17
Match length
                  39
% identity
NCBI Description
                  (AL021890) putative protein [Arabidopsis thaliana]
                  146672
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  3.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146673
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  653
E value
                  1.0e-68
```

```
156
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146674
Seq. No.
                  LIB3168-077-P1-K1-E10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g166610
BLAST score
                  34
                  6.0e-10
E value
Match length
                  94
% identity
                  84
                  A.thaliana at 2S2 gene encoding albumin 2S subunit 2,
NCBI Description
                  complete cds
Seq. No.
                  146675
Seq. ID
                  LIB3168-077-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  62
E value
                  6.0e-55
Match length
                  119
% identity
                  86
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146676
                  LIB3168-077-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  662
```

E value 1.0e-69 Match length 146 % identity 87

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146677

Seq. ID LIB3168-077-P1-K1-E2

Method BLASTX NCBI GI g3337356 BLAST score 597 E value 5.0e-62 Match length 118 % identity 99

NCBI Description (AC004481) putative protein transport protein SEC61 alpha

subunit [Arabidopsis thaliana]

Seq. No. 146678

LIB3168-077-P1-K1-E3 Seq. ID

Method BLASTN

```
g4691223
NCBI GI
BLAST score
                  407
E value
                  0.0e + 00
Match length
                  441
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
NCBI Description
                   (ESSA project)
Seq. No.
                  146679
                  LIB3168-077-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  120
BLAST score
                   7.0e-23
E value
Match length
                  85
                  87
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                   146680
Seq. No.
                  LIB3168-077-P1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2264321
BLAST score
                   328
                   0.0e + 00
E value
                   472
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXM12, complete sequence [Arabidopsis thaliana]
                   146681
Seq. No.
                   LIB3168-077-P1-K1-E8
Seq. ID
Method
                   BLASTX
                   q3860247
NCBI GI
BLAST score
                   659
E value
                   3.0e-69
Match length
                   131
% identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   146682
Seq. No.
                   LIB3168-077-P1-K1-E9
Seq. ID
                   BLASTN
Method
NCBI GI
                   q166610
                   127
BLAST score
                   4.0e-65
E value
Match length
                   269
                   90
% identity
                   A.thaliana at2S2 gene encoding albumin 2S subunit 2,
NCBI Description
                   complete cds
                   146683
Seq. No.
                   LIB3168-077-P1-K1-F1
Seq. ID
                   BLASTX
Method
                   g112682
NCBI GI
```

BLAST score

- (

```
3.0e-76
E value
Match length
                  149
                  92
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir_ $08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146684
                  LIB3168-077-P1-K1-F10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g136739
BLAST score
                  459
                  8.0e-46
E value
Match length
                  142
% identity
                  65
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi_67061_pir__XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi 218001 dbj BAA00570 (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  146685
Seq. ID
                  LIB3168-077-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  3.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146686
Seq. ID
                  LIB3168-077-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q4539005
BLAST score
                  348
E value
                  8.0e-33
Match length
                  149
% identity
NCBI Description
                  (AL049481) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  146687
Seq. ID
                  LIB3168-077-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  282
E value
                  6.0e-36
Match length
                  82
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

cruciferin seed storage protein [Arabidopsis thaliana]

```
146688
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4325282
BLAST score
                  306
E value
                  7.0e-28
Match length
                  59
% identity
                  93
NCBI Description
                  (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
                  >gi 4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                  [Arabidopsis thaliana]
                  146689
Seq. No.
                  LIB3168-077-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  655
                  8.0e-69
E value
Match length
                  149
                  83
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  tha\overline{\text{liana}} >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146690
Seq. ID
                  LIB3168-077-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  691
E value
                  5.0e-73
Match length
                  139
% identity
                  94
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146691
                  LIB3168-077-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  459
E value
                  7.0e-46
Match length
                  147
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir $08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146692
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-F8
Method
                  BLASTX
```

```
NCBI GI
                   q267073
BLAST score
                  638
E value
                   7.0e-67
Match length
                  117
                   100
% identity
                  TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir__JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi_1\overline{1}668\overline{98} (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  146693
                  LIB3168-077-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  a1628583
BLAST score
                  642
E value
                   3.0e-67
Match length
                  123
% identity
                   100
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146694
                  LIB3168-077-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  265
E value
                   3.0e-42
Match length
                  126
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir_ S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146695
                  LIB3168-077-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2392769
BLAST score
                   272
E value
                   6.0e-24
                  100
Match length
% identity
                   50
                   (AC002534) putative histone deacetylase [Arabidopsis
NCBI Description
                   thaliana]
                   146696
Seq. No.
                  LIB3168-077-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  620
E value
                   9.0e-65
Match length
                  119
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
```



## cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146697 Seq. ID LIB3168-077-P1-K1-G2 Method BLASTX NCBI GI g112681 BLAST score 737 2.0e-78 E value 139 Match length 99 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana

146698

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. Seq. ID

LIB3168-077-P1-K1-G3

Method BLASTN
NCBI GI g4584841
BLAST score 30
E value 4.0e-07
Match length 476
% identity 45

NCBI Description Genomic sequence for Arabidopsis thaliana BAC T23E23,

complete sequence

Seq. No. 146699

Seq. ID LIB3168-077-P1-K1-G4

Method BLASTX
NCBI GI g404690
BLAST score 219
E value 1.0e-17
Match length 89
% identity 45

NCBI Description (L19075) cytochrome P450 [Catharanthus roseus]

Seq. No. 146700

Seq. ID LIB3168-077-P1-K1-G5

Method BLASTX
NCBI GI g3157931
BLAST score 276
E value 2.0e-45
Match length 96
% identity 99

NCBI Description (AC002131) Similar to pyrophosphate-dependent

phosphofuctokinase beta subunit gb\_Z32850 from Ricinus communis. ESTs gb\_N65773, gb\_N64925 and gb\_F15232 come

from this gene. [Arabidopsis thaliana]

Seq. No. 146701

Seq. ID LIB3168-077-P1-K1-G7

Method BLASTX
NCBI GI g112741
BLAST score 771
E value 2.0e-82
Match length 144

```
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1_{-} (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  146702
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q136739
BLAST score
                  453
E value
                  4.0e-45
Match length
                  142
% identity
                  64
                  UTP--GLUCOSE-1-PHOSPHATE URIDYLYLTRANSFERASE (UDP-GLUCOSE
NCBI Description
                  PYROPHOSPHORYLASE) (UDPGP) >gi 67061 pir XNPOU
                  UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) -
                  potato >gi_218001_dbj_BAA00570_ (D00667) UDP-glucose
                  pyrophosphorylase precursor [Solanum tuberosum]
Seq. No.
                  146703
Seq. ID
                  LIB3168-077-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q3747050
BLAST score
                  326
E value
                  3.0e-30
Match length
                  69
% identity
NCBI Description
                  (AF093540) ribosomal protein L26 [Zea mays]
Seq. No.
                  146704
Seq. ID
                  LIB3168-077-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  615
E value
                  4.0e-64
Match length
                  138
% identity
                  86
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146705
                  LIB3168-077-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170503
BLAST score
                  622
E value
                  4.0e-65
Match length
                  124
% identity
                  98
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
NCBI Description
```

>gi\_322503\_pir\_\_JC1452 translation initiation factor

```
eIF-4A1 - Arabidopsis thaliana >qi 16554 emb CAA46188
                  (X65052) eukaryotic translation initiation factor 4A-1
                  [Arabidopsis thaliana]
                  146706
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2605714
               489
BLAST score
                  2.0e-49
E value
Match length
                  115
                  83
% identity
                  (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
NCBI Description
                  thalianal
                  146707
Seq. No.
                  LIB3168-077-P1-K1-H2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2114077
BLAST score
                  160
E value
                  1.0e-84
Match length
                  419
% identity
                  95
                  Arabidopsis thaliana DNA for larger subunit of Rubisco,
NCBI Description
                  beta subunit of coupling factor one, partial cds
Seq. No.
                  146708
Seq. ID
                  LIB3168-077-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  523
E value
                  1.0e-53
Match length
                  102
% identity
                  99
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146709
Seq. ID
                  LIB3168-077-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g2129659
BLAST score
                  412
                  2.0e-40
E value
                  129
Match length
                  69
% identity
NCBI Description
                  oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
                  (L40954) oleosin [Arabidopsis thaliana]
Seq. No.
                  146710
                  LIB3168-077-P1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4220633
BLAST score
                  117
                  6.0e-59
E value
Match length
                  197
% identity
                  95
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K7J8, complete sequence [Arabidopsis thaliana]
                  146711
Seq. No.
Seq. ID
                  LIB3168-077-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1561730
BLAST score
                  153
E value
                  6.0e-10
Match length
                  58
                  47
% identity
                  (U65491) Dreg-3 protein [Drosophila melanogaster]
NCBI Description
Seq. No.
                  146712
                  LIB3168-077-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2605714
BLAST score
                  185
E value
                  1.0e-49
Match length
                  125
% identity
NCBI Description
                  (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                  thaliana]
Seq. No.
                  146713
                  LIB3168-078-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2959729
                  399
BLAST score
E value
                  0.0e+00
Match length
                  418
                  99
% identity
                  Arabidopsis thaliana mRNA for GATA transcription factor
NCBI Description
Seq. No.
                  146714
                  LIB3168-078-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  413
E value
                  2.0e-40
Match length
                  92
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146715
                  LIB3168-078-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  283
E value
                  2.0e-25
Match length
                  54
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

```
146716
Seq. No.
Seq. ID
                   LIB3168-078-P1-K1-A2
Method
                   BLASTN
NCBI GI
                   g16231
BLAST score
                   159
                    2.0e-84
E value
Match length
                   183
% identity
                    97
NCBI Description
                   Arabidopsis CRA1 gene for 12S seed storage protein
                   >qi 166675 gb M37247 ATHCRA1AA A.thaliana 12S storage
                   protein CRA1 gene, exons 1-4
Seq. No.
                   146717
Seq. ID
                   LIB3168-078-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   775
E value
                   7.0e-83
Match length
                   152
% identity
                    97
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146718
Seq. ID
                   LIB3168-078-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   g112740
BLAST score
                   269
E value
                    1.0e-23
Match length
                   117
% identity
                    52
NCBI Description
                   NAPIN 2 PRECURSOR (1.7S SEED STORAGE PROTEIN)
                   >gi_81691_pir__A25997 napin precursor (napA) - rape
                   >gi 16715\overline{3} (J\overline{02}586) prepronapin [Brassica napus] >gi 167155
                    (J02798) napin [Brassica napus]
Seq. No.
                   146719
Seq. ID
                   LIB3168-078-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   760
E value
                    4.0e-81
Match length
                   151
% identity
NCBI Description
                    (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146720
Seq. No.
Seq. ID
                   LIB3168-078-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   424
```

9.0e-42 E value Match length 96 % identity 88 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi\_2842495 emb CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146721 Seq. ID LIB3168-078-P1-K1-A7 Method BLASTX NCBI GI q112682 BLAST score 636 E value 1.0e-66 Match length 146 % identity 82 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 146722 Seq. ID LIB3168-078-P1-K1-A8 Method BLASTX NCBI GI q2129657 BLAST score 50 E value 5.0e-53 Match length 142 % identity 82 NCBI Description oleosin isoform - Arabidopsis thaliana >gi\_987014\_emb\_CAA90877\_ (Z54164) oleosin [Arabidopsis
thaliana] >gi\_987016\_emb\_CAA90878\_ (Z54165) oleosin [Arabidopsis thaliana] Seq. No. 146723 LIB3168-078-P1-K1-A9 Seq. ID Method BLASTX NCBI GI g112681 BLAST score 696 E value 1.0e-73 Match length 156 % identity 87 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir\_ S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 146724

Seq. ID LIB3168-078-P1-K1-B1

Method BLASTX NCBI GI g2129657 BLAST score 454 E value 3.0e-45 Match length 120 79 % identity

NCBI Description oleosin isoform - Arabidopsis thaliana

```
>gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                   [Arabidopsis thaliana]
Seq. No.
                   146725
                   LIB3168-078-P1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   4.65
E value
                   1.0e-46
Match length
                   91
                   97
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146726
Seq. No.
                   LIB3168-078-P1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   522
                   3.0e-53
E value
Match length
                   112
% identity
                   91
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146727
Seq. No.
Seq. ID
                   LIB3168-078-P1-K1-B12
Method
                   BLASTN
NCBI GI
                   g2924729
BLAST score
                   330
                   0.0e+00
E value
Match length
                   341
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNA5, complete sequence [Arabidopsis thaliana]
                   146728
Seq. No.
Seq. ID
                   LIB3168-078-P1-K1-B2
Method
                   BLASTX
NCBI GI
                   g4204299
BLAST score
                   625
E value
                   2.0e-65
Match length
                   125
% identity
                   95
                   (ACO03027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   146729
Seq. ID
                   LIB3168-078-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   589
E value
                   4.0e-61
Match length
                   151
```

```
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146730
Seq. ID
                  LIB3168-078-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  536
E value
                  6.0e-55
Match length
                  120
% identity
                  87
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146731
Seq. ID
                  LIB3168-078-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  543
E value
                  1.0e-55
Match length
                  132
% identity
                  81
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146732
Seq. ID
                  LIB3168-078-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  589
E value
                  5.0e-61
                  120
Match length
% identity
                  95
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146733
Seq. ID
                  LIB3168-078-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  549
E value
                  2.0e-56
Match length
                  103
```

100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146734

Seq. ID LIB3168-078-P1-K1-B9

```
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  628
                  1.0e-65
E value
                  123
Match length
% identity
                  98
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146735
Seq. No.
                  LIB3168-078-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2735841
BLAST score
                  157
E value
                  1.0e-10
                  73
Match length
% identity
                  49
NCBI Description (AF010283) No definition line found [Sorghum bicolor]
Seq. No.
                  146736
Seq. ID
                  LIB3168-078-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q4510397
BLAST score
                  629
E value
                  9.0e-66
Match length
                  138
% identity
                  87
NCBI Description (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
Seq. No.
                  146737
                  LIB3168-078-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3184281
BLAST score
                  388
E value
                  1.0e-37
Match length
                  120
% identity
                  (AC004136) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  146738
                  LIB3168-078-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  665
E value
                  5.0e-70
Match length
                  150
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
```

Seq. No. 146739

Seq. ID LIB3168-078-P1-K1-C4

Method BLASTX

```
NCBI GI
                  q1628583
BLAST score
                  573
E value
                  2.0e-59
Match length
                  117
                  94
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146740
                  LIB3168-078-P1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3402745
BLAST score
                  64
E value
                  2.0e-27
Match length
                  289
                  85
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5
                  (ESSAII project)
                  146741
Seq. No.
Seq. ID
                  LIB3168-078-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  570
E value
                  5.0e-59
Match length
                  109
                  96
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146742
Seq. ID
                  LIB3168-078-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  558
E value
                  2.0e-57
Match length
                  123
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146743
Seq. ID
                  LIB3168-078-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q2129767
BLAST score
                  631
                  4.0e-66
E value
Match length
                  130
% identity
NCBI Description
                  vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
```

NCBI GI

BLAST score

```
precursor - Arabidopsis thaliana >gi 1805364 dbj BAA09615
                  (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3168-078-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  746
E value
                  2.0e-79
Match length
                  143
% identity
                  99
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146745
Seq. No.
                  LIB3168-078-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  616
                  3.0e-64
E value
Match length
                  125
% identity
                  94
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146746
Seq. No.
Seq. ID
                  LIB3168-078-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  q2244747
BLAST score
                  39
E value
                  6.0e-13
Match length
                  122
% identity
                  82
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  146747
Seq. ID
                  LIB3168-078-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1173103
BLAST score
                  569
E value
                  9.0e-59
Match length
                  98
% identity
NCBI Description
                  RIBONUCLEASE 1 PRECURSOR >gi 561998 (U05206) ribonuclease
                   [Arabidopsis thaliana] >gi_3461823 (AC004138) ribonuclease,
                  RNS1 [Arabidopsis thaliana]
Seq. No.
                  146748
Seq. ID
                  LIB3168-078-P1-K1-D2
Method
                  BLASTN
```

g1628582

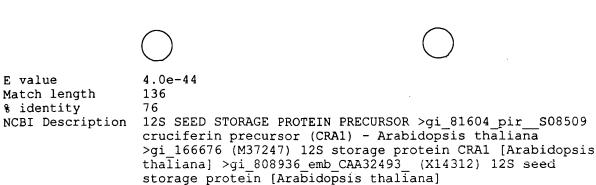
```
5.0e - 34
E value
Match length
                  202
                  91
% identity
                  Arabidopsis thaliana 12S cruciferin seed storage protein
NCBI Description
                  (ATCRU3) gene, complete cds
Seq. No.
                  146749
Seq. ID
                  LIB3168-078-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q2842474
BLAST score
                  18
E value
                  1.6e+00
                  93
Match length
% identity
                  90
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                  (ESSAII project)
                  146750
Seq. No.
Seq. ID
                  LIB3168-078-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2583125
BLAST score
                  582
E value
                  2.0e-60
Match length
                  128
% identity
                  (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  146751
Seq. ID
                  LIB3168-078-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g112737
                  593
BLAST score
                  2.0e-61
E value
Match length
                  141
                  79
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146752
Seq. ID
                  LIB3168-078-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  512
E value
                  4.0e-52
                  127
Match length
% identity
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
```

[Arabidopsis thaliana]

>gi\_987014\_emb\_CAA90877\_ (Z54164) oleosin [Arabidopsis
thaliana] >gi\_987016\_emb\_CAA90878\_ (Z54165) oleosin

```
146753
Seq. No.
Seq. ID
                  LIB3168-078-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  630
                  5.0e-66
E value
Match length
                  123
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146754
Seq. No.
                  LIB3168-078-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  a1628583
                  618
BLAST score
                  1.0e-64
E value
                  123
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146755
Seq. ID
                  LIB3168-078-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q112741
                  645
BLAST score
E value
                  1.0e-67
Match length
                  119
% identity
                  100
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  146756
Seq. No.
Seq. ID
                  LIB3168-078-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q1628583
                   608
BLAST score
                   3.0e-63
E value
Match length
                  123
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146757
                  LIB3168-078-P1-K1-E2
Seq. ID
Method
                  BLASTX
                  q112681
NCBI GI
```

BLAST score



Seq. No. 146758 LIB3168-078-P1-K1-E3

Seq. ID BLASTX Method NCBI GI q112737 BLAST score 490 3.0e-54 E value Match length 124 82

NCBI Description

% identity

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

146759 Seq. No.

Seq. ID LIB3168-078-P1-K1-E4

Method BLASTX NCBI GI q112682 597 BLAST score 4.0e-62 E value Match length 138

82 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB (Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146760

LIB3168-078-P1-K1-E5 Seq. ID

Method BLASTX g1628583 NCBI GI BLAST score 558 2.0e-59 E value 175 Match length % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146761

LIB3168-078-P1-K1-E6 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 580 E value 5.0e-60

```
123
Match length
% identity
                   90
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146762
Seq. ID
                  LIB3168-078-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q2497543
BLAST score
                  184
E value
                   1.0e-13
Match length
                   59
% identity
                   64
                  PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi 542061 pir S41379
NCBI Description
                  pyruvate kinase - common tobacco >gi 444023 emb CAA82628
                   (Z29492) pyruvate kinase [Nicotiana tabacum]
                  146763
Seq. No.
Seq. ID
                  LIB3168-078-P1-K1-E8
Method
                  BLASTX
NCBI GI
                   g1628583
BLAST score
                   66
E value
                   2.0e-57
                   137
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146764
                   LIB3168-078-P1-K1-E9
Seq. ID
Method
                   BLASTN
                   q4006885
NCBI GI
                   289
BLAST score
E value
                   1.0e-161
Match length
                   425
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
Seq. No.
                   146765
                   LIB3168-078-P1-K1-F1
Seq. ID
Method
                   BLASTX
                   q4204299
NCBI GI
                   481
BLAST score
E value
                   1.0e-48
Match length
                   99
                   95
% identity
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   146766
                   LIB3168-078-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   420
```

Seq. ID

```
3.0e-41
E value
Match length
                   114
                   75
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146767
Seq. ID
                   LIB3168-078-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q112737
BLAST score
                   663
E value
                   1.0e-69
Match length
                   140
                   89
% identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
Seq. No.
                   146768
Seq. ID
                   LIB3168-078-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q1113941
BLAST score
                   97
E value
                   2.0e-03
Match length
                   77
% identity
NCBI Description
                   (U40713) Pv42p [Phaseolus vulgaris]
                   146769
Seq. No.
Seq. ID
                   LIB3168-078-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q4406773
BLAST score
                   397
E value
                   2.0e-50
Match length
                   137
% identity
                   49
NCBI Description
                   (AC006836) putative cell division control protein 48
                   [Arabidopsis thaliana]
Seq. No.
                   146770
Seq. ID
                   LIB3168-078-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q2815905
BLAST score
                   184
E value
                   8.0e-14
Match length
                   72
% identity
                   (AF043734) Pros45 proteosome subunit homolog [Drosophila
NCBI Description
                   melanogaster]
Seq. No.
                   146771
```

LIB3168-078-P1-K1-F6

```
Method
                  BLASTN
NCBI GI
                  a4191771
BLAST score
                  383
E value
                  0.0e + 00
Match length
                  467
% identity
                  Arabidopsis thaliana chromosome II BAC F3P11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146772
Seq. ID
                  LIB3168-078-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  506
E value
                  2.0e-51
Match length
                  107
                  92
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146773
Seq. No.
                  LIB3168-078-P1-K1-F8
Seq. ID
Method
                  BLASTX
                  g112681
NCBI GI
BLAST score
                  549
E value
                  2.0e-56
Match length
                  129
                  83
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146774
Seq. No.
Seq. ID
                  LIB3168-078-P1-K1-F9
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  559
E value
                  9.0e-58
Match length
                  112
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146775
                  LIB3168-078-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g21911
BLAST score
                  154
E value
                  4.0e-10
Match length
                  66
% identity
                  42
NCBI Description (X62625) vicilin [Theobroma cacao]
```

```
Seq. No.
                   146776
 Seq. ID
                   LIB3168-078-P1-K1-G10
 Method
                   BLASTN
 NCBI GI
                   g3461810
 BLAST score
                   237
 E value
                   1.0e-130
Match length
                   352
 % identity
                   97
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T17M13 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   146777
Seq. ID
                   LIB3168-078-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g112741
BLAST score
                   616
E value
                   2.0e-64
Match length
                   118
% identity
                   97
NCBI Description
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi 68855_pir__NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi_4490712_emb CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
Seq. No.
                   146778
Seq. ID
                   LIB3168-078-P1-K1-G12
Method
                  BLASTX
NCBI GI
                   g3176874
BLAST score
                   805
E value
                   2.0e-86
Match length
                   160
% identity
                   96
NCBI Description
                   (AF065639) cucumisin-like serine protease [Arabidopsis
                  thaliana]
Seq. No.
                  146779
Seq. ID
                  LIB3168-078-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g4773906
BLAST score
                  507
E value
                  2.0e-51
Match length
                  109
% identity
                  89
NCBI Description
                  (AF074021) putative symbiosis-related protein [Arabidopsis
                  thaliana]
Seq. No.
                  146780
Seq. ID
                  LIB3168-078-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q128859
BLAST score
                  739
E value
                  1.0e-78
Match length
                  154
% identity
                  88
```

```
NADH-PLASTOQUINONE OXIDOREDUCTASE SUBUNIT J (ORF 158)
NCBI Description
                  >gi_82206_pir__A05194 hypothetical protein 158 - common
                  tobacco chloroplast >gi_11836 emb CAA77356 (Z00044) NADH
                  dehydrogenase 30kD subunit [Nicotiana tabacum]
                  >gi 225204 prf 1211235AJ ORF 158 [Nicotiana tabacum]
Seq. No.
                  146781
                  LIB3168-078-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  634
E value
                  2.0e-66
Match length
                  142
% identity
                  90
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146782
                  LIB3168-078-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  613
E value
                  6.0e-64
Match length
                  130
% identity
                  88
NCBI Description
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi_395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >qi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146783
                  LIB3168-078-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3980378
BLAST score
                  473
                  4.0e-59
E value
Match length
                  113
% identity
                  (AC004561) putative RNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
                  146784
```

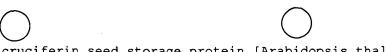
Seq. No.

LIB3168-078-P1-K1-H1 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 630 E value 6.0e-66 Match length 142 % identity 87

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S



## cruciferin seed storage protein [Arabidopsis thaliana]

146785 Seq. No. Seq. ID LIB3168-078-P1-K1-H10 Method BLASTN NCBI GI g4220510 BLAST score 171 3.0e-91 E value 340 Match length 100 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18

(ESSAII project)

Seq. No. 146786

Seq. ID LIB3168-078-P1-K1-H11

Method BLASTX
NCBI GI g112737
BLAST score 348
E value 5.0e-33
Match length 96
% identity 73

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 146787

Seq. ID LIB3168-078-P1-K1-H2

Method BLASTX
NCBI GI g3434971
BLAST score 305
E value 7.0e-28
Match length 102
% identity 63

NCBI Description (AB008105) ethylene responsive element binding factor 3

[Arabidopsis thaliana]

Seq. No. 146788

Seq. ID LIB3168-078-P1-K1-H3

Method BLASTX
NCBI GI g3927831
BLAST score 630
E value 5.0e-66
Match length 124
% identity 55

NCBI Description (AC005727) similar to mouse ankyrin 3 [Arabidopsis

thaliana]

Seq. No. 146789

Seq. ID LIB3168-078-P1-K1-H4

Method BLASTX
NCBI GI g1628583
BLAST score 782
E value 1.0e-83

NCBI GI

q112682

```
Match length
                  158
% identity
                  97
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146790
Seq. ID
                  LIB3168-078-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  660
E value
                  2.0e-69
Match length
                  126
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146791
Seq. ID
                  LIB3168-078-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  574
E value
                  2.0e-59
Match length
                  117
% identity
                  94
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146792
                  LIB3168-078-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  600
E value
                  2.0e-62
Match length
                  123
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146793
                  LIB3168-078-P1-K1-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757405
BLAST score
                  314
E value
                  1.0e-176
Match length
                  375
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOJ10, complete sequence
Seq. No.
                  146794
                  LIB3168-078-P1-K1-H9
Seq. ID
Method
                  BLASTX
```

BLAST score

```
BLAST score
                  555
                  3.0e-57
E value
                  118
Match length
                  88
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937_emb CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146795
                  LIB3168-079-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  353
                  2.0e-33
E value
                  75
Match length
% identity
                  87
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  146796
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-A11
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  597
                  4.0e-62
E value
Match length
                  122
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146797
                  LIB3168-079-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  q112681
NCBI GI
                  534
BLAST score
                  1.0e-54
E value
Match length
                  141
                  77
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146798
                  LIB3168-079-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112739
```

1.0e-42 E value Match length 131 % identity 68 NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi\_4490711\_emb\_CAB38845.1\_ (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana] Seq. No. 146799 LIB3168-079-P1-K1-A6 Seq. ID Method BLASTX NCBI GI q112682 BLAST score 578 7.0e-60 E value 135 Match length 81 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605\_pir\_\_S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed storage protein [Arabidopsis thaliana] 146800 Seq. No. Seq. ID LIB3168-079-P1-K1-A7 BLASTN Method q2894557 NCBI GI 331 BLAST score 0.0e+00E value Match length 343 % identity 99 Arabidopsis thaliana DNA chromosome 4, BAC clone T805 NCBI Description (ESSAII project) Seq. No. 146801 LIB3168-079-P1-K1-A8 Seq. ID Method BLASTX g112681 NCBI GI BLAST score 574 E value 2.0e-59 Match length 134 % identity 84 NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed storage protein [Arabidopsis thaliana] 146802 Seq. No.

Seq. ID LIB3168-079-P1-K1-A9

Method BLASTX
NCBI GI g1402904
BLAST score 682
E value 5.0e-72
Match length 131

```
% identity
                  (X98313) peroxidase [Arabidopsis thaliana]
NCBI Description
                  146803
Seq. No.
                  LIB3168-079-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  595
E value
                  8.0e-62
Match length
                  139
                  83
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146804
Seq. No.
                  LIB3168-079-P1-K1-B10
Seq. ID
Method
                  BLASTX
                  g112682
NCBI GI
                  565
BLAST score
E value
                  5.0e-61
                  135
Match length
                  89
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  tha\overline{1}iana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146805
Seq. No.
                  LIB3168-079-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1628583
BLAST score
                   597
                   4.0e-62
E value
Match length
                  114
% identity
                   100
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   146806
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q112681
BLAST score
                   511
E value
                   5.0e-52
Match length
                   144
                   76
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                  LIB3168-079-P1-K1-B2
Seq. ID
```

```
BLASTN
Method
NCBI GI
                  g2842474
BLAST score
                  24
                  1.0e-03
E value
                  367
Match length
                  74
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                   (ESSAII project)
Seq. No.
                  146808
                  LIB3168-079-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  39
E value
                  3.0e-13
Match length
                  98
                  85
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                   (ESSAII project)
                  146809
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  526
E value
                  1.0e-53
Match length
                  134
                  77
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146810
Seq. ID
                  LIB3168-079-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q2760165
BLAST score
                  319
E value
                  1.0e-179
Match length
                  393
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146811
Seq. ID
                  LIB3168-079-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  590
E value
                  3.0e-61
Match length
                  120
% identity
                  95
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146812 Seq. ID LIB3168-079-P1-K1-B7 Method BLASTX NCBI GI q1628583 BLAST score 736 E value 2.0e-78 Match length 147 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 146813 Seq. No. LIB3168-079-P1-K1-B8 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 103 E value 5.0e-58 Match length 119 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146814 Seq. ID LIB3168-079-P1-K1-C1 Method BLASTX NCBI GI g2285885 BLAST score 682 E value 5.0e-72 Match length 147 95 % identity NCBI Description (D89631) sulfate transporter [Arabidopsis thaliana] Seq. No. 146815 Seq. ID LIB3168-079-P1-K1-C10 Method BLASTX g1628583 NCBI GI BLAST score 585 E value 1.0e-60 Match length 111 100 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 146816 Seq. No. LIB3168-079-P1-K1-C11 Seq. ID BLASTX Method NCBI GI q112682 BLAST score 684 E value 3.0e-72

Match length 141 % identity 91

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_\$08510

cruciferin precursor (CRB) - Arabidopsis thaliana >gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 146817

Seq. ID LIB3168-079-P1-K1-C12

Method BLASTX
NCBI GI g112682
BLAST score 621
E value 6.0e-65
Match length 130
% identity 89

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146818

Seq. ID LIB3168-079-P1-K1-C2

Method BLASTX
NCBI GI g1628583
BLAST score 578
E value 6.0e-60
Match length 123
% identity 88

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146819

Seq. ID LIB3168-079-P1-K1-C3

Method BLASTX
NCBI GI g1628583
BLAST score 474
E value 1.0e-47
Match length 138

Match length 138 % identity 73

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146820

Seq. ID LIB3168-079-P1-K1-C5

Method BLASTX
NCBI GI g1628583
BLAST score 538
E value 3.0e-58
Match length 120
% identity 89

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146821

Seq. ID LIB3168-079-P1-K1-C6

```
Method
                  BLASTX
NCBI GI
                  g3236242
BLAST score
                  491
E value
                  1.0e-49
Match length
                  111
% identity
NCBI Description
                  (AC004684) putative ribosomal protein L36 [Arabidopsis
Seq. No.
                  146822
Seq. ID
                  LIB3168-079-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  681
                  7.0e-72
E value
Match length
                  146
% identity
                  94
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146823
                  LIB3168-079-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  175
E value
                  6.0e-13
Match length
                  69
                  58
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146824
                  LIB3168-079-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3935151
BLAST score
                  678
E value
                  1.0e-71
Match length
                  127
% identity
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
NCBI Description
                  146825
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g3367500
BLAST score
                  81
E value
                  3.0e-38
Match length
                  97
% identity
                  96
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
```

TO: 93489, complete sequence [Arabidopsis thaliana]

```
146826
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  565
E value
                  3.0e-58
Match length
                  108
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146827
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g58298
BLAST score
                  47
E value
                  9.0e-18
Match length
                  96
                  84
% identity
                  Synthetic DNA for A.thaliana ats1A leader spliced to
NCBI Description
                  B.thuringiensis CryIA(c)
                  146828
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g484640
BLAST score
                  169
                  5.0e-12
E value
Match length
                  31
                  97
% identity
NCBI Description 2S albumin, AT2S5 - Arabidopsis thaliana (fragment)
                  146829
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  88
                  4.0e-42
E value
Match length
                  106
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146830
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  539
                  2.0e-55
E value
Match length
                  101
                  99
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
```

3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi\_4490712\_emb\_CAB38846.1\_(AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

146831
LIB3168-079-P1-K1-D6
BLASTX

Method BLASTX
NCBI GI g1628583
BLAST score 165
E value 5.0e-12
Match length 35
% identity 91

Seq. No.

Seq. ID

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146832

Seq. ID LIB3168-079-P1-K1-D7

Method BLASTX
NCBI GI 9477819
BLAST score 216
E value 9.0e-18
Match length 55
% identity 76

NCBI Description mitochondrial processing peptidase (EC 3.4.99.41) beta

chain precursor - potato >gi\_410634\_bbs\_136741 cytochrome c reductase-processing peptidase subunit II, MPP subunit II, P53 [potatoes, var. Marfona, tuber, Peptide Mitochondrial,

530 aa]

Seq. No. 146833

Seq. ID LIB3168-079-P1-K1-D8

Method BLASTX
NCBI GI g112681
BLAST score 565
E value 2.0e-58
Match length 122
% identity 89

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146834

Seq. ID LIB3168-079-P1-K1-D9

Method BLASTX
NCBI GI g112682
BLAST score 625
E value 2.0e-65
Match length 143
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed



## storage protein [Arabidopsis thaliana]

Seq. No. 146835 Seq. ID LIB3168-079-P1-K1-E10 Method BLASTX NCBI GI g3873913 BLAST score 183 E value 1.0e-13 Match length 114 % identity 37 NCBI Description (Z71258) similar to Flavin-binding monooxygenase-like [Caenorhabditis elegans] Seq. No. 146836 Seq. ID LIB3168-079-P1-K1-E11 Method BLASTX NCBI GI g135858 BLAST score 292 2.0e-26 E value 57 Match length 100 % identity NCBI Description TONOPLAST INTRINSIC PROTEIN, ALPHA (ALPHA TIP) >qi 99760 pir S22201 tonoplast intrinsic protein alpha -Arabidopsis thaliana >gi 16182 emb CAA45114 (X63551) tonoplast intrinsic protein: alpha-TIP(Ara) [Arabidopsis thaliana] >gi\_166623 (M84343) tonoplast intrinsic protein [Arabidopsis thaliana] >gi\_445128\_prf\_\_1908432A tonoplast intrinsic protein alpha [Arabidopsis thaliana] Seq. No. 146837 LIB3168-079-P1-K1-E2 Seq. ID Method BLASTN NCBI GI q1628582 BLAST score 29 1.0e-06 E value 282 Match length % identity 60 NCBI Description Arabidopsis thaliana 12S cruciferin seed storage protein (ATCRU3) gene, complete cds Seq. No. 146838 Seq. ID LIB3168-079-P1-K1-E3 Method BLASTN NCBI GI q557693 BLAST score 264 1.0e-147 E value Match length 316

Seq. No. 146839

% identity

NCBI Description

Seq. ID LIB3168-079-P1-K1-E5

Method BLASTX
NCBI GI g82051
BLAST score 130
E value 3.0e-26

subunit (AGB1) mRNA, complete cds

Arabidopsis thaliana Columbia GTP binding protein beta

Seq. No.

146844

```
Match length
                  120
% identity
                  47
NCBI Description
                  lipid body-associated membrane protein - carrot
                  >gi 259453 bbs_117620 (S47635) lipid body membrane
                  protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                  180 aa] [Daucus carota]
Seq. No.
                  146840
Seq. ID
                  LIB3168-079-P1-K1-E6
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  497
E value
                  2.0e-50
Match length
                  137
                  74
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146841
Seq. ID
                  LIB3168-079-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g4539378
BLAST score
                  234
E value
                  1.0e-129
Match length
                  445
                  96
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21
                  (ESSA project)
Seq. No.
                  146842
Seq. ID
                  LIB3168-079-P1-K1-F1
                  BLASTX
Method
NCBI GI
                  g112737
BLAST score
                  363
                  9.0e-40
E value
                  108
Match length
                  75
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  146843
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g1669387
BLAST score
                  605
                  5.0e-63
E value
Match length
                  119
                  100
% identity
NCBI Description (U41998) actin 2 [Arabidopsis thaliana]
```

```
LIB3168-079-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  365
E value
                  8.0e-35
Match length
                  138
% identity
                  58
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146845
                  LIB3168-079-P1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2842474
                  133
BLAST score
E value
                  1.0e-68
Match length
                  314
                  86
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                  (ESSAII project)
                  146846
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  q166611
                  77
BLAST score
E value
                  3.0e-35
                  253
Match length
% identity
                  83
                  A.thaliana at 2S3 gene encoding albumin 2S subunit 3,
NCBI Description
                  complete cds
                  146847
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  533
                  1.0e-54
E value
Match length
                  103
                  96
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146848
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q1628583
                  523
BLAST score
                  2.0e-53
E value
Match length
                  121
% identity
                  88
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
```



```
cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146849
Seq. ID
                  LIB3168-079-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   q2961542
BLAST score
                   636
E value
                   1.0e-66
Match length
                   116
% identity
                   98
NCBI Description
                   (AF050463) zinc finger transcription factor [Arabidopsis
                   thaliana]
Seq. No.
                   146850
Seq. ID
                  LIB3168-079-P1-K1-F9
Method
                  BLASTX
                   g4204298
NCBI GI
BLAST score
                   529
                   4.0e-54
E value
Match length
                   101
                   99
% identity
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   146851
Seq. ID
                  LIB3168-079-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g4204299
BLAST score
                   53
E value
                   1.0e-48
Match length
                   110
                   89
% identity
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   146852
Seq. ID
                  LIB3168-079-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1070654
BLAST score
                   208
E value
                   4.0e-26
Match length
                  91
% identity
NCBI Description
                  cruciferin 4 precursor - rape
                  146853
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g4337025
BLAST score
                  561
                  7.0e-58
E value
Match length
                  133
% identity
NCBI Description
                   (AF123253) AIM1 protein [Arabidopsis thaliana]
```

146854

LIB3168-079-P1-K1-G6

Seq. No. Seq. ID

```
Method
                  BLASTX
NCBI GI
                  g1076416
BLAST score
                  161
E value
                  1.0e-11
Match length
                  59
% identity
                  63
NCBI Description
                  sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor -
                  Arabidopsis thaliana >qi 2129745 pir S71437 sulfite
                  reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis
                  thaliana >gi 804953 emb CAA89154 (Z49217) sulfite
                  reductase [Arabidopsis thaliana]
                  146855
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q2781345
BLAST score
                  206
E value
                  3.0e-16
                  97
Match length
% identity
                  49
NCBI Description (AC003113) F2401.2 [Arabidopsis thaliana]
                  146856
Seq. No.
                  LIB3168-079-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  415
                  7.0e-41
E value
                  91
Match length
% identity
                  87
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146857
Seq. No.
Seq. ID
                  LIB3168-079-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2708741
BLAST score
                  579
                  5.0e-60
E value
Match length
                  113
% identity
                  (AC003952) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  146858
Seq. No.
                  LIB3168-079-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3808062
BLAST score
                  155
                  3.0e-10
E value
                  64
Match length
% identity
NCBI Description (AB019195) PV100 [Cucurbita maxima]
                  146859
Seq. No.
```

```
Seq. ID
                  LIB3168-079-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q2062164
BLAST score
                  418
E value
                  4.0e-41
Match length
                  136
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  146860
Seq. ID
                  LIB3168-079-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  q16236
BLAST score
                  69
E value
                  2.0e-30
Match length
                  162
                  86
% identity
                  Arabidopsis CRB gene for 12S seed storage protein
NCBI Description
                  >qi 166677 qb M37248 ATHCRBAA A.thaliana 12S storage
                  protein CRA1 gene, exons 1-4
                  146861
Seq. No.
                  LIB3168-079-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  525
E value
                  1.0e-53
                  100
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146862
Seq. No.
                  LIB3168-079-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  385
                  2.0e-37
E value
                  113
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146863
Seq. No.
                  LIB3168-079-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  g1592677
NCBI GI
BLAST score
                  239
                  4.0e-20
E value
                  122
Match length
% identity
NCBI Description
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
                  146864
Seq. No.
```

```
LIB3168-079-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2984196
BLAST score
                  207
E value
                  2.0e-16
Match length
                  110
% identity
                  (AE000764) ribosomal protein L11 [Aquifex aeolicus]
NCBI Description
Seq. No.
                  146865
                  LIB3168-080-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2914700
BLAST score
                  391
                  5.0e-38
E value
Match length
                  99
% identity
NCBI Description
                  (AC003974) tRNA-processing protein SEN3-like [Arabidopsis
                  thaliana
                  146866
Seq. No.
Seq. ID
                  LIB3168-080-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q2654208
BLAST score
                  460
                  4.0e-46
E value
Match length
                  120
% identity
                  (AF035456) heat shock 70 protein [Spinacia oleracea]
NCBI Description
                  >qi 2773050 (AF039083) heat shock 70 protein [Spinacia
                  oleracea]
Seq. No.
                  146867
                  LIB3168-080-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  559
E value
                  1.0e-57
                  119
Match length
% identity
                  89
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146868
Seq. ID
                  LIB3168-080-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  657
E value
                  4.0e-69
Match length
                  128
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
```

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

BLAST score

BLAST score

Match length

% identity

```
thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146869
                  LIB3168-080-P1-K1-A4
                  BLASTX
                  q1628583
                  247
                  1.0e-32
                  91
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146870
                  LIB3168-080-P1-K1-A6
                  BLASTX
                  g112681
                  526
                  9.0e-54
                  133
                  80
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
```

E value Match length % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604 pir S08509 NCBI Description >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana]

146871 Seq. No. LIB3168-080-P1-K1-B1 Seq. ID Method BLASTX NCBI GI q1628583 BLAST score 697 8.0e-74E value 140

Match length % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

146872 Seq. No. Seq. ID LIB3168-080-P1-K1-B10

Method BLASTX NCBI GI q4585882 BLAST score 474 E value 1.0e-47 Match length 99 % identity

NCBI Description (AC005850) PSI type III chlorophyll a/b-binding protein

[Arabidopsis thaliana]

Seq. No. 146873

Seq. ID LIB3168-080-P1-K1-B11

Method BLASTX NCBI GI g1628583 BLAST score 543

9.0e-56 E value Match length 113 % identity 93 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146874 LIB3168-080-P1-K1-B2 Seq. ID Method BLASTN NCBI GI g395200 BLAST score 66 E value 4.0e-29 Match length 118 % identity A.thaliana 2S albumin gene isoforms 3 and 4, complete CDS's NCBI Description 146875 Seq. No. LIB3168-080-P1-K1-B4 Seq. ID Method BLASTN NCBI GI q4454022 BLAST score 309 1.0e-173 E value 383 Match length 95 % identity Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16 NCBI Description (ESSAII project) 146876 Seq. No. Seq. ID LIB3168-080-P1-K1-B5 Method BLASTX NCBI GI g112737 BLAST score 491 9.0e-50 E value 110 Match length % identity 85 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870 (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana] 146877 Seq. No. Seg. ID LIB3168-080-P1-K1-B6 Method BLASTX NCBI GI q1628583 BLAST score 338

Method BLASTX
NCBI GI g1628583
BLAST score 338
E value 6.0e-32
Match length 72
% identity 86

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146878

```
Seq. ID
                  LIB3168-080-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2129657
BLAST score
                  202
E value
                  7.0e-16
Match length
                  59
% identity
NCBI Description
                  oleosin isoform - Arabidopsis thaliana
                  >gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878_ (Z54165) oleosin
                  [Arabidopsis thaliana]
                  146879
Seq. No.
Seq. ID
                  LIB3168-080-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g4756963
BLAST score
                  40
                  2.0e-13
E value
                  94
Match length
                  91
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                  (ESSA project)
                  146880
Seq. No.
                  LIB3168-080-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  312
                  4.0e-29
E value
Match length
                  76
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146881
Seq. ID
                  LIB3168-080-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q3193297
BLAST score
                  580
E value
                  4.0e-60
Match length
                  126
% identity
NCBI Description
                  (AF069298) similar to epoxide hydrolases [Arabidopsis
                  thaliana]
Seq. No.
                  146882
Seq. ID
                  LIB3168-080-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  614
E value
                  3.0e-64
Match length
                  124
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

Seq. ID

```
146883
Seq. No.
                   LIB3168-080-P1-K1-C12
Seq. ID
Method
                   BLASTX
                   g1170191
NCBI GI
BLAST score
                   523
                   2.0e-53
E value
                   115
Match length
                   92
% identity
NCBI Description
                   HOMEOBOX PROTEIN HD1 >gi 1076449 pir S47535
                   homeodomain-containing protein - rape
                   >gi_453949_emb_CAA82314_ (Z29073) homeodomain-containing
protein [Brassica napus] >gi_1090522_prf__2019252A homeobox
                   protein [Brassica napus]
Seq. No.
                   146884
                   LIB3168-080-P1-K1-C4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   576
E value
                   1.0e-59
Match length
                   132
                   83
% identity
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146885
Seq. ID
                   LIB3168-080-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   q112681
BLAST score
                   94
E value
                   3.0e-54
Match length
                   115
% identity
                   95
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146886
Seq. ID
                   LIB3168-080-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   203
E value
                   1.0e-16
Match length
                   56
% identity
                   80
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   146887
```

LIB3168-080-P1-K1-C8

```
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  536
E value
                  5.0e-55
Match length
                  103
% identity
                  99
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146888
Seq. No.
                  LIB3168-080-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  70
E value
                  1.0e-50
Match length
                  119
                  93
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146889
Seq. No.
Seq. ID
                  LIB3168-080-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  498
E value
                  1.0e-50
                  104
Match length
                  93
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146890
Seq. No.
                  LIB3168-080-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4704730
BLAST score
                  43
E value
                  4.0e-22
Match length
                  91
% identity
NCBI Description (AF121355) peroxiredoxin TPx1 [Arabidopsis thaliana]
Seq. No.
                  146891
                  LIB3168-080-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  491
                  1.0e-49
E value
                  107
Match length
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
```

storage protein [Arabidopsis thaliana]

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

NCBI GI

BLAST score

g2688544

169

Seq. No. 146892 LIB3168-080-P1-K1-D2 Seq. ID Method BLASTX NCBI GI g112681 BLAST score 210 E value 5.0e-17 Match length 72 58 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis tha $\overline{1}$ iana] >gi\_808936\_emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] 146893 Seq. No. Seq. ID LIB3168-080-P1-K1-D4 BLASTX Method g112682 NCBI GI BLAST score 622 5.0e-65 E value 137 Match length 87 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir\_S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed storage protein [Arabidopsis thaliana] 146894 Seq. No. LIB3168-080-P1-K1-D5 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 335 1.0e-31 E value 83 Match length % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 146895 Seq. ID LIB3168-080-P1-K1-D7 Method BLASTN NCBI GI g3250673 BLAST score 54 1.0e-21 E value 289 Match length 58 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project) 146896 Seq. No. Seq. ID LIB3168-080-P1-K1-D8 Method BLASTX

```
5.0e-12
E value
Match length
                  89
% identity
                  36
NCBI Description
                   (AE001163) 4-methyl-5(b-hydroxyethyl)-thiazole
                  monophosphate biosynthesis protein (thiJ) [Borrelia
                  burgdorferi]
Seq. No.
                  146897
Seq. ID
                  LIB3168-080-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  q4753645
BLAST score
                  94
E value
                  8.0e-46
Match length
                  139
% identity
                  96
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17N18
                  (ESSA project)
                  146898
Seq. No.
                  LIB3168-080-P1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1877523
BLAST score
                  249
E value
                  1.0e-138
Match length
                  253
% identity
                  100
NCBI Description
                  Arabidopsis thaliana BAC T7I23, complete sequence
                  [Arabidopsis thaliana]
                  146899
Seq. No.
                  LIB3168-080-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  495
                  3.0e-50
E value
                  94
Match length
                  97
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146900
                  LIB3168-080-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q18058
BLAST score
                  45
E value
                  3.0e-16
Match length
                  157
% identity
                  88
NCBI Description Citrus limon cistron for 26S ribosomal RNA
                  146901
Seq. No.
Seq. ID
                  LIB3168-080-P1-K1-E12
Method
                  BLASTX
NCBI GI
```

q112681

```
BLAST score
E value
                  5.0e-28
Match length
                  72
% identity
                  82
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146902
Seq. ID
                  LIB3168-080-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g4510392
BLAST score
                  48
E value
                  2.0e-18
Match length
                  133
% identity
                  81
                  Arabidopsis thaliana chromosome II BAC T17D12 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  146903
                  LIB3168-080-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267073
BLAST score
                  470
E value
                  2.0e-47
Match length
                  88
% identity
NCBI Description
                  TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin
                  beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
                  146904
Seq. No.
                  LIB3168-080-P1-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4572664
BLAST score
                  101
                  9.0e-50
E value
                  149
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F25P17 genomic
                  sequence, complete sequence
Seq. No.
                  146905
                  LIB3168-080-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  192
E value
                  8.0e-15
Match length
                  49
% identity
                  76
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
```

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed



## storage protein [Arabidopsis thaliana]

Seq. No. 146906 Seq. ID LIB3168-080-P1-K1-E8 Method BLASTX NCBI GI q112681

BLAST score 258 E value 4.0e-23 Match length 110 % identity 63

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146907

Seq. ID LIB3168-080-P1-K1-F1

Method BLASTX NCBI GI q112681 BLAST score 295 E value 2.0e-28 95 Match length 71 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

146908 Seq. No.

LIB3168-080-P1-K1-F10 Seq. ID

Method BLASTX q1628583 NCBI GI BLAST score 420 1.0e-41 E value Match length 84 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146909

Seq. ID LIB3168-080-P1-K1-F12

Method BLASTX NCBI GI q1628583 BLAST score 476 E value 4.0e-48 Match length 97

% identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146910

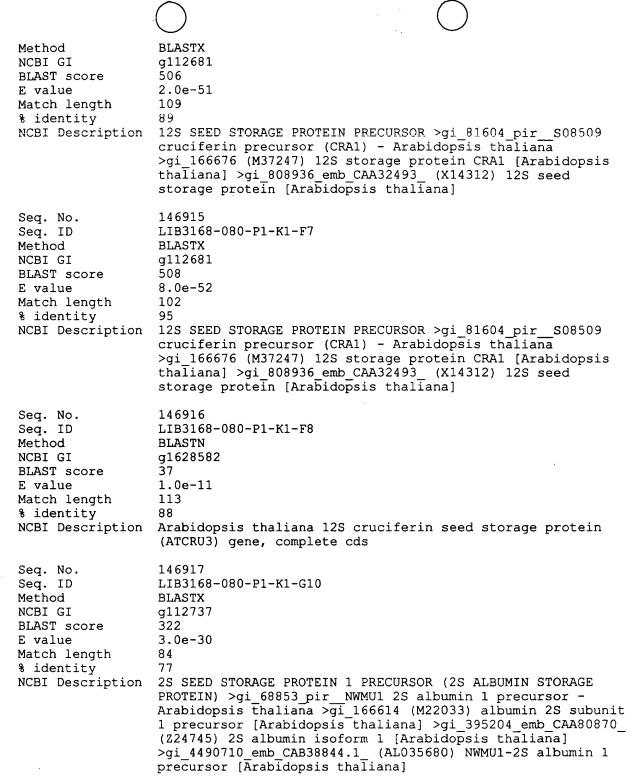
LIB3168-080-P1-K1-F2 Seq. ID

Method BLASTX

```
g112741
NCBI GI
BLAST score
                  491
E value
                  9.0e-50.
Match length
                  94
                  95
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146911
Seq. ID
                  LIB3168-080-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  152
E value
                  4.0e-10
                  83
Match length
                  47
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146912
Seq. ID
                  LIB3168-080-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                  46
E value
                  2.0e-13
Match length
                  48
% identity
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                  >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
Seq. No.
                  146913
Seq. ID
                  LIB3168-080-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  56
E value
                  4.0e-23
Match length
                  125
% identity
                  56
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor ~
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
```

Seq. ID LIB3168-080-P1-K1-F6

Seq. No.



Seq. ID LIB3168-080-P1-K1-G11

Method BLASTN NCBI GI g4691223

Seq. No.

```
BLAST score
                  0.0e + 00
E value
Match length
                  404
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                  (ESSA project)
                  146919
Seq. No.
                  LIB3168-080-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112739
                  195
BLAST score
E value
                  4.0e-15
Match length
                  84
% identity
                  55
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  146920
Seq. No.
Seq. ID
                  LIB3168-080-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  553
E value
                  5.0e-57
Match length
                  111
% identity
                  95
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146921
Seq. ID
                  LIB3168-080-P1-K1-G6
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  301
E value
                  8.0e-38
Match length
                  95
% identity
                  89
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146922
                  LIB3168-080-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  643
E value
                  2.0e-67
                  122
Match length
                  97
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
```

PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi\_4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

 Seq. No.
 146923

 Seq. ID
 LIB3168-080-P1-K1-G8

 Method
 BLASTX

 NCBI GI
 g112681

 BLAST score
 536

E value 6.0e-55
Match length 132
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146924

Seq. ID LIB3168-080-P1-K1-G9

Method BLASTX
NCBI GI g112682
BLAST score 545
E value 5.0e-56
Match length 129
% identity 81

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146925

Seq. ID LIB3168-080-P1-K1-H1

Method BLASTN
NCBI GI 94097693
BLAST score 37
E value 6.0e-12
Match length 109
% identity 83

NCBI Description Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete

cds

Seq. No. 146926

Seq. ID LIB3168-080-P1-K1-H3

Method BLASTN
NCBI GI g4469002
BLAST score 61

E value 8.0e-26 Match length 164 8 identity 84

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 146927

```
LIB3168-080-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  189
                  3.0e-14
E value
Match length
                  84
                  54
% identity
NCBI Description
                  oleosin isoform - Arabidopsis thaliana
                  >gi 987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                  thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                  [Arabidopsis thaliana]
Seq. No.
                  146928
Seq. ID
                  LIB3168-080-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  g16231
BLAST score
                  37
                  6.0e-12
E value
Match length
                  117
% identity
                  82
NCBI Description
                  Arabidopsis CRA1 gene for 12S seed storage protein
                  >qi 166675 qb M37247 ATHCRA1AA A.thaliana 12S storage
                  protein CRA1 gene, exons 1-4
Seq. No.
                  146929
Seq. ID
                  LIB3168-080-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  187
                  1.0e-14
E value
Match length
                  53
% identity
                  74
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >qi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146930
                  LIB3168-080-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  497
                  2.0e-50
E value
Match length
                  111
% identity
                  93
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146931
                  LIB3168-080-P1-K1-H9
Seq. ID
Method
                  BLASTN
                  q4006885
NCBI GI
BLAST score
                  269
```

..

```
1.0e-150
E value
Match length
                  330
% identity
                  95
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  146932
Seq. ID
                  LIB3168-082-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  54
E value
                  1.0e-77
Match length
                  147
                  92
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146933
Seq. No.
Seg. ID
                  LIB3168-082-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  q2275194
BLAST score
                  389
                  0.0e + 00
E value
Match length
                  401
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T08I13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  146934
Seq. No.
Seq. ID
                  LIB3168-082-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  614
E value
                  4.0e-64
Match length
                  120
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146935

Seq. ID LIB3168-082-P1-K1-A2

Method BLASTX NCBI GI q112737 BLAST score 581 E value 4.0e-60 Match length 122

% identity 90

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >qi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

NCBI Description

thalianal

```
precursor [Arabidopsis thaliana]
                  146936
Seq. No.
Seq. ID
                  LIB3168-082-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q3023190
BLAST score
                  393
                  4.0e-38
E value
                  84
Match length
                  93
% identity
                  14-3-3-LIKE PROTEIN 16R >qi 1888459 emb CAA72381 (Y11685)
NCBI Description
                  14-3-3 protein [Solanum tuberosum]
                  146937
Seq. No.
                  LIB3168-082-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  659
                  2.0e-69
E value
                  138
Match length
% identity
                  91
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  146938
Seq. No.
                  LIB3168-082-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3367576
BLAST score
                   594
E value
                   1.0e-61
                  130
Match length
% identity
NCBI Description
                   (ALO31135) NAM / CUC2 -like protein [Arabidopsis thaliana]
Seq. No.
                  146939
                  LIB3168-082-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2252634
BLAST score
                  217
E value
                   2.0e-17
Match length
                  82
% identity
NCBI Description
                  (U95973) hypothetical protein [Arabidopsis thaliana]
                  146940
Seq. No.
Seq. ID
                  LIB3168-082-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4678226
BLAST score
                  561
E value
                   6.0e-58
Match length
                   131
% identity
```

(AC007135) putative 40S ribosomal protein S14 [Arabidopsis

```
146941
Seq. No.
                  LIB3168-082-P1-K1-B11
Seq. ID
Method
                  BLASTN
                  q1402874
NCBI GI
BLAST score
                  91
E value
                  1.0e-43
Match length
                  119
% identity
                  95
NCBI Description
                  A.thaliana 81kb genomic sequence
Seq. No.
                  146942
                  LIB3168-082-P1-K1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  126
E value
                  6.0e-65
Match length
                  130
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                  (ESSAII project)
Seq. No.
                  146943
                  LIB3168-082-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3152581
BLAST score
                  519
E value
                  6.0e-53
Match length
                  115
% identity
NCBI Description
                  (AC002986) Similar to E. coli sulfurtransferase (rhodanese)
                  qb AE00338. ESTs qb T03984, qb T03983 and qb W43228 come
                  from this gene. [Arabidopsis thaliana]
Seq. No.
                  146944
                  LIB3168-082-P1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589434
BLAST score
                  306
E value
                  1.0e-172
Match length
                  446
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNJ7, complete sequence
Seq. No.
                  146945
                  LIB3168-082-P1-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2262155
BLAST score
                  85
E value
                  6.0e-40
Match length
                  335
% identity
                  87
NCBI Description
                  DNA sequence of Arabidopsis thaliana BAC F5J6 from
                  chromosome IV, complete sequence [Arabidopsis thaliana]
```

Seq. No.

```
LIB3168-082-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4165488
BLAST score
                  622
E value
                  5.0e-65
Match length
                  117
% identity
                  98
                   (AJ132399) alpha-tubulin 3 [Hordeum vulgare]
NCBI Description
Seq. No.
                  146947
                  LIB3168-082-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159705
BLAST score
                  393
E value
                  0.0e + 00
Match length
                  401
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGD8, complete sequence
Seq. No.
                  146948
Seq. ID
                  LIB3168-082-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  43
E value
                  3.0e - 36
Match length
                  121
                  67
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146949
Seq. ID
                  LIB3168-082-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  625
E value
                  2.0e-65
Match length
                  142
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146950
Seq. ID
                  LIB3168-082-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q3212869
BLAST score
                  592
E value
                  2.0e-61
Match length
                  123
```

Match length

% identity

416 95

```
% identity
NCBI Description
                  (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  146951
                  LIB3168-082-P1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2264321
BLAST score
                  141
                  2.0e-73
E value
Match length
                  386
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXM12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146952
                  LIB3168-082-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3482913
BLAST score
                  230
                  5.0e-19
E value
Match length
                  119
                  35
% identity
                  (AC003970) Similar to MtN21, gi 2598575, Megicago
NCBI Description
                  truncatula nodulation induced gene [Arabidopsis thaliana]
Seq. No.
                  146953
Seq. ID
                  LIB3168-082-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
                  2.0e-65
E value
Match length
                  120
                  100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146954
Seq: ID
                  LIB3168-082-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  514
                  3.0e-52
E value
Match length
                  111
% identity
                  91
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146955
                  LIB3168-082-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4678266
BLAST score
                  189
                  1.0e-102
E value
```

Match length

NCBI Description

% identity

139 82

```
NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8
                  (ESSA project)
Seq. No.
                  146956
                  LIB3168-082-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  516
E value
                  1.0e-52
Match length
                  139
                  75
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  146957
Seq. No.
Seq. ID
                  LIB3168-082-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  606
E value
                  3.0e-63
Match length
                  113
% identity
                  99
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146958
                  LIB3168-082-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  102
E value
                  6.0e-57
Match length
                  120
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146959
                  LIB3168-082-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  597
E value
                  5.0e-62
```

12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir \$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

146960 Seq. No.

Seq. ID LIB3168-082-P1-K1-D10

Method BLASTN NCBI GI g3335170 BLAST score 111 1.0e-55 E value 278 Match length 95 % identity

Arabidopsis thaliana embryo-specific protein 3 (ATS3) gene, NCBI Description

complete cds

Seq. No. 146961

LIB3168-082-P1-K1-D11 Seq. ID

BLASTX Method g112681 NCBI GI 119 BLAST score 4.0e-06 E value 104 Match length % identity 52

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

146962 Seq. No.

LIB3168-082-P1-K1-D3 Seq. ID

Method BLASTX q112682 NCBI GI 621 BLAST score 7.0e-65 E value 142 Match length % identity 82

12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 146963

LIB3168-082-P1-K1-D4 Seq. ID

Method BLASTX NCBI GI g129817 BLAST score 417 6.0e-41 E value Match length 113 % identity 80

BASIC PEROXIDASE E PRECURSOR >gi 81653 pir JU0458 NCBI Description

peroxidase (EC 1.11.1.7) E - Arabidopsis thaliana

>gi 166807 (M58381) peroxidase [Arabidopsis thaliana]

146964 Seq. No.

LIB3168-082-P1-K1-D5 Seq. ID

```
BLASTX
Method
NCBI GI
                  q112681
BLAST score
                  623
E value
                  4.0e-65
Match length
                  132
% identity
                  91
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146965
                  LIB3168-082-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  478
E value
                  2.0e-48
Match length
                  95
% identity
                  97
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146966
Seq. ID
                  LIB3168-082-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  q2264314
BLAST score
                  419
E value
                  0.0e + 00
Match length
                  427
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146967
Seq. ID
                  LIB3168-082-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g899608
BLAST score
                  587
E value
                  5.0e-61
Match length
                  120
% identity
NCBI Description
                  (U29158) polyubiquitin [Zea mays]
Seq. No.
                  146968
                  LIB3168-082-P1-K1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264306
BLAST score
                  50
E value
                  4.0e-19
Match length
                  54
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBK5, complete sequence [Arabidopsis thaliana]
```

146969

Seq. No.

Seq. ID

Method

NCBI GI

```
Seq. ID
                  LIB3168-082-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  398
E value
                  1.0e-38
Match length
                  109
% identity
                  77
NCBI Description
                  oleosin isoform - Arabidopsis thaliana
                  >qi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                  [Arabidopsis thaliana]
Seq. No.
                  146970
Seq. ID
                  LIB3168-082-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  717
E value
                  4.0e-76
Match length
                  135
                  99
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >qi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >qi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146971
Seq. ID
                  LIB3168-082-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  499
E value
                  1.0e-50
Match length
                  120
% identity
                  82
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146972
Seq. ID
                  LIB3168-082-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  q4512656
BLAST score
                  422
E value
                  0.0e + 00
Match length
                  430
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
Seq. No.
                  146973
```

18459

LIB3168-082-P1-K1-E2

BLASTX

g1628583

```
BLAST score
                  2.0e-65
E value
                  120
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  146974
Seq. No.
                  LIB3168-082-P1-K1-E3
Seq. ID
Method
                  BLASTX
                  q2501296
NCBI GI
BLAST score
                  248
                  4.0e-21
E value
Match length
                  115
                  41
% identity
                  DNA GYRASE SUBUNIT B >gi_1652801_dbj_BAA17720 (D90908) DNA
NCBI Description
                  gyrase B subunit [Synechocystis sp.]
                  146975
Seq. No.
Seq. ID
                  LIB3168-082-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g4581146
BLAST score
                  309
E value
                  9.0e-29
Match length
                  64
% identity
                  (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                  cytoplasmic [Arabidopsis thaliana]
Seq. No.
                  146976
                  LIB3168-082-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454050
BLAST score
                  161
                  6.0e-11
E value
Match length
                  40
% identity
                  (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
                  146977
Seq. No.
Seq. ID
                  LIB3168-082-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  566
                  2.0e-58
E value
                  137
Match length
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146978
```

```
Seq. ID
                   LIB3168-082-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   650
E value
                   3.0e-68
Match length
                   137
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   146979
Seq. ID
                   LIB3168-082-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q2129657
BLAST score
                  433
E value
                   8.0e-43
Match length
                   116
% identity
                   78
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                   >qi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                   thaliana] \geq gi_987016_{emb}_{CAA90878}_{CAA90878} (Z54165) oleosin
                   [Arabidopsis thaliana]
Seq. No.
                   146980
Seq. ID
                  LIB3168-082-P1-K1-F1
Method
                  BLASTN
NCBI GI
                   q4191771
BLAST score
                   411
E value
                   0.0e + 00
Match length
                   435
% identity
                   98
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3P11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  146981
Seq. ID
                  LIB3168-082-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                   674
E value
                   4.0e-71
Match length
                  132
% identity
                   99
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  146982
Seq. ID
                  LIB3168-082-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3023516
BLAST score
                  492
E value
                  6.0e-50
Match length
                  112
% identity
                  85
```

NCBI Description PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE PRECURSOR

```
(DXP SYNTHASE) >gi_1399261 (U27099) DEF [Arabidopsis
thaliana]
```

```
Seq. No.
                  146983
                  LIB3168-082-P1-K1-F12
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146984
Seq. ID
                  LIB3168-082-P1-K1-F2
Method
                  BLASTX
                  q112681
NCBI GI
BLAST score
                  739
                  1.0e-78
E value
Match length
                  145
                  99
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146985
Seq. ID
                  LIB3168-082-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  651
E value
                  2.0e-68
Match length
                  127
                  98
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146986
Seq. ID
                  LIB3168-082-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  567
E value
                  1.0e-58
Match length
                  141
% identity
                  79
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
```

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 146987

Method BLASTX NCBI GI g2921158

Seq. ID

LIB3168-082-P1-K1-F7

Seq. No.

```
BLAST score
E value
                  4.0e-75
Match length
                  144
% identity
                  99
NCBI Description
                  (AF022909) ClpC [Arabidopsis thaliana]
                  146988
Seq. No.
                  LIB3168-082-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  468
                  6.0e-47
E value
Match length
                  131
% identity
                  73
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146989
Seq. ID
                  LIB3168-082-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146990
Seq. ID
                  LIB3168-082-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2253579
BLAST score
                  159
E value
                  8.0e-11
Match length
                  119
% identity
                  42
NCBI Description
                 (U78721) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  146991
                  LIB3168-082-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1350634
BLAST score
                  395
E value
                  2.0e-38
Match length
                  76
% identity
                  99
NCBI Description
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L23
                  >gi 12213 emb CAA46567 (X65615) ribosomal protein L23
                  [Sinapis alba]
```

```
Seq. ID
                  LIB3168-082-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q2924779
BLAST score
                  658
E value
                  3.0e-69
Match length
                  130
% identity
NCBI Description
                  (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
                  thaliana] >qi 2981616 dbj BAA25248 (AB008854)
                  3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                  >qi 2981618 dbj BAA25249 (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
Seq. No.
                  146993
Seq. ID
                  LIB3168-082-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g3600030
BLAST score
                  521
                  4.0e-53
E value
Match length
                  118
% identity
NCBI Description
                  (AF080119) contains similarity to ankyrin repeats (Pfam:
                  ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis
                  thaliana)
Seq. No.
                  146994
Seq. ID
                  LIB3168-082-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
                  2.0e-65
E value
                  120
Match length
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  146995
Seq. ID
                  LIB3168-082-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  604
E value
                  6.0e-63
Match length
                  117
                  97
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >qi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  146996
Seq. ID
                  LIB3168-082-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q112681
```

```
BLAST score
                  7.0e-63
E value
Match length
                  139
% identity
                  84
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146997
                  LIB3168-082-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  614
E value
                  5.0e-64
Match length
                  142
% identity
                  82
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146998
Seq. ID
                  LIB3168-082-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  547
E value
                  3.0e-56
Match length
                  126
% identity
                  84
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  146999
                  LIB3168-082-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220514
BLAST score
                  307
                  5.0e-28
E value
Match length
                  74
% identity
                  73
NCBI Description
                  (AL035356) putative protein [Arabidopsis thaliana]
                  147000
Seq. No.
                  LIB3168-082-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  315
E value
                  5.0e-29
Match length
                  93
                  73
% identity
NCBI Description oleosin isoform - Arabidopsis thaliana
```

```
>gi_987014_emb_CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                   [Arabidopsis thaliana]
Seq. No.
                  147001
Seq. ID
                  LIB3168-082-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2160151
BLAST score
                   629
E value
                  8.0e-66
Match length
                  136
% identity
                  89
                   (AC000375) Strong similarity to Brassica aspartic protease
NCBI Description
                   (gb X77260). [Arabidopsis thaliana]
Seq. No.
                  147002
                  LIB3168-082-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                   452
E value
                   3.0e-45
Match length
                  115
% identity
                  78
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  147003
Seq. ID
                  LIB3168-082-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2961378
BLAST score
                  565
E value
                   3.0e-58
Match length
                  135
% identity
NCBI Description
                  (AL022141) putative protein [Arabidopsis thaliana]
Seq. No.
                  147004
Seq. ID
                  LIB3168-082-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                   625
                  2.0e-65
E value
Match length
                  120
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147005
Seq. ID
                  LIB3168-082-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  599
E value
                  3.0e-62
Match length
                  141
% identity
NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
```

ve?



PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710\_emb\_CAB38844.1\_(AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 147006

Seq. ID LIB3168-082-P1-K1-H5

Method BLASTX
NCBI GI g585536
BLAST score 584
E value 1.0e-60
Match length 105
% identity 100

NCBI Description MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE) >gi 1362006 pir S56653 thioglucosidase (EC 3.2.3.1) -

Arabidopsis thaliana >gi\_304115 (L11454) thioglucosidase [Arabidopsis thaliana] >gi 871990 emb CAA55786 (X79194)

thioglucosidase [Arabidopsis thaliana]

Seq. No. 147007

Seq. ID LIB3168-082-P1-K1-H6

Method BLASTX
NCBI GI g1628583
BLAST score 546
E value 4.0e-56
Match length 110
% identity 95

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147008

Seq. ID LIB3168-082-P1-K1-H7

Method BLASTX
NCBI GI g112681
BLAST score 643
E value 2.0e-67
Match length 132
% identity 92

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147009

Seq. ID LIB3168-082-P1-K1-H8

Method BLASTX
NCBI GI g266693
BLAST score 423
E value 9.0e-42
Match length 106
% identity 82

NCBI Description OLEOSIN >gi\_282875\_pir\_\_S22538 oleosin - Arabidopsis

thaliana >gi\_16405\_emb\_CAA44225\_ (X62353) oleosin

[Arabidopsis thaliana] >gi\_4455257\_emb\_CAB36756.1\_(AL035523) oleosin, 18.5K [Arabidopsis thaliana]

Seq. No. 147010

Seq. ID LIB3168-082-P1-K1-H9

Method BLASTX
NCBI GI g4539335
BLAST score 152
E value 6.0e-10
Match length 93
% identity 41

NCBI Description (AL035539) putative protein [Arabidopsis thaliana]

Seq. No. 147011

Seq. ID LIB3168-083-P1-K1-A1

Method BLASTX
NCBI GI g112739
BLAST score 345
E value 1.0e-32
Match length 109
% identity 67

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi\_4490711\_emb\_CAB38845.1\_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 147012

Seq. ID LIB3168-083-P1-K1-A11

Method BLASTX
NCBI GI g112737
BLAST score 251
E value 2.0e-21
Match length 115
% identity 48

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204 emb\_CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147013

Seq. ID LIB3168-083-P1-K1-A2

Method BLASTX
NCBI GI g4204299
BLAST score 105
E value 8.0e-64
Match length 127
% identity 100

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 147014

```
LIB3168-083-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  386
E value
                  1.0e-46
Match length
                  119
% identity
                  82
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147015
                  LIB3168-083-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3236234
BLAST score
                  362
E value
                  0.0e+00
Match length
                  378
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13M22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147016
Seq. ID
                  LIB3168-083-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  571
E value
                  5.0e-59
Match length
                  137
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147017
Seq. ID
                  LIB3168-083-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  390
E value
                  9.0e-38
Match length
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147018
Seq. ID
                  LIB3168-083-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  708
E value
                  4.0e-75
Match length
                  133
% identity
```

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi\_4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3
precursor [Arabidopsis thaliana]

Seq. No. 147019

Seq. ID LIB3168-083-P1-K1-B2

Method BLASTX
NCBI GI g112682
BLAST score 609
E value 2.0e-63
Match length 126

% identity 90
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147020

Seq. ID LIB3168-083-P1-K1-B4

Method BLASTX
NCBI GI g1628583
BLAST score 342
E value 1.0e-32
Match length 77

% identity 86

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147021

Seq. ID LIB3168-083-P1-K1-B7

Method BLASTN
NCBI GI g21157
BLAST score 110
E value 4.0e-55
Match length 170
% identity 92

NCBI Description S.alba 18S, 5.8S & 25S rRNA genes

Seq. No. 147022

Seq. ID LIB3168-083-P1-K1-B9

Method BLASTX
NCBI GI g4584542
BLAST score 42
E value 1.0e-60

E value 1.0e Match length 128 % identity 97

NCBI Description (AL049608) putative protein [Arabidopsis thaliana]

Seq. No. 147023

Seq. ID LIB3168-083-P1-K1-C10

Method BLASTN NCBI GI g4079614

```
BLAST score
E value
                  5.0e-50
Match length
                  332
                  92
% identity
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  147024
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  598
E value
                  4.0e-62
Match length
                  146
                  79
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit,
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  147025
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  90
E value
                  9.0e-73
Match length
                  145
                  97
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147026
                  LIB3168-083-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q99688
BLAST score
                  460
                  3.0e-46
E value
                  99
Match length
                  90
% identity
                  translation elongation factor eEF-1 alpha chain (gene A4) -
NCBI Description
                  Arabidopsis thaliana >gi 295789 emb CAA34456 (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
                  147027
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  389
E value
                  1.0e-37
Match length
                  135
                  59
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
```

Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710\_emb\_CAB38844.1\_(AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana]

Seq. No. 147028

Seq. ID LIB3168-083-P1-K1-C8

Method BLASTN
NCBI GI g2760171
BLAST score 37
E value 2.0e-11
Match length 104
% identity 85

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MPA24, complete sequence [Arabidopsis thaliana]

Seq. No. 147029

Seq. ID LIB3168-083-P1-K1-C9

Method BLASTX
NCBI GI g1628583
BLAST score 537
E value 5.0e-55
Match length 120
% identity 87

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147030

Seq. ID LIB3168-083-P1-K1-D1

Method BLASTX
NCBI GI g1628583
BLAST score 612
E value 9.0e-64
Match length 120
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147031

Seq. ID LIB3168-083-P1-K1-D10

Method BLASTX
NCBI GI g1628583
BLAST score 438
E value 6.0e-69
Match length 146
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147032

Seq. ID LIB3168-083-P1-K1-D11

Method BLASTX NCBI GI g112737 BLAST score E value 5.0e-62 Match length 145 % identity 79 NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870 (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana] 147033 Seq. No. LIB3168-083-P1-K1-D12 Seq. ID BLASTX Method NCBI GI g112681 BLAST score 392 E value 4.0e-38 87 Match length 87 % identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi\_166676 (M37247) 12S storage protein CRA1 (Arabidopsis  $tha\overline{liana}$  >gi\_808936\_emb\_CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] 147034 Seq. No. Seq. ID LIB3168-083-P1-K1-D2 Method BLASTX NCBI GI g2454182 BLAST score 407 9.0e-40 E value Match length 116 % identity 71 NCBI Description (U80185) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana] 147035 Seq. No. Seq. ID LIB3168-083-P1-K1-D4 Method BLASTX NCBI GI g112681 BLAST score 547 E value 3.0e-56 Match length 111 93 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana]

Seq. No. 147036

Seq. ID LIB3168-083-P1-K1-D6

Method BLASTX
NCBI GI g112682
BLAST score 549
E value 2.0e-56

BLAST score

E value

632 4.0e-66

```
Match length
                  78
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147037
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-D7
Method
                  BLASTX
                  q2894568
NCBI GI
BLAST score
                  503
E value
                  5.0e-51
Match length
                  145
% identity
                  71
                  (AL021890) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  147038
Seq. ID
                  LIB3168-083-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  a166609
                  147
BLAST score
                  7.0e-77
E value
Match length
                  415
                  91
% identity
                  A.thaliana at2S1 gene encoding albumin 2S subunit 1,
NCBI Description
                  complete cds
                  147039
Seq. No.
                  LIB3168-083-P1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4587582
                  87
BLAST score
                  3.0e-41
E value
Match length
                  261
                  93
% identity
                  Arabidopsis thaliana chromosome II BAC T16B14 genomic
NCBI Description
                  sequence, complete sequence
                  147040
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  q4206762
                  235
BLAST score
                  1.0e-129
E value
                  363
Match length
                  95
% identity
                  Arabidopsis thaliana cell wall-plasma membrane linker
NCBI Description
                  protein homolog (CWLP) mRNA, complete cds
                  147041
Seq. No.
                  LIB3168-083-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3687228
```

```
Match lëngth
                  95
% identity
                  (AC005169) putative malate dehydrogenase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  147042
                  LIB3168-083-P1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3299824
BLAST score
                  367
E value
                  0.0e+00
Match length
                  375
                  99
% identity
NCBI Description
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
                  near 17 cM, complete sequence [Arabidopsis thaliana]
                  147043
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  597
                  5.0e-62
E value
Match length
                  138
% identity
                  84
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  147044
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q132866
BLAST score
                  441
                  9.0e-44
E value
Match length
                  91
% identity
                  CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 >gi 71086 pir R5NT2
NCBI Description
                  ribosomal protein L2 - common tobacco chloroplast
                  >gi_435269_emb_CAA77384_ (Z00044) ribosomal protein L2
                  [Nicotiana tabacum] >gi 1223691 emb CAA77409 (Z00044)
                  ribosomal protein L2 [Nicotiana tabacum]
                  >gi 225238 prf 1211235BW ribosomal protein L2 [Nicotiana
                  tabacum]
                  147045
Seq. No.
                  LIB3168-083-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  362
E value
                  2.0e-34
Match length
                  103
% identity
                  76
```

NCBI Description oleosin isoform - Arabidopsis thaliana



>gi\_987014\_emb\_CAA90877\_ (Z54164) oleosin [Arabidopsis
thaliana] >gi\_987016\_emb\_CAA90878\_ (Z54165) oleosin
[Arabidopsis thaliana]

Seq. No. 147046

Seq. ID LIB3168-083-P1-K1-E7

Method BLASTX
NCBI GI g2129767
BLAST score 608
E value 2.0e-63
Match length 122
% identity 93

NCBI Description vacuolar processing enzyme (EC 3.4.22.-) isozyme beta precursor - Arabidopsis thaliana >gi\_1805364\_dbj\_BAA09615\_

(D61394) beta-VPE [Arabidopsis thaliana]

Seq. No. 147047

Seq. ID LIB3168-083-P1-K1-E9

Method BLASTX
NCBI GI g1628583
BLAST score 574
E value 2.0e-59
Match length 113
% identity 97

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147048

Seq. ID LIB3168-083-P1-K1-F10

Method BLASTX
NCBI GI g1628583
BLAST score 125
E value 3.0e-26
Match length 71
% identity 93

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147049

Seq. ID LIB3168-083-P1-K1-F11

Method BLASTX
NCBI GI g1628583
BLAST score 376
E value 1.0e-36
Match length 80
% identity 94

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147050

Seq. ID LIB3168-083-P1-K1-F12

Method BLASTX NCBI GI g3242706 BLAST score 314

```
8.0e-32
E value
Match length
                  124
% identity
                  64
                   (AC003040) cyclin-dependent kinase inhibitor protein
NCBI Description
                  [Arabidopsis thaliana] >gi_3550262 (AF079587)
                  cyclin-dependent kinase inhibitor; ICK1 [Arabidopsis
                  thaliana]
                  147051
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2160151
BLAST score
                  550
                  2.0e-56
E value
                  129
Match length
                  84
% identity
                  (AC000375) Strong similarity to Brassica aspartic protease
NCBI Description
                   (gb_X77260). [Arabidopsis thaliana]
                  147052
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  q2924257
BLAST score
                  28
                  7.0e-06
E value
Match length
                  143
                  90
% identity
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                  147053
Seq. ID
                  LIB3168-083-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  142
                  7.0e-09
E value
Match length
                  95
                  58
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147054
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-F5
                  BLASTN
Method
NCBI GI
                  g3695372
BLAST score
                  65
E value
                  2.0e-28
Match length
                  153
% identity
                  86
NCBI Description Arabidopsis thaliana BAC F1104
```

Seq. No. 147055

Seq. ID LIB3168-083-P1-K1-F6

Method BLASTX NCBI GI g4510397

```
BLAST score
E value
                  6.0e-14
Match length
                  61
                  72
% identity
NCBI Description
                  (AC006587) putative preproMP27-MP32 [Arabidopsis thaliana]
                  147056
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  44
                  1.0e-46
E value
                  116
Match length
% identity
                  84
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  tha\overline{1}iana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147057
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g4220640
BLAST score
                  133
E value
                  1.0e-68
Match length
                  280
% identity
                  86
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPE11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147058
Seq. ID
                  LIB3168-083-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q4580461
                  503
BLAST score
E value
                  5.0e-51
Match length
                  111
% identity
                  (AC006081) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  147059
Seq. ID
                  LIB3168-083-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  496
                  3.0e-50
E value
Match length
                  126
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147060
Seq. ID
                  LIB3168-083-P1-K1-G12
Method
                  BLASTX
NCBI GI
```

g1628583

Seq. No.

Seq. ID

Method

147065

BLASTX

LIB3168-083-P1-K1-G7

```
BLAST score
                  3.0e-60
E value
Match length
                  123
% identity
                  98
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147061
Seq. ID
                  LIB3168-083-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g4336436
BLAST score
                  528
E value
                  6.0e-54
Match length
                  149
% identity
                  70
NCBI Description
                  (AF092432) protein phosphatase type 2C [Lotus japonicus]
                  147062
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q2832777
BLAST score
                  276
E value
                  2.0e-24
Match length
                  114
% identity
NCBI Description
                  (AL021086) /prediction=(method:; /prediction=(method:;
                  /match=(desc:; /match=(desc:; /match=(desc:; /match=(desc:;
                  EST embl AA735498 AA735498 comes from the 5' UTR
                  [Drosophila melanogaster]
Seq. No.
                  147063
Seq. ID
                  LIB3168-083-P1-K1-G5
Method
                  BLASTN
NCBI GI
                  q3406756
BLAST score
                  43
E value
                  5.0e-15
Match length
                  104
% identity
NCBI Description
                  Arabidopsis thaliana rac-like GTP binding protein Arac6
                  (Arac6) mRNA, complete cds
Seq. No.
                  147064
Seq. ID
                  LIB3168-083-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  82
E value
                  2.0e-54
Match length
                  119
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

```
NCBI GI
BLAST score
                  255
E value
                  3.0e-22
Match length
                  65
% identity
                  77
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) > gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (224744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147066
Seq. No.
                  LIB3168-083-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1750376
BLAST score
                  56
                  2.0e-58
E value
Match length
                  138
                  62
% identity
NCBI Description
                  (U80808) ubiquitin activating enzyme [Arabidopsis thaliana]
                  >qi 3150409 (AC004165) ubiquitin activating enzyme (UBA1)
                  [Arabidopsis thaliana]
                  147067
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  q3659908
BLAST score
                  131
E value
                  2.0e-67
Match length
                  263
                  100
% identity
                  Arabidopsis thaliana histidyl-tRNA synthetase mRNA,
NCBI Description
                  complete cds
                  147068
Seq. No.
                  LIB3168-083-P1-K1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4159712
BLAST score
                  308
                  1.0e-173
E value
Match length
                  324
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWI23, complete sequence
                  147069
Seq. No.
Seq. ID
                  LIB3168-083-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g112743
               669
BLAST score
                  2.0e-70
E value
Match length
                  143
% identity
                  88
NCBI Description
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
```

Arabidopsis thaliana >gi\_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi\_395202\_emb\_CAA80869\_(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi\_4490713\_emb\_CAB38847.1\_ (AL035680) NWMU4-2S albumin 4 precursor [Arabidopsis thaliana]

 Seq. No.
 147070

 Seq. ID
 LIB3168-083-P1-K1-H3

 Method
 BLASTN

NCBI GI g4100059
BLAST score 380
E value 0.0e+00
Match length 396
% identity 50

NCBI Description Arabidopsis thaliana AthlecRK4 pseudogene, complete sequence, receptor lectin kinase 3 (AthlecRK3) gene, complete cds, and AthlecRK2 pseudogene, complete sequence

 Seq. No.
 147071

 Seq. ID
 LIB3168-083-P1-K1-H4

 Method
 BLASTX

NCBI GI g1628583
BLAST score 130
E value 4.0e-71
Match length 146
% identity 98

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147072

Seq. ID LIB3168-083-P1-K1-H5

Method BLASTX
NCBI GI g112741
BLAST score 598
E value 3.0e-62
Match length 129
% identity 88

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi\_4490712 emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 147073 Seq. ID LIB3168-083-P1-K1-H7

Method BLASTX
NCBI GI g2961378
BLAST score 45
E value 6.0e-41
Match length 139
% identity 43

NCBI Description (AL022141) putative protein [Arabidopsis thaliana]

Seq. No. 147074

```
Seq. ID
                  LIB3168-083-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  467
E value
                  8.0e-47
Match length
                  131
% identity
                  73
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (224745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147075
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  475
                  9.0e-48
E value
                  117
Match length
                  79
% identity
NCBI Description
                  (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
                  147076
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2244897
BLAST score
                  719
                  2.0e-76
E value
Match length
                  142
                  99
% identity
NCBI Description (Z97338) hypothetical protein [Arabidopsis thaliana]
                  147077
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g16472
BLAST score
                  416
                  0.0e+00
E value
Match length
                  420
                  100
% identity
NCBI Description A.thaliana rRNA repeat unit, most frequent IGR type
                  147078
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q3273743
BLAST score
                  620
                  9.0e-65
E value
Match length
                  118
                  100
% identity
                  (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                  thaliana] >gi_3786019 (AC005499) unknown protein
                  [Arabidopsis thaliana]
```

```
147079
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  143
E value
                  1.0e-74
Match length
                  350
% identity
                  82
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
                  147080
Seq. No.
                  LIB3168-084-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
                  620
BLAST score
                  9.0e-65
E value
Match length
                  120
% identity
                  99
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147081
                  LIB3168-084-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  46
E value
                  1.0e-27
                  77
Match length
% identity
                  78
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147082
Seq. ID
                  LIB3168-084-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  618
                  2.0e-64
E value
                  120
Match length
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147083
Seq. No.
                  LIB3168-084-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2661422
BLAST score
                  580
E value
                  4.0e-60
Match length
                  119
```

Method BLASTX
NCBI GI g1628583
BLAST score 573
E value 3.0e-59
Match length 144
% identity 78

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147085

Seq. ID LIB3168-084-P1-K1-A8

Method BLASTX
NCBI GI g112681
BLAST score 545
E value 6.0e-56
Match length 144
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147086

Seq. ID LIB3168-084-P1-K1-A9

Method BLASTN
NCBI GI g511598
BLAST score 346
E value 0.0e+00
Match length 390
% identity 32

NCBI Description Arabidopsis thaliana cell wall protein (APTR-1) gene,

complete cds

Seq. No. 147087

Seq. ID LIB3168-084-P1-K1-B1

Method BLASTX
NCBI GI g112682
BLAST score 582
E value 2.0e-60
Match length 126
% identity 87

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb\_CAA32494\_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

NCBI Description

trachomatis]





```
Seq. No.
                   147088
Seq. ID
                  LIB3168-084-P1-K1-B10
Method
                  BLASTX
NCBI GI
                   g2605714
BLAST score
                  514
E value
                   2.0e-52
Match length
                  122
% identity
                   84
NCBI Description
                   (AF026275) beta-tonoplast intrinsic protein [Arabidopsis
                   thaliana]
                   147089
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q4204299
BLAST score
                   685
E value
                   2.0e-72
Match length
                  134
                   99
% identity .
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   147090
                  LIB3168-084-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  512
E value
                   3.0e-52
Match length
                  98
% identity
                   99
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543
                                                              (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  147091
Seq. ID
                  LIB3168-084-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q3660465
BLAST score
                  542
E value
                   8.0e-56
Match length
                  110
                   98
% identity
                   (AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  147092
Seq. ID
                  LIB3168-084-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q3328490
BLAST score
                  156
E value
                  3.0e-10
                  86
Match length
% identity
                  47
```

(AE001283) tRNA Pseudouridine Synthase [Chlamydia

```
Seq. No.
                  147093
                  LIB3168-084-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  689
E value
                  7.0e-73
Match length
                  144
% identity
                  94
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147094
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q2459446
BLAST score
                  589
E value
                  4.0e-61
                  132
Match length
% identity
                   (AC002332) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thalianal
                  147095
Seq. No.
                  LIB3168-084-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2708747
BLAST score
                  500
                  8.0e-51
E value
Match length
                  97
% identity
                   (AC003952) putative glycine-rich, zinc-finger DNA-binding
NCBI Description
                  protein [Arabidopsis thaliana]
                  147096
Seq. No.
                  LIB3168-084-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  469
                   4.0e-47
E value
                  138
Match length
% identity
                  72
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147097
Seq. ID
                  LIB3168-084-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  655
E value
                  6.0e-69
Match length
                  133
% identity
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
```

cruciferin precursor (CRB) - Arabidopsis thaliana >gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed

Seq. No. 147098

Seq. ID LIB3168-084-P1-K1-C10

Method BLASTX
NCBI GI g1526424
BLAST score 579
E value 6.0e-60
Match length 129
% identity 46

NCBI Description (D64140) LEA protein in group 3 [Arabidopsis thaliana]

storage protein [Arabidopsis thaliana]

Seq. No. 147099

Seq. ID LIB3168-084-P1-K1-C11

Method BLASTX
NCBI GI g112743
BLAST score 632
E value 4.0e-66
Match length 133
% identity 89

NCBI Description 2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68856\_pir\_\_NWMU4 2S albumin 4 precursor - Arabidopsis thaliana >gi\_166617 (M22033) albumin 2S subunit 4 precursor [Arabidopsis thaliana] >gi\_395202\_emb\_CAA80869\_

(Z24744) 2S albumin isoform 4 [Arabidopsis thaliana] >gi\_4490713\_emb\_CAB38847.1\_ (AL035680) NWMU4-2S albumin 4

precursor [Arabidopsis thaliana]

Seq. No. 147100

Seq. ID LIB3168-084-P1-K1-C12

Method BLASTX
NCBI GI g112682
BLAST score 595
E value 7.0e-62
Match length 138
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsīs thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi\_808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147101

Seq. ID LIB3168-084-P1-K1-C2

Method BLASTX
NCBI GI g2252866
BLAST score 279
E value 9.0e-25

Match length 59 % identity 93

NCBI Description (AF013294) contains region of similarity to SYT

[Arabidopsis thaliana]

Seq. No. 147102

```
Seq. ID
                  LIB3168-084-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g1109699
BLAST score
                  609
E value
                  2.0e-63
Match length
                  118
% identity
NCBI Description
                  (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
                  147103
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1871192
BLAST score
                  155
E value
                  3.0e-10
                  59
Match length
% identity
                  (U90439) Cys3His zinc finger protein isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  147104
Seq. ID
                  LIB3168-084-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  609
                  2.0e-63 ·
E value
                  140
Match length
                  82
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147105
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-C6
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  319
E value
                  2.0e-29
                  76
Match length
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147106
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-C7
Method
                  BLASTX
                  g1429207
NCBI GI
BLAST score
                  636
                  1.0e-66
E value
Match length
                  123
% identity
NCBI Description (X99224) annexin [Arabidopsis thaliana]
Seq. No.
                  147107
```

```
Seq. ID
                  LIB3168-084-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4584110
BLAST score
                  299
                  4.0e-27
E value
Match length
                  111
% identity
                  53
NCBI Description (AJ133639) SAH7 protein [Arabidopsis thaliana]
                  147108
Seq. No.
                  LIB3168-084-P1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112682
                  591
BLAST score
                  2.0e-61
E value
                  137
Match length
                  82
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir_ S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147109
Seq. No.
                  LIB3168-084-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  753
E value
                  2.0e-80
Match length
                  143
                  99
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147110
Seq. No.
                  LIB3168-084-P1-K1-D10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4159709
BLAST score
                  361
E value
                  0.0e + 00
Match length
                  421
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLN21, complete sequence
                  147111
Seq. No.
                  LIB3168-084-P1-K1-D11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g133959
BLAST score
                  263
                  6.0e-23
E value
                  56
Match length
                  91
% identity
NCBI Description CHLOROPLAST 30S RIBOSOMAL PROTEIN S4 >gi 81526 pir A30833
```

```
ribosomal protein S4 - spinach chloroplast >gi_343377
(M16878) ribosomal protein S4 [Spinacia oleracea]
>gi_225464_prf__1303355A ribosomal protein S4 [Spinacia oleracea]

147112
LIB3168-084-P1-K1-D12
BLASTN
g3449326
88
1.0e-41
315
```

 Seq. No.
 147113

 Seq. ID
 LIB3168-084-P1-K1-D2

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 267

 E value
 2.0e-23

Match length 65 % identity 83

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

 Seq. No.
 147114

 Seq. ID
 LIB3168-084-P1-K1-D3

 Method
 BLASTX

 NCBI GI
 g2911042

 BLAST score
 535

 F value
 7.0e-55

BLAST score 535 E value 7.0e-55 Match length 111 % identity 99

NCBI Description (AL021961) Phosphoglycerate dehydrogenase - like protein [Arabidopsis thaliana]

Seq. No. 147115

Seq. ID LIB3168-084-P1-K1-D4

Method BLASTN
NCBI GI g3228389
BLAST score 387
E value 0.0e+00
Match length 395
% identity 99

NCBI Description Genomic sequence for Arabidopsis thaliana BAC F17L21,

complete sequence [Arabidopsis thaliana]

Seq. No. 147116

Seq. ID LIB3168-084-P1-K1-D5

Method BLASTX
NCBI GI g2446981
BLAST score 626
E value 2.0e-65
Match length 120

Seq. ID

```
% identity
NCBI Description
                  (AB005560) AtGDI2 [Arabidopsis thaliana]
                  >gi_2569936_emb_CAA04727_ (AJ001397) GDI2 [Arabidopsis
                  thalianal
Seq. No.
                  147117
                  LIB3168-084-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3434975
BLAST score
                  142
E value
                  1.0e-08
Match length
                  31
% identity
                  (AB008107) ethylene responsive element binding factor 5
NCBI Description
                  [Arabidopsis thaliana]
                  147118
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  685
                  2.0e-72
E value
Match length
                  128
                  99
% identity
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >qi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  147119
Seq. ID
                  LIB3168-084-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  703
                  2.0e-74
E value
                  133
Match length
                  98
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147120
Seq. ID
                  LIB3168-084-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  q3869067
                  401
BLAST score
E value
                  0.0e + 00
                  430
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MCK7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147121
```

18491

LIB3168-084-P1-K1-E1

```
Method
NCBI GI
                  q4756963
BLAST score
                  350
                  0.0e + 00
E value
Match length
                  354
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                  (ESSA project)
                  147122
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-E10
                  BLASTX
Method
                  q3080530
NCBI GI
BLAST score
                  160
                  8.0e-11
E value
Match length
                  121
% identity
NCBI Description
                 (AL022600) hypothetical protein [Schizosaccharomyces pombe]
                  147123
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q2315449
BLAST score
                  292
E value
                  3.0e-26
Match length
                  131
                  43
% identity
                  (AF016448) similar to Saccharomyces cerevisiae nuclear
NCBI Description
                  protein SNF7 (SP:P39929)in one region and the chromosome
                  segregation protein SMC2 (SP:P38989) in another
                  [Caenorhabditis elegans]
                  147124
Seq. No.
                  LIB3168-084-P1-K1-E12
Seq. ID
Method
                  BLASTX
                  g1107501
NCBI GI
                  369
BLAST score
E value
                  2.0e-35
Match length
                  91
% identity
                  (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
NCBI Description
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb_{Z17604}, gb_{H76594}, gb_{AA597972} and gb_{AA394824} come from
                  this gene. [Arabidopsis thaliana]
                  147125
Seq. No.
                  LIB3168-084-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
                  789
BLAST score
                  1.0e-84
E value
Match length
                  145
% identity
                  99
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) > gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868_
```

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] 147126 LIB3168-084-P1-K1-E4 BLASTX q112739 483 1.0e-48 133 73 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205 emb CAA80871 (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana] 147127 LIB3168-084-P1-K1-E5 BLASTN q4199934 352 0.0e + 00392 97 NCBI Description Genomic sequence for Arabidopsis thaliana BAC T3P18, complete sequence [Arabidopsis thaliana] 147128 LIB3168-084-P1-K1-E6 BLASTX g3914386 206 3.0e-16 87 ALLERGEN MF1 >gi\_3445490\_dbj\_BAA32435\_ (AB011804) MF1 [Malassezia furfur] 147129 LIB3168-084-P1-K1-E7

NCBI Description

Seq. No.

Seq. ID

NCBI GI

E value.

Seq. No. Seq. ID

BLAST score

Match length

% identity

Method NCBI GI

E value

Seq. No.

Seq. ID

E value

BLAST score

Match length % identity

Method NCBI GI

BLAST score

Match length

% identity

Method

Seq. No.

Seq. ID Method BLASTX NCBI GI g3157937 BLAST score 653 1.0e-68 E value Match length 131 % identity

NCBI Description (AC002131) Identical to aspartic proteinase cDNA gb U51036 from A. thaliana. ESTs gb\_N96313, gb\_T21893, gb\_R30158, gb\_T21482, gb\_T43650, gb\_R64749, gb\_R65157, gb\_T88269,

gb\_T44552, gb\_T22542, gb\_T76533, gb\_T44350, gb\_Z34591,

gb\_AA728734, gb

Seq. No. 147130

```
LIB3168-084-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  620
E value
                  9.0e-65
Match length
                  120
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147131
                  LIB3168-084-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  696
E value
                  1.0e-73
                  140
Match length
                  99
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147132
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  351
E value
                  3.0e-33
Match length
                  102
                  75
% identity
NCBI Description
                  oleosin isoform - Arabidopsis thaliana
                  >gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                  [Arabidopsis thaliana]
Seq. No.
                  147133
                  LIB3168-084-P1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g166609
BLAST score
                  217
E value
                  1.0e-119
Match length
                  217
                  100
% identity
                  A.thaliana at 2S1 gene encoding albumin 2S subunit 1,
NCBI Description
                  complete cds
Seq. No.
                  147134
                  LIB3168-084-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263515
BLAST score
                  277
E value
                  1.0e-24
Match length
                  138
% identity
                  54
```

```
NCBI Description (AC004044) hypothetical protein [Arabidopsis thaliana]
                  147135
Seq. No.
Seq. ID
                  LIB3168-084-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1070654
BLAST score
                  318
E value
                  2.0e-50
Match length
                  131
% identity
                  71
NCBI Description cruciferin 4 precursor - rape
Seq. No.
                  147136
                  LIB3168-084-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  608
E value
                  2.0e-63
Match length
                  120
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147137
                  LIB3168-084-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  197
E value
                  3.0e-15
Match length
                  65
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147138
Seq. ID
                  LIB3168-084-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  474
E value
                  1.0e-47
Match length
                  131
% identity
                  73
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
```

Seq. No. 147139

precursor [Arabidopsis thaliana]

2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871\_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

```
LIB3168-084-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  56
                  1.0e-61
E value
Match length
                  136
% identity
                  90
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147140
Seq. ID
                  LIB3168-084-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  q4263540
BLAST score
                  39
                  5.0e-13
E value
                  55
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T6A13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147141
Seq. ID
                  LIB3168-084-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  618
                  2.0e-64
E value
                  144
Match length
% identity
                  83
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147142
Seq. ID
                  LIB3168-084-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  641
E value
                  3.0e-67
Match length
                  144
% identity
                  79
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >qi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  147143
Seq. ID
                  LIB3168-084-P1-K1-G6
Method
                  BLASTN
                  q4733952
NCBI GI
BLAST score
                  95
E value
                  4.0e-46
Match length
                  219
% identity
NCBI Description Arabidopsis thaliana chromosome I BAC F23H11 genomic
```





```
sequence, complete sequence
Seq. No.
                  147144
Seq. ID
                  LIB3168-084-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  588
                  5.0e-61
E value
                  138
Match length
% identity
                  81
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147145
                  LIB3168-084-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432839
BLAST score
                  144
                  6.0e-09
E value
Match length
                  85
                  22
% identity
NCBI Description (AC006283) unknown protein [Arabidopsis thaliana]
                  147146
Seq. No.
                  LIB3168-084-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  659
E value
                  2.0e-69
Match length
                  138
% identity
                  91
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147147
                  LIB3168-084-P1-K1-H1
Seq. ID
```

Method BLASTX NCBI GI g2129657 271 BLAST score E value 7.0e-24 Match length 90 % identity

NCBI Description oleosin isoform - Arabidopsis thaliana

>qi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 147148

Seq. ID LIB3168-084-P1-K1-H10

Method BLASTN NCBI GI q4757411

```
BLAST score
E value
                  1.0e-164
Match length
                  376
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MXC7, complete sequence
Seq. No.
                  147149
Seq. ID
                  LIB3168-084-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2191135
BLAST score
                  446
                  2.0e-44
E value
Match length
                  118
% identity
NCBI Description
                  (AF007269) A IG002N01.14 gene product [Arabidopsis
                  thaliana]
Seq. No.
                  147150
                  LIB3168-084-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  590
E value
                  3.0e~61
Match length
                  137
% identity
                  82
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir $08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147151
Seq. ID
                  LIB3168-084-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  719
E value
                  2.0e-76
Match length
                  143
% identity
                  99
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147152
Seq. ID
                  LIB3168-084-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  546
E value
                  4.0e-56
Match length
                  138
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
```

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147153



Seq. ID LIB3168-084-P1-K1-H4 Method BLASTX NCBI GI q137578

NCBI GI g137578 BLAST score 255 E value 5.0e-22 Match length 106 % identity 44

NCBI Description VICILIN PRECURSOR (ALPHA-GLOBULIN A) (CLONE GC72-A) >gi\_81545\_pir\_\_S06398 alpha-globulin type A precursor ~

upland cotton >gi\_167371 (M19378) vicilin precursor [Gossypium hirsutum] >gi\_207906 (M18027) alpha globulin A [Artificial gene] >gi\_226119\_prf\_\_1410330A vicilin gene A

[Saguinus oedipus]

Seq. No. 147154

Seq. ID LIB3168-084-P1-K1-H5

Method BLASTX
NCBI GI g112682
BLAST score 588
E value 5.0e-61
Match length 124
% identity 89

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir \$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147155

Seq. ID LIB3168-084-P1-K1-H6

Method BLASTX
NCBI GI g112682
BLAST score 598
E value 3.0e-62
Match length 128
% identity 90

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147156

Seq. ID LIB3168-084-P1-K1-H9

Method BLASTX
NCBI GI g1628583
BLAST score 618
E value 2.0e-64
Match length 120
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147157

Seq. ID LIB3168-086-P1-K1-A1

Method BLASTX

NCBI GI q3738288 BLAST score 407 E value 5.0e-40 Match length 82 % identity NCBI Description (AC005309) auxin-responsive GH3-like protein (Arabidopsis thaliana] 147158 Seq. No. Seq. ID LIB3168-086-P1-K1-A10 Method BLASTX NCBI GI g2795809 BLAST score 362 E value 2.0e-34 Match length 96 73 % identity NCBI Description (AC003674) putative expansin [Arabidopsis thaliana] Seq. No. 147159 LIB3168-086-P1-K1-A11 Seq. ID Method BLASTX NCBI GI g112682 BLAST score 511 E value 6.0e-52 Match length 140 75 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana]  $>gi_808937_emb_CAA32494_ (X14313)$  12S seed storage protein [Arabidopsis thaliana] 147160 Seq. No. LIB3168-086-P1-K1-A12 Seq. ID Method BLASTX NCBI GI q3335169 BLAST score 645 E value 1.0e-67 Match length 130 % identity NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana] >gi 4455197 emb\_CAB36520.1\_ (AL035440) embryo-specific protein 1 (ATS1) [Arabidopsis thaliana] Seq. No. 147161 LIB3168-086-P1-K1-A3

Seq. ID

Method BLASTN NCBI GI q3894179 BLAST score 412 E value 0.0e + 00Match length 431 99 % identity

Arabidopsis thaliana chromosome II BAC F13H10 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 147162

LIB3168-086-P1-K1-A4 Seq. ID

```
Method
                  BLASTX
                  g112737
NCBI GI
BLAST score
                  588
E value
                  5.0e-61
Match length
                  140
% identity
                  81
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147163
Seq. ID
                  LIB3168-086-P1-K1-A5
                  BLASTN
Method
NCBI GI
                  g3242700
BLAST score
                  369
                  0.0e + 00
E value
Match length
                  475
                  95
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F26B6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147164
Seq. ID
                  LIB3168-086-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3914996
BLAST score
                  739
E value
                  1.0e-78
Match length
                  142
                  99
% identity
NCBI Description
                  PHOSPHOSERINE AMINOTRANSFERASE PRECURSOR (PSAT)
                  >gi 1665831 dbj BAA13640 (D88541) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi 2804260 dbj BAA24441 (AB010408) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
                  >gi_3367581_emb_CAA20033_ (AL031135) phosphoserine
                  aminotransferase [Arabidopsis thaliana]
Seq. No.
                  147165
Seq. ID
                  LIB3168-086-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  q112739
```

BLAST score 358 4.0e-34 E value 110 Match length

67

% identity NCBI Description

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871 (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

```
Seq. No.
                  LIB3168-086-P1-K1-A9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  561
                  7.0e-58
E value
                  134
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147167
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-B1
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  466
                  7.0e-47
E value
Match length
                  109
% identity
                  82
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147168
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  876
                  1.0e-94
E value
                  176
Match length
                  98
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147169
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g4585924
BLAST score
                  542
                  2.0e-55
E value
Match length
                  174
% identity
NCBI Description (AC007211) hypothetical protein [Arabidopsis thaliana]
                  147170
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2564045
BLAST score
                  204
                  1.0e-111
E value
Match length
                  530
% identity
                  97
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
```

Seq. ID

```
K8K14, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147171
Seq. ID
                  LIB3168-086-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  q2564044
BLAST score
                  131
                  2.0e-67
E value
                  191
Match length
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19P17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147172
                  LIB3168-086-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131336
BLAST score
                  324
E value
                  6.0e-30
                  73
Match length
% identity
NCBI Description
                  PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi 72715 pir F2NTOP
                  photosystem II phosphoprotein psbH - common tobacco
                  chloroplast >gi 11857 emb CAA77374 (Z00044) PSII 10kD
                  phosphoprotein [Nicotiana tabacum]
                  >gi 225225 prf 1211235BG photosystem II 10kD
                  phosphoprotein [Nicotiana tabacum]
Seq. No.
                  147173
Seq. ID
                  LIB3168-086-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  542
E value
                  1.0e-55
Match length
                  118
                  87
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147174
Seq. ID
                  LIB3168-086-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  g3482964
BLAST score
                  167
E value
                  6.0e-89
Match length
                  323
                  88
% identity
                  Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
NCBI Description
                  (ESSAII project)
Seq. No.
                  147175
```

18503

LIB3168-086-P1-K1-B8

```
Method
NCBI GI
                  g112739
BLAST score
                  475
E value
                  1.0e-47
Match length
                  148
% identity
                  66
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147176
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q3128189
BLAST score
                  171
                  2.0e-19
E value
                  93
Match length
% identity
                  (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
NCBI Description
                  147177
Seq. No.
                  LIB3168-086-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  541
E value
                  1.0e-55
Match length
                  111
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147178
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  q3869071
BLAST score
                  450
E value
                  0.0e + 00
Match length
                  477
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MIL23, complete sequence [Arabidopsis thaliana]
                  147179
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  q3869071
BLAST score
                  453
                  0.0e + 00
E value
Match length
                  536
% identity
                  96
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
```

MIL23, complete sequence [Arabidopsis thaliana]

```
147180
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g4262222
BLAST score
                  601
E value
                  1.0e-62
Match length
                  119
% identity
                  (AC006200) putative RNA helicase A, 3' partial [Arabidopsis
NCBI Description
                  thaliana]
                  147181
Seq. No.
                  LIB3168-086-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3776561
BLAST score
                  531
E value
                  3.0e-54
Match length
                  119
                  95
% identity
NCBI Description
                  (AC005388) Identical to DNA for acyl carrier protein (ACP)
                  gene A2 gb X57699 from A. thaliana. ESTs gb W43252,
                  gb_T42821, gb_N65229, gb_N97267, gb_F15491 and gb_AA040955
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  147182
Seq. ID
                  LIB3168-086-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2894599
BLAST score
                  182
                  2.0e-13
E value
Match length
                  125
% identity
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  147183
                  LIB3168-086-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3047104
BLAST score
                  623
E value
                  5.0e-65
Match length
                  123
% identity
NCBI Description
                  (AF058919) No definition line found [Arabidopsis thaliana]
Seq. No.
                  147184
                  LIB3168-086-P1-K1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2961346
BLAST score
                  271
E value
                  1.0e-23
Match length
                  121
% identity
                  (AL022140) pectinesterase like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  147185
```

```
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2795809
BLAST score
                   330
E value
                   8.0e-31
Match length
                   79
% identity
NCBI Description
                   (AC003674) putative expansin [Arabidopsis thaliana]
Seq. No.
                   147186
                   LIB3168-086-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112741
BLAST score
                   847
E value
                   3.0e-91
Match length
                   160
                   97
% identity
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
                   147187
Seq. No.
Seq. ID
                   LIB3168-086-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g2651296
BLAST score
                   633
E value
                   4.0e-66
Match length
                   152
% identity
NCBI Description
                   (AC002336) b-zip DNA-binding protein [Arabidopsis thaliana]
Seq. No.
                   147188
Seq. ID
                   LIB3168-086-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q4406780
BLAST score ·
                   632
E value
                   5.0e-66
Match length
                   154
% identity
                   82
NCBI Description
                   (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                   147189
                   LIB3168-086-P1-K1-D2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3080430
BLAST score
                   466
E value
                   0.0e + 00
                   513
Match length
                   98
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
NCBI Description
                   (ESSAII project)
```

```
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-D3
                  BLASTN
Method
NCBI GI
                  g2842474
BLAST score
                  278
                  1.0e-155
E value
Match length
                  325
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                   (ESSAII project)
                  147191
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  455
E value
                  2.0e-45
Match length
                  114
% identity
                  81
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605_pir_ S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147192
                  LIB3168-086-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2146741
BLAST score
                  77
                  3.0e-33
E value
                  98
Match length
                  77
% identity
                  isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2) -
NCBI Description
                  Arabidopsis thaliana >gi_1293565 (U49259) isopentenyl
                  diphosphate:dimethylallyl diphosphate isomerase
                   [Arabidopsis thaliana]
Seq. No.
                  147193
                  LIB3168-086-P1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159709
                  155
BLAST score
E value
                  7.0e-82
                  251
Match length
% identity
                  90
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLN21, complete sequence
Seq. No.
                  147194
                  LIB3168-086-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                  607
E value
                  3.0e-63
Match length
                  150
% identity
                  79
```

```
(AC003027) lcl_prt_seq No definition line found
NCBI Description
                  [Arabidopsis thaliana]
                  147195
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  288
E value
                  7.0e-26
Match length
                  65
% identity
NCBI Description
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
                  147196
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  44
                  4.0e-58
E value
Match length
                  144
                  90
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147197
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3273743
BLAST score
                  536
                  6.0e-55
E value
Match length
                  118
                  89
% identity
NCBI Description
                   (AF057357) lipid transfer protein 2 precursor [Arabidopsis
                  thaliana] >gi 3786019 (AC005499) unknown protein
                  [Arabidopsis thaliana]
                  147198
Seq. No.
                  LIB3168-086-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160133
                  150
BLAST score
E value
                  3.0e-10
Match length
                  49
% identity
NCBI Description
                   (AC000375) Strong similarity to Arabidopsis
                  gb_X91953,F19K23.3,F19K23.15. ESTs
                  gb T21984,gb ATTS0219,gb ATTS0207,gb T21984 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  147199
Seq. ID
                  LIB3168-086-P1-K1-E4
                  BLASTX
Method
NCBI GI
                  g112741
BLAST score
                  753
E value
                  2.0e-80
```

```
Match length
% identity
                  99
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147200
Seq. No.
                  LIB3168-086-P1-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2760171
BLAST score
                  193
                  1.0e-104
E value
                  392
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MPA24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147201
                  LIB3168-086-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3449320
BLAST score
                  381
                  0.0e+00
E value
                  473
Match length
                  95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRB17, complete sequence [Arabidopsis thaliana]
                  147202
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  q112682
                  594
BLAST score
                  1.0e-61
E value
Match length
                  141
                  84
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147203
Seq. ID
                  LIB3168-086-P1-K1-E8
Method
                  BLASTX
```

Method BLASTX
NCBI GI g2738248
BLAST score 461
E value 1.0e-64
Match length 154
% identity 88

NCBI Description (U97200) cobalamin-independent methionine synthase

[Arabidopsis thaliana]

```
Seq. No.
                   147204
Seq. ID
                   LIB3168-086-P1-K1-E9
Method
                   BLASTN
NCBI GI
                   q987013
BLAST score
                   204
                   1.0e-111
E value
                   300
Match length
% identity
                   92
                   A.thaliana mRNA for oleosin (isoform; 841 bp)
NCBI Description
                   >gi 987015 emb Z54165 ATOLEOSN3 A.thaliana mRNA for oleosin
                   (isoform; 841 bp)
Seq. No.
                   147205
                   LIB3168-086-P1-K1-F1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4100568
BLAST score
                   83
E value
                   3.0e-39
Match length
                   95
% identity
                   98
NCBI Description
                  Arabidopsis thaliana fatty acid desaturase/cytochrome b5
                   fusion protein mRNA, complete cds
Seq. No.
                   147206
Seq. ID
                   LIB3168-086-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   q3063690
BLAST score
                   218
E value
                   1.0e-119
Match length
                   437
% identity
                   94
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
                   (ESSAII project)
Seq. No.
                   147207
Seq. ID
                   LIB3168-086-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q4544419
BLAST score
                   598
E value
                   4.0e-62
Match length
                   148
% identity
NCBI Description
                  (AC006955) unknown protein [Arabidopsis thaliana]
Seq. No.
                   147208
Seq. ID
                   LIB3168-086-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q4204298
BLAST score
                   582
E value
                   3.0e-60
Match length
                   152
                   77
% identity
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   147209
Seq. ID
                  LIB3168-086-P1-K1-F3
```

% identity

```
Method
                  BLASTX
NCBI GI
                  q112743
BLAST score
                  704
E value
                  1.0e-74
Match length
                  148
% identity
                  89
NCBI Description
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                   (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147210
Seq. ID
                  LIB3168-086-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  549
E value
                  2.0e-56
Match length
                  112
                  99
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147211
Seq. ID
                  LIB3168-086-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g2661422
BLAST score
                  740
E value
                  1.0e-78
Match length
                  144
% identity
                  99
                   (AJ001342) Putative S-phase-specific ribosomal protein
NCBI Description
                   [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1
                   (AL023094) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana]
Seq. No.
                  147212
Seq. ID
                  LIB3168-086-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g4006897
BLAST score
                  42
E value
                  8.0e-43
Match length
                  112
% identity
NCBI Description (299708) globulin-like protein [Arabidopsis thaliana]
Seq. No.
                  147213
Seq. ID
                  LIB3168-086-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  277
E value
                  1.0e-27
Match length
                  96
```

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495 emb CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147214 Seq. ID LIB3168-086-P1-K1-F8 Method BLASTX NCBI GI g112741 BLAST score 457 9.0e-51 E value 101 Match length 94 % identity NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] 147215 Seq. No. Seq. ID LIB3168-086-P1-K1-F9 Method BLASTX NCBI GI g112682 BLAST score 716 E value 5.0e-76 145 Match length 92 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605 pir\_\_S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 147216 Seq. ID LIB3168-086-P1-K1-G11 Method BLASTX NCBI GI q3660465 BLAST score 471 4.0e-47 E value Match length 91 % identity (AJ001753) Inositol 1,3,4-Trisphosphate 5/6 kinase NCBI Description [Arabidopsis thaliana] Seq. No. 147217 Seq. ID LIB3168-086-P1-K1-G12 Method BLASTX NCBI GI q112741 BLAST score 885 E value 1.0e-95 Match length 164 99 % identity 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868 Seq. No.

Seq. ID

E value

Seq. No. Seq. ID

Method NCBI GI

BLAST score

Match length

% identity

BLAST score E value

Match length

% identity

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score

Match length

% identity

Method NCBI GI

```
(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147218
                  LIB3168-086-P1-K1-G2
                  BLASTX
                  q3335171
                  673
                  6.0e-71
                  134
                  96
NCBI Description (AF067858) embryo-specific protein 3 [Arabidopsis thaliana]
                  147219
                  LIB3168-086-P1-K1-G3
                  BLASTN
                  g3128136
                  255
                  1.0e-141
                  471
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1F13, complete sequence [Arabidopsis thaliana]
                  147220
                  LIB3168-086-P1-K1-G4
                  BLASTX
                  g112741
                  846
                  4.0e-91
                  157
                  100
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147221
                  LIB3168-086-P1-K1-G5
                  BLASTX
                  q1628583
                  642
                  3.0e-67
```

Seq. No. Seq. ID Method NCBI GI BLAST score

E value 123 Match length 100 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

147222 Seq. No.

LIB3168-086-P1-K1-G6 Seq. ID

Method BLASTX NCBI GI g1628583

```
BLAST score
E value
                  7.0e-65
Match length
                  120
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 125
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147223
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  524
                  2.0e-53
E value
                  120
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147224
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g3241916
                  321
BLAST score
                  0.0e+00
E value
Match length
                  469
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15N18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147225
Seq. ID
                  LIB3168-086-P1-K1-G9
                  BLASTN
Method
                  q4006885
NCBI GI
BLAST score
                  324
                  0.0e + 00
E value
Match length
                  452
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
Seq. No.
                  147226
Seq. ID
                  LIB3168-086-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g3318611
BLAST score
                  339
                  1.0e-31
E value
Match length
                  66
% identity
                  (AB016063) mitochondrial phosphate transporter [Glycine
NCBI Description
                  max]
Seq. No.
                  147227
Seq. ID
                  LIB3168-086-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  q4757414
```

```
BLAST score
E value
                  0.0e+00
Match length
                  483
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
Seq. No.
                  147228
Seq. ID
                  LIB3168-086-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q4006914
BLAST score
                  609
E value
                  1.0e-63
                  119
Match length
% identity
NCBI Description
                  (Z99708) serine C-palmitoyltransferase like protein
                  [Arabidopsis thaliana]
Seq. No.
                  147229
                  LIB3168-086-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
                  709
BLAST score
E value
                  4.0e-75
Match length
                  163
                  89
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir_ NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147230
                  LIB3168-086-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  435
E value
                  3.0e - 43
Match length
                  99
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147231
Seq. No.
Seq. ID
                  LIB3168-086-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  g4220632
BLAST score
                  131
                  2.0e-67
E value
Match length
                  387
% identity
                  92
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
```

```
K6M13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147232
Seq. ID
                  LIB3168-086-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2160191
BLAST score
                  50
E value
                  1.0e-04
Match length
                  75
% identity
                  81
NCBI Description
                  (ACO00132) Identical to A. thaliana AtK-1 (gb X79279).
                  [Arabidopsis thaliana]
Seq. No.
                  147233
                  LIB3168-086-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  42
                  1.0e-32
E value
                  94
Match length
                  86
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >qi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147234
                  LIB3168-086-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  588
                  6.0e-61
E value
                  130
Match length
% identity
                  87.
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147235
Seq. No.
                  LIB3168-086-P1-K1-H8
Seg. ID
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  619
E value
                  3.0e-85
Match length
                  160
% identity
                  92
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
```

Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

```
(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]
```

```
Seq. No.
                   147236
                   LIB3168-087-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112741
BLAST score
                   665
E value
                   5.0e-70
Match length
                   142
% identity
                   89
```

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

```
      Seq. No.
      147237

      Seq. ID
      LIB3168-087-P1-K1-A11

      Method
      BLASTX

      NCBI GI
      g112741

      BLAST score
      435

      E value
      3.0e-43
```

Match length 98 % identity 84

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

```
      Seq. No.
      147238

      Seq. ID
      LIB3168-087-P1-K1-A12

      Method
      BLASTX

      NCBI GI
      g3157947

      RLAST score
      298
```

NCBI GI g3157947
BLAST score 298
E value 5.0e-49
Match length 131
% identity 54

NCBI Description (AC002131) Similar to protein gb\_Z74962 from Brassica oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb\_T21954, gb\_T04283, gb\_Z37609, gb\_N37366,

gb\_R90704, gb\_F15500 and gb\_F14353 come from this gene.

[Arabidopsis tha

Seq. No. 147239

Seq. ID LIB3168-087-P1-K1-A4

Method BLASTX
NCBI GI g112682
BLAST score 412
E value 1.0e-40
Match length 94

BLAST score

Match length

E value

465

123

2.0e-46

```
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147240
                  LIB3168-087-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4038491
BLAST score
                  155
E value
                  3.0e-10
Match length
                  110
% identity
                  (AJ131705) poly(ADP-ribose) polymerase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  147241
Seq. ID
                  LIB3168-087-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  301
                  2.0e-27
E value
Match length
                  56
% identity
                  100
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147242
Seq. ID
                  LIB3168-087-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  460
                  4.0e-46
E value
                  115
Match length
                  77
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147243
Seq. ID
                  LIB3168-087-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g2129657
```

% identity NCBI Description oleosin isoform - Arabidopsis thaliana >gi\_987014\_emb CAA90877 (Z54164) oleosin [Arabidopsis thaliana]  $\overline{>}$ gi  $\overline{9}87016$  em $\overline{b}$  CAA90878\_ (Z54165) oleosin [Arabidopsis thaliana] Seq. No. 147244 Seq. ID LIB3168-087-P1-K1-B1 BLASTX Method NCBI GI q1628583 BLAST score 527 7.0e-54 E value 120 Match length 84 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147245 LIB3168-087-P1-K1-B10 Seq. ID BLASTX Method NCBI GI g112737 714 BLAST score E value 1.0e-75 Match length 164 83 % identity 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870 (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana] Seq. No. 147246 LIB3168-087-P1-K1-B11 Seq. ID BLASTX Method NCBI GI q1628583 325 BLAST score E value 2.0e-30 89 Match length % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147247

Seq. ID LIB3168-087-P1-K1-B2

Method BLASTX
NCBI GI g1628583
BLAST score 239
E value 3.0e-56
Match length 128
% identity 88

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

```
147248
Seq. No.
                   LIB3168-087-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   249
E value
                   2.0e-21
Match length
                   49
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   147249
Seq. No.
                   LIB3168-087-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q99742
BLAST score
                   373
                   5.0e-36
E value
Match length
                   94
                   79
% identity
                   2-dehydro-3-deoxyphosphoheptonate aldolase (EC 4.1.2.15) 1
NCBI Description
                   - Arabidopsis thaliana
                   147250
Seq. No.
Seq. ID
                   LIB3168-087-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   q112681
                   854
BLAST score
                   4.0e-92
E value
Match length
                   172
                   97
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir__S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   tha\overline{\text{liana}} >gi 808936 emb CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   147251
Seq. No.
                   LIB3168-087-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   416
                   6.0e-41
E value
                   113
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   147252
Seq. No.
Seq. ID
                   LIB3168-087-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   474
                   8.0e-48
E value
                   114
Match length
```

NCBI GI

g112682

```
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147253
Seq. ID
                   LIB3168-087-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g112737
BLAST score
                   687
E value
                   1.0e-72
Match length
                   146
                   90
% identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi_4490710_emb_CAB38844.1 (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
                   147254
Seq. No.
Seq. ID
                   LIB3168-087-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   581
E value
                   5.0e-60
Match length
                   120
% identity
                   94
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147255
Seq. ID
                   LIB3168-087-P1-K1-C4
Method
                   BLASTN
NCBI GI
                   q3600045
BLAST score
                   180
E value
                   1.0e-96
Match length
                   372
                   94
% identity
NCBI Description Arabidopsis thaliana BAC F2P3
Seq. No.
                   147256
Seq. ID
                   LIB3168-087-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g3859696
BLAST score
                   190
E value
                   2.0e-14
Match length
                   132
% identity
                   33
NCBI Description (AL033497) unknown hypothetical protein [Candida albicans]
Seq. No.
                   147257
Seq. ID
                   LIB3168-087-P1-K1-C6
Method
                   BLASTX
```

```
BLAST score
E value
                  9.0e-47
Match length
                  109
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147258
                  LIB3168-087-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  642
                  3.0e-67
E value
Match length
                  123
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147259
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-C8
                  BLASTX
Method
NCBI GI
                  g4455338
BLAST score
                  687
                  1.0e-72
E value
Match length
                  133
                  100
% identity
NCBI Description (AL035525) putative protein [Arabidopsis thaliana]
Seq. No.
                  147260
Seq. ID
                  LIB3168-087-P1-K1-C9
                  BLASTX
Method
NCBI GI
                  q112681
BLAST score
                  744
                  3.0e-79
E value
Match length
                  141
% identity
                  99
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147261
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  358
                  4.0e-34
E value
                  89
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
```

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                  147262
Seq. ID
                  LIB3168-087-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g3551247
BLAST score
                  740
E value
                  9.0e-79
Match length
                  155
% identity
                  (AB012703) 181 [Daucus carota]
NCBI Description
                  147263
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-D11
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  644
E value
                  1.0e-67
Match length
                  127
                  96
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147264
                  LIB3168-087-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  698
E value
                  6.0e-74
                  140
Match length
                  96
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147265
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  678
E value
                  1.0e-71
Match length
                  142
                  92
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147266
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-D3
                  BLASTX
Method
NCBI GI
                  g1345973
BLAST score
                  389
                  9.0e-38
E value
                  92
Match length
                  79
% identity
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi 541882 pir JQ2335 omega-3 fatty acid desaturase (EC
```

```
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi_3420053 (AC004680) omega-3 fatty acid desaturase [Arabidopsis thaliana]

147267
LIB3168-087-P1-K1-D4
BLASTX
g4455300
174
2.0e-12
```

 Seq. No.
 147268

 Seq. ID
 LIB3168-087-P1-K1-D5

 Method
 BLASTX

 NCBI GI
 g2832625

 BLAST score
 523

39

BLAST score 523
E value 2.0e-53
Match length 116
% identity 84

Seq. No. Seq. ID

Method

NCBI GI

E value Match length

BLAST score

NCBI Description (AL021711) putative protein [Arabidopsis thaliana]

Seq. No. 147269 Seq. ID LIB3168-087-P1-K1-D6

Method BLASTN
NCBI GI g12208
BLAST score 268
E value 1.0e-149
Match length 358
% identity 92

NCBI Description Sinapis alba plastid trnQ and psbK genes for tRNA-Glu and K proteiH of photosystem II

Seq. No. 147270

Seq. ID LIB3168-087-P1-K1-D7

Method BLASTN
NCBI GI g3176694
BLAST score 415
E value 0.0e+00
Match length 415
% identity 100

NCBI Description Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 147271

Seq. ID LIB3168-087-P1-K1-D8

Method BLASTX
NCBI GI g1628583
BLAST score 491
E value 7.0e-50

E value

2.0e-50

```
99
Match length
                   97
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147272
Seq. ID
                  LIB3168-087-P1-K1-D9
Method
                   BLASTN
NCBI GI
                   q4454022
BLAST score
                   260
                   1.0e-144
E value
                   375
Match length
                   96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F9D16
NCBI Description
                   (ESSAII project)
Seq. No.
                   147273
Seq. ID
                  LIB3168-087-P1-K1-E1
Method
                  BLASTX
NCBI GI
                   g1107501
                   389
BLAST score
E value
                   1.0e-37
                   96
Match length
% identity
                   (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
NCBI Description
                  Match to gb_X91954 orf gene product from A. thaliana. ESTs
                   gb Z17604, gb H76594, gb AA597972 and gb AA394824 come from
                   this gene. [Arabidopsis thaliana]
                   147274
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-E10
Method
                  BLASTX
                   g3776005
NCBI GI
BLAST score
                   484
                   6.0e-49
E value
                  110
Match length
                   86
% identity
NCBI Description
                  (AJ010466) RNA helicase [Arabidopsis thaliana]
                   147275
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   g1871173
BLAST score
                  242
E value
                   1.0e-133
                  349
Match length
                   93
% identity
                  Arabidopsis thaliana chromosome II BAC T06D20 genomic
NCBI Description
                  sequence, complete sequence
                  147276
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-E12
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  497
```

```
Match length
                  98
% identity
                  96
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147277
Seq. ID
                  LIB3168-087-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  645
                  1.0e-84
E value
Match length
                  158
                  92
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147278
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q112682
                  785
BLAST score
E value
                  5.0e-84
Match length
                  176
                  86
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147279
                  LIB3168-087-P1-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3510339
BLAST score
                  262
E value
                  1.0e-145
Match length
                  355
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3K7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147280
Seq. ID
                  LIB3168-087-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  521
E value
                  4.0e-53
Match length
                  103
% identity
NCBI Description
                  (AC003027) 1cl prt seq No definition line found
                  [Arabidopsis thaliana]
```

Seq. No. 147281

```
Seq. ID
                  LIB3168-087-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  470
E value
                  4.0e-47
Match length
                  133
% identity
                  72
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147282
Seq. No.
                  LIB3168-087-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  665
E value
                  4.0e-70
                  127
Match length
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147283
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g399091
BLAST score
                  780
E value
                  2.0e-83
Match length
                  175
                  89
% identity
                  PYROPHOSPHATE-ENERGIZED VACUOLAR MEMBRANE PROTON PUMP
NCBI Description
                  (PYROPHOSPHATE-ENERGIZED INORGANIC PYROPHOSPHATASE)
                  (H+-PPASE) >gi_282878_pir__A38230 inorganic pyrophosphatase
                  (EC 3.6.1.1), H+-translocating pyrophosphate-energized -
                  Arabidopsis thaliana >gi_166634 (M81892) vacuolar
                  H+-phosphatase [Arabidopsis thaliana]
Seq. No.
                  147284
Seq. ID
                  LIB3168-087-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g112681
                  691
BLAST score
E value
                  4.0e-73
                  134
Match length
                  97
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
```

Seq. No. 147285

storage protein [Arabidopsis thaliana]

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

```
Seq. ID
                  LIB3168-087-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  621
E value
                  5.0e-65
Match length
                  119
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein {Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147286
                  LIB3168-087-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  252
E value
                  9.0e-22
Match length
                  81
% identity
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                  >gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                  [Arabidopsis thaliana]
                  147287
Seq. No.
                  LIB3168-087-P1-K1-F2
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4406776
BLAST score
                  384
E value
                  0.0e + 00
                  489
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14H2O genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  147288
Seq. No.
                  LIB3168-087-P1-K1-F3
Seq. ID
Method
                  BLASTX
                  g3193331
NCBI GI
BLAST score
                  177
                  7.0e-13
E value
Match length
                  45
% identity
NCBI Description
                  (AF069299) No definition line found [Arabidopsis thaliana]
                  147289
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  615
E value
                  3.0e-64
Match length
                  132
                  89
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
```

## storage protein [Arabidopsis thaliana]

```
Seq. No.
                  147290
                  LIB3168-087-P1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3821780
BLAST score
                  37
                  3.0e-11
E value
Match length
                  37
                  100
% identity
NCBI Description Xenopus laevis cDNA clone 27A6-1
Seq. No.
                  147291
Seq. ID
                  LIB3168-087-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  g2264302
BLAST score
                  286
E value
                  1.0e-160
Match length
                  385
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147292
Seq. ID
                  LIB3168-087-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g1171870
BLAST score
                  152
E value
                  9.0e-10
                  88
Match length
                  33
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT (COMPLEX
NCBI Description
                  I-19KD) (CI-19KD) (COMPLEX I-PGIV) (CI-PGIV)
                  >gi 89670 pir S16208 NADH dehydrogenase (ubiquinone) (EC
                  1.6.5.3) 19K chain - bovine >gi 599681_emb_CAA42218
                  (X59697) 19 kDa subunit of NADH:ubiquinone oxidoreductase
                  complex (complex I) [Bos taurus]
                  147293
Seq. No.
                  LIB3168-087-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1526412
                  286
BLAST score
                  1.0e-160
E value
Match length
                  330
% identity
                  97
                  Arabidopsis thaliana ATPK19 mRNA for ribosomal-protein S6
NCBI Description
                  kinase homolog, complete cds
Seq. No.
                  147294
Seq. ID
                  LIB3168-087-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  893
E value
                  1.0e-96
Match length
                  164
                  100
% identity
```

```
2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147295
                  LIB3168-087-P1-K1-G10
                  BLASTX
                  q115783
                  561
```

Seq. ID Method NCBI GI BLAST score 7.0e-58 E value Match length 109 % identity 97

Seq. No.

CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

147296 Seq. No. Seq. ID LIB3168-087-P1-K1-G12 Method BLASTN q3798730 NCBI GI

BLAST score 45 3.0e-16 E value Match length 73 90 % identity

Arabidopsis thaliana transgenic line C DNA NCBI Description

147297 Seq. No. Seq. ID LIB3168-087-P1-K1-G2 Method BLASTX

NCBI GI q1628583 BLAST score 625 E value 3.0e-65 Match length 120 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147298

Seq. ID LIB3168-087-P1-K1-G4

Method BLASTN NCBI GI q4512656 BLAST score 151 E value 3.0e-79Match length 357 % identity 84

NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic

sequence, complete sequence

147299 Seq. No.

LIB3168-087-P1-K1-G5 Seq. ID

Method BLASTX

```
q1628583
NCBI GI
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147300
                  LIB3168-087-P1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  607
E value
                  2.0e-63
Match length
                  123
% identity
                  93
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir_RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  147301
                  LIB3168-087-P1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3046854
BLAST score
                  329
E value
                  0.0e + 00
Match length
                  473
% identity
                  94
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRG7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147302
Seq. ID
                  LIB3168-087-P1-K1-G8
Method
                  BLASTX
                  q1354272
NCBI GI
BLAST score
                  671
                  1.0e-70
E value
Match length
                  143
% identity
                  86
                  (U51036) aspartic proteinase [Arabidopsis thaliana]
NCBI Description
                  147303
Seq. No.
                  LIB3168-087-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2507477
BLAST score
                  184
E value
                  2.0e-13
Match length
                  120
                  37
% identity
                  TRANSALDOLASE A >gi_1788807 (AE000333) transaldolase A
NCBI Description
                  [Escherichia coli] >gi_1799888_dbj_BAA16339_ (D90875)
                  similar to [PIR Accession Number S40535] [Escherichia coli]
                  >gi_2337774_dbj_BAA21821_ (D13159) transaldolase
```

[Escherichia coli]

NCBI GI

g82051

```
Seq. No.
                   147304
Seq. ID
                  LIB3168-087-P1-K1-H1
Method
                  BLASTX
NCBI GI
                   g3894193
BLAST score
                   431
E value
                   2.0e-42
Match length
                   137
                   59
% identity
NCBI Description
                   (AC005662) putative strictosidine synthase [Arabidopsis
                   147305
Seq. No.
Seq. ID
                  LIB3168-087-P1-K1-H12
Method
                   BLASTN
NCBI GI
                   q3046853
BLAST score
                   140
E value
                   4.0e-73
Match length
                   148
                   99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRA19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   147306
Seq. ID
                   LIB3168-087-P1-K1-H3
Method
                  BLASTX
NCBI GI
                   q112739
BLAST score
                   470
E value
                   4.0e-47
Match length
                   131
% identity
                   73
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                   Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                   2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                   (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                   >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                   precursor [Arabidopsis thaliana]
Seq. No.
                   147307
                   LIB3168-087-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131336
BLAST score
                   247
E value
                   5.0e-21
Match length
                   58
% identity
                  PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi 72715_pir__F2NT0P
NCBI Description
                  photosystem II phosphoprotein psbH - common tobacco
                   chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD
                  phosphoprotein [Nicotiana tabacum]
                  >gi_225225_prf__1211235BG photosystem II 10kD
phosphoprotein [Nicotiana tabacum]
Seq. No.
                  147308
Seq. ID
                  LIB3168-087-P1-K1-H6
Method
                  BLASTX
```

```
BLAST score
                  368
E value
                  4.0e-35
Match length
                  151
                  50
% identity
NCBI Description
                  lipid body-associated membrane protein - carrot
                  >gi 259453 bbs 117620 (S47635) lipid body membrane
                  protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                  180 aa] [Daucus carota]
Seq. No.
                  147309
                  LIB3168-087-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q633890
BLAST score
                  450
E value
                  1.0e-44
Match length
                  150
% identity
NCBI Description
                  ($72926) glucose and ribitol dehydrogenase homolog [Hordeum
                  vulgare]
Seq. No.
                  147310
Seq. ID
                  LIB3168-087-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  653
E value
                  1.0e-68
Match length
                  119
% identity
                  100
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147311
Seq. ID
                  LIB3168-088-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  605
E value
                  5.0e-63
Match length
                  117
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147312
                  LIB3168-088-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1255951
BLAST score
                  227
E value
                  7.0e-32
Match length
                  103
% identity
                  70
NCBI Description (X96932) PS60 [Nicotiana tabacum]
```

```
147313
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g1336807
BLAST score
                  265
                   3.0e-23
E value
                  100
Match length
                  56
% identity
                   (S81193) CEN=GTP-binding protein homolog
NCBI Description
                   [Antirrhinum=snapdragons, Peptide, 181 aa] [Antirrhinum]
                  >gi 1587482 prf 2206476A CEN gene [Antirrhinum sp.]
                  147314
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-A2
                  BLASTX
Method
NCBI GI
                  g3342249
BLAST score
                  528
                   4.0e-54
E value
Match length
                  106
                   98
% identity
NCBI Description
                   (AF047719) GA3 [Arabidopsis thaliana] >gi_3342251
                   (AF047720) GA3 [Arabidopsis thaliana]
Seq. No.
                  147315
Seq. ID
                  LIB3168-088-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g82051
                  331
BLAST score
E value
                   6.0e-31
Match length
                  124
                   53
% identity
                  lipid body-associated membrane protein - carrot
NCBI Description
                  >gi 259453 bbs_117620 (S47635) lipid body membrane
                  protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,
                  180 aa] [Daucus carota]
                  147316
Seq. No.
                  LIB3168-088-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  597
E value
                   4.0e-62
Match length
                  113
                  98
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147317
                  LIB3168-088-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  554
E value
                  5.0e-57
```

```
Match length
                  125
% identity
                  86
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 125 seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147318
Seq. ID
                  LIB3168-088-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q4584346
BLAST score
                  420
E value
                  2.0e-41
                  91
Match length
                  90
% identity
                  (AC007127) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  147319
                  LIB3168-088-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112739
                  187
BLAST score
                  2.0e-14
E value
Match length
                  41
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147320
Seq. ID
                  LIB3168-088-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4539301
BLAST score
                  120
E value
                  1.0e-12
Match length
                  66
% identity
NCBI Description
                  (AL049480) putative mitochondrial protein [Arabidopsis
                  thaliana]
Seq. No.
                  147321
Seq. ID
                  LIB3168-088-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  628
E value
                  8.0e-66
Match length
                  121
% identity
                  98
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
```

thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed



storage protein [Arabidopsis thaliana]

Seq. No. 147322

Seq. ID LIB3168-088-P1-K1-B1

Method BLASTX
NCBI GI g112741
BLAST score 686
E value 2.0e-72
Match length 127
% identity 100

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 147323

Seq. ID LIB3168-088-P1-K1-B10

Method BLASTX
NCBI GI g112682
BLAST score 618
E value 1.0e-64
Match length 131
% identity 91

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147324

Seq. ID LIB3168-088-P1-K1-B11

Method BLASTX
NCBI GI g112737
BLAST score 426
E value 4.0e-42
Match length 121
% identity 71

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi\_4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147325

Seq. ID LIB3168-088-P1-K1-B12

Method BLASTX
NCBI GI g3241945
BLAST score 144
E value 5.0e-09
Match length 65
% identity 43

NCBI Description (AC004625) unknown protein [Arabidopsis thaliana]

```
147326
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  736
E value
                  2.0e-78
Match length
                  136
                  100
% identity
NCBI Description
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
                  >gi 4455197 emb CAB36520.1 (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
                  147327
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-B3
                  BLASTX
Method
NCBI GI
                  g548847
BLAST score
                  253
E value
                  9.0e-22
                  51
Match length
                  98
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                  >gi_1086182_pir__S39501 ribosomal protein S12 -
                  curled-leaved tobacco >gi 225248 prf 1211235CG ribosomal
                  protein S12 [Nicotiana tabacum]
                  147328
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g3241922
BLAST score
                  137
                  2.0e-71
E value
Match length
                  168
                  96
% identity
                 Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLM24, complete sequence [Arabidopsis thaliana]
                  147329
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  556
                  3.0e-57
E value
Match length
                  131
% identity
                  81
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147330
Seq. ID
                  LIB3168-088-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  301
E value
                  1.0e-27
```

```
102
Match length
% identity
                  62
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147331
Seq. ID
                  LIB3168-088-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1172676
BLAST score
                  384
E value
                  2.0e-37
Match length
                  80
                  93
% identity
                  PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN)
NCBI Description
                  (CP43) >gi 1262709 dbj_BAA04424.1_ (D17510) PSII 44kDa
                  protein [Pinus thunbergii]
                  147332
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  522
E value
                  2.0e-53
Match length
                  104
% identity
                  95
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147333
Seq. ID
                  LIB3168-088-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3808062
                  .175
BLAST score
E value
                  1.0e-12
                  73
Match length
% identity
NCBI Description (AB019195) PV100 [Cucurbita maxima]
Seq. No.
                  147334
Seq. ID
                  LIB3168-088-P1-K1-C10
                  BLASTN
Method
NCBI GI
                  g2656026
BLAST score
                  258
E value
                  1.0e-143
                  325
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MDF20

BLAST score

```
Seq. No.
                   147335
Seq. ID
                   LIB3168-088-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g2129657
BLAST score
                   335
E value
                   2.0e-31
Match length
                   97
% identity
                   74
NCBI Description
                   oleosin isoform - Arabidopsis thaliana
                   >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                   [Arabidopsis thaliana]
Seq. No.
                   147336
Seq. ID
                   LIB3168-088-P1-K1-C2
Method
                   BLASTX
NCBI GI
                   g2444271
                   561
BLAST score
E value
                   7.0e-58
Match length
                   123
% identity
                   85
NCBI Description
                   (AF019637) putative amino acid or GABA permease
                   [Arabidopsis thaliana]
Seq. No.
                   147337
Seq. ID
                   LIB3168-088-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q112737
BLAST score
                   533
E value
                   1.0e-54
Match length
                   130
                   79
% identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                   Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                   1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (224745) 2S albumin isoform 1 [Arabidopsis thaliana]
                   >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                   precursor [Arabidopsis thaliana]
Seq. No.
                   147338
Seq. ID
                   LIB3168-088-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   718
E value
                   3.0e-76
Match length
                   136
                   100
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147339
Seq. ID
                   LIB3168-088-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   q4468103
```

```
E value
                  1.0e-132
Match length
                  417
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
                  (ESSA project)
Seq. No.
                  147340
Seq. ID
                  LIB3168-088-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g3128139
BLAST score
                  392
                  0.0e + 00
E value
                  396
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIK19, complete sequence [Arabidopsis thaliana]
                  147341
Seq. No.
                  LIB3168-088-P1-K1-C8
Seq. ID
                  BLASTX
Method
                  q112681
NCBI GI
BLAST score
                  510
                  6.0e-52
E value
                  134
Match length
                  78
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147342
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  523
                  1.0e-53
E value
Match length
                  112
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147343
Seq. No.
Sea. ID
                  LIB3168-088-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  54
                  2.0e-38
E value
                  89
Match length
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
```

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed



## storage protein [Arabidopsis thaliana]

Seq. No. 147344 Seq. ID LIB3168-088-P1-K1-E12 Method BLASTN NCBI GI g3108248 BLAST score 54 E value 1.0e-21 Match length 111 % identity 87

147345

NCBI Description Gossypium barbadense clone pXP027 repetitive DNA sequence

Seq. ID LIB3168-088-P1-K1-E5 Method BLASTX NCBI GI g112739 BLAST score 468 E value 5.0e-47

Match length 131 73 % identity

Seq. No.

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor -

Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_

1. ........

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 147346

Seq. ID LIB3168-088-P1-K1-E6

Method BLASTX NCBI GI g3929649 BLAST score 237 E value 4.0e-20 Match length 62 % identity

(AJ131205) mitochondrial NAD-dependent malate dehydrogenase NCBI Description

[Arabidopsis thaliana]

Seq. No. 147347

Seq. ID LIB3168-088-P1-K1-E7

Method BLASTN NCBI GI g3449314 BLAST score 307 E value 1.0e-172 Match length 370 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K22F20, complete sequence [Arabidopsis thaliana]

147348 Seq. No.

Seq. ID LIB3168-088-P1-K1-E8

Method BLASTN NCBI GI g2864607 BLAST score 331 E value 0.0e + 00Match length 358

```
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                   (ESSAII project)
                  147349
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g2138315
BLAST score
                  289
E value
                  1.0e-161
Match length
                  383
                  99
% identity
                  Arabidopsis thaliana root hair defective 3 (RHD3) gene,
NCBI Description
                  complete cds
Seq. No.
                  147350
                  LIB3168-088-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  521
E value
                  3.0e-53
Match length
                  108
% identity
                  92
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147351
Seq. ID
                  LIB3168-088-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  g2459406
BLAST score
                  120
E value
                  4.0e-61
Match length
                  212
% identity
                  92
                  Arabidopsis thaliana chromosome II BAC F4P9 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147352
Seq. ID
                  LIB3168-088-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  277
E value
                  4.0e-25
                  73
Match length
% identity
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  147353
Seq. ID
                  LIB3168-088-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  592
E value
                  1.0e-61
```

125 Match length % identity 89 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis tha $\overline{\text{liana}}$  >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 147354 LIB3168-088-P1-K1-F2 Seq. ID Method BLASTX NCBI GI g112739 BLAST score 432 E value 9.0e-43 124 Match length 70 % identity 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871 (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana] Seq. No. 147355 Seq. ID LIB3168-088-P1-K1-F3 Method BLASTX NCBI GI g1628583 BLAST score 356 E value 8.0e-34 Match length 69 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147356 Seq. ID LIB3168-088-P1-K1-F5 Method BLASTX NCBI GI g112681 BLAST score 276 1.0e-24 E value 72 Match length % identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 147357 Seq. ID LIB3168-088-P1-K1-F6 Method **BLASTX** 

NCBI GI g112682 BLAST score 572

E value 3.0e-59 Match length 119

```
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   147358
Seq. ID
                  LIB3168-088-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  g2760172
BLAST score
                   402
E value
                   0.0e + 00
Match length
                   406
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   147359
                  LIB3168-088-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4455229
BLAST score
                   371
E value
                   0.0e+00
Match length
                   375
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23
                   (ESSAII project)
                   147360
Seq. No.
Seq. ID
                  LIB3168-088-P1-K1-F9
Method
                  BLASTX
NCBI GI
                   g4204299
BLAST score
                   674
E value
                   4.0e-71
Match length
                  129
% identity
                   99
NCBI Description,
                   (AC003027) 1cl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   147361
Seq. ID
                  LIB3168-088-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2335094
BLAST score
                  232
E value
                  3.0e-25
Match length
                  63
% identity
NCBI Description
                   (AC002339) putative polygalacturonase [Arabidopsis
                  thaliana]
Seq. No.
                  147362
Seq. ID
                  LIB3168-088-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  591
E value
                  2.0e-61
```

Match length 137 % identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir \$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 125 seed

storage protein [Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3168-088-P1-K1-G11

147363

Method BLASTX NCBI GI q2494896 BLAST score 242 E value 4.0e-21 Match length 54 81 % identity

EUKARYOTIC TRANSLATION INITIATION FACTOR 3 DELTA SUBUNIT NCBI Description

(EIF-3 DELTA) (EIF3 P36) (TGF-BETA RECEPTOR INTERACTING PROTEIN 1) (TRIP-1) >gi 2129749 pir S60256 TGF-beta receptor interacting protein 1 homolog - Arabidopsis

thaliana >gi 1036803 (U36765) TGF-beta receptor interacting

protein 1 homolog [Arabidopsis thaliana]

Seq. No. 147364

Seq. ID LIB3168-088-P1-K1-G12

Method BLASTX NCBI GI g1628583 BLAST score 668 E value 2.0e-70 132 Match length 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147365

Seq. ID LIB3168-088-P1-K1-G3

Method BLASTX NCBI GI q112741 BLAST score 695 E value 1.0e-73 Match length 129 100 % identity

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi 4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 147366

Seq. ID LIB3168-088-P1-K1-G5

Method BLASTX NCBI GI g1628583 BLAST score 646 E value 7.0e-68

```
126
Match length
% identity
                  98
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147367
Seq. ID
                  LIB3168-088-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  g2264320
BLAST score
                  214
                  1.0e-117
E value
                  377
Match length
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXI10, complete sequence [Arabidopsis thaliana]
                  147368
Seq. No.
                  LIB3168-088-P1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4557061
                  328
BLAST score
E value
                  0.0e + 00
Match length
                   400
                   96
% identity
                  Arabidopsis thaliana chromosome II BAC F23M2 genomic
NCBI Description
                  -sequence, complete sequence
Seq. No.
                  147369
                  LIB3168-088-P1-K1-G9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4455229
                  170
BLAST score
E value
                  1.0e-90
Match length
                  256
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23
NCBI Description
                   (ESSAII project)
Seq. No.
                  147370
Seq. ID
                  LIB3168-088-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                   610
E value
                   1.0e-63
Match length
                  120
% identity
                   98
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147371
Seq. ID
                  LIB3168-088-P1-K1-H10
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  73
E value
                  6.0e-45
```

101 Match length % identity NCBI Description

(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No.

147372

LIB3168-088-P1-K1-H2 Seq. ID

Method BLASTN NCBI GI g2618600 BLAST score 342 0.0e+00 E value 374 Match length 98 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MDC12, complete sequence [Arabidopsis thaliana]

Seq. No.

147373

LIB3168-088-P1-K1-H3 Seq. ID

BLASTX Method g3044212 NCBI GI 580 BLAST score E value 4.0e-60 134 Match length 87 % identity

(AF057043) acyl-CoA oxidase [Arabidopsis thaliana] NCBI Description

Seq. No.

LIB3168-088-P1-K1-H5 Seq. ID

147374

Method BLASTN NCBI GI q4544435 BLAST score 252 E value 1.0e-140 252 Match length

100 % identity

Arabidopsis thaliana chromosome II BAC F14M13 genomic NCBI Description

sequence, complete sequence

Seq. No. 147375

LIB3168-088-P1-K1-H6 Seq. ID

Method BLASTX NCBI GI g112681 BLAST score 575 2.0e-59 E value 114 Match length 100 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

147376 Seq. No.

LIB3168-089-P1-K1-A1 Seq. ID

Method BLASTX NCBI GI q112681 BLAST score 199

5.0e-16 E value 45 Match length 82 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604\_pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRAl [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 147377 LIB3168-089-P1-K1-A10 Seq. ID Method BLASTX g112741 NCBI GI 597 BLAST score E value 4.0e-62 Match length 133 84 % identity 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] Seq. No. 147378 Seq. ID LIB3168-089-P1-K1-A11 Method BLASTX NCBI GI g112741 BLAST score 648 E value 4.0e-68 Match length 121 % identity 100 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] Seq. No. 147379 LIB3168-089-P1-K1-A2 Seq. ID Method BLASTX NCBI GI q4204299 BLAST score 568 E value 1.0e-58 Match length 115 % identity (AC003027) lcl prt seq No definition line found NCBI Description

[Arabidopsis thaliana]

Seq. No. 147380

Seq. ID LIB3168-089-P1-K1-A3

MethodBLASTXNCBI GIg112743BLAST score739

```
E value
                  1.0e-78
Match length
                  148
                  93
% identity
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147381
                  LIB3168-089-P1-K1-A4
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4558586
BLAST score
                  161
                  1.0e-85
E value
Match length
                  193
                  96
% identity
                  Arabidopsis thaliana chromosome 1 BAC T518 sequence,
NCBI Description
                  complete sequence
Seq. No.
                  147382
                  LIB3168-089-P1-K1-A5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2832629
                  190
BLAST score
E value
                  2.0e-14
Match length
                  125
% identity
                  (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                  thaliana]
                  147383
Seq. No.
                  LIB3168-089-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
                  623
BLAST score
E value
                  4.0e-65
Match length
                  143
                  85
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 125 seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147384
Seq. ID
                  LIB3168-089-P1-K1-A7
Method
                  BLASTX
                  g112741
NCBI GI
BLAST score
                  175
                  4.0e-13
E value
                  67
Match length
% identity
                  57
NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
```

Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi\_4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 147385

Seq. ID LIB3168-089-P1-K1-A8

Method BLASTX
NCBI GI g112741
BLAST score 613
E value 6.0e-64
Match length 122
% identity 93

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>gi\_4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 147386

Seq. ID LIB3168-089-P1-K1-A9

Method BLASTX
NCBI GI g1628583
BLAST score 545
E value 6.0e-56
Match length 112

% identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147387

Seq. ID LIB3168-089-P1-K1-B10

Method BLASTX
NCBI GI g112681
BLAST score 523
E value 2.0e-53
Match length 131
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147388

Seq. ID LIB3168-089-P1-K1-B11

Method BLASTX
NCBI GI g1628583
BLAST score 636
E value 1.0e-66
Match length 127
% identity 96

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis



thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

147389 Seq. No.

LIB3168-089-P1-K1-B2 Seq. ID

Method BLASTX NCBI GI q1628583 755 BLAST score E value 1.0e-80 Match length 153 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147390

LIB3168-089-P1-K1-B3 Seq. ID

BLASTX Method g1628583 NCBI GI BLAST score 95 E value 1.0e-57 148

Match length 77 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

147391 Seq. No.

Seq. ID LIB3168-089-P1-K1-B4

BLASTX Method NCBI GI g2129773 BLAST score 554 E value 5.0e-57

Match length 106 % identity

NCBI Description xyloglucan endotransglycosylase-related protein XTR3 -

Arabidopsis thaliana (fragment) >gi\_1244752 (U43485)

xyloglucan endotransglycosylase-related protein

[Arabidopsis thaliana]

Seq. No. 147392

Seq. ID LIB3168-089-P1-K1-B5

Method BLASTX NCBI GI g1628583 555 BLAST score E value 4.0e-57 Match length 143 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147393

LIB3168-089-P1-K1-B6 Seq. ID

Method BLASTX q1628583 NCBI GI BLAST score 672

```
E value
                  7.0e - 71
Match length
                  141
% identity
                  92
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147394
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  607
E value
                  3.0e-63
Match length
                  148
% identity
                  79
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir $08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsīs thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147395
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  615
E value
                  4.0e-64
Match length
                  148
                  79
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__$08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147396
Seq. ID
                  LIB3168-089-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  604
E value
                  7.0e-63
Match length
                  120
                  97
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147397
Seq. ID
                  LIB3168-089-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  478
E value
                  4.0e-48
```

Match length 106 % identity 89

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

## cruciferin seed storage protein [Arabidopsis thaliana]

147398 Seq. No. Seq. ID LIB3168-089-P1-K1-C10 Method BLASTX NCBI GI q112682 BLAST score 527 7.0e-59 E value Match length 146

81

% identity 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

147399 Seq. No.

LIB3168-089-P1-K1-C11 Seq. ID

Method BLASTX NCBI GI g112682 BLAST score 556 E value 3.0e-57 Match length 116 90 % identity

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi 166678 (M37248) 12S storage protein CRB [Arabidopsis

thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147400

LIB3168-089-P1-K1-C2 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 69 E value 2.0e-52 Match length 108 % identity 99

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147401

LIB3168-089-P1-K1-C3 Seq. ID

Method BLASTX NCBI GI q112681 BLAST score 518 E value 9.0e-53 139 Match length % identity 76

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

147402 Seq. No.

```
LIB3168-089-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4689386
                  342
BLAST score
                  4.0e-32
E value
                  77
Match length
% identity
NCBI Description
                  (AF139468) photosystem I reaction center subunit III [Vigna
                  radiata]
                  147403
Seq. No.
                  LIB3168-089-P1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q112681
                  593
BLAST score
                  1.0e-61
E value
                  114
Match length
                  96
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147404
                  LIB3168-089-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  609
E value
                  2.0e-63
                  120
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147405
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  176
E value
                  2.0e-26
Match length
                  124
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147406
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  401
E value
                  5.0e-39
Match length
                  89
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
```

Seq. No. Seq. ID

Method

NCBI GI

E value

Seq. No. Seq. ID

Method

NCBI GI

E value

Seq. No. Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

BLAST score

Match length

% identity

BLAST score

Match length % identity

```
thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147407
                  LIB3168-089-P1-K1-D11
                  BLASTX
                  g112682
                  630
                  6.0e-66
                  139
                  88
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147408
                  LIB3168-089-P1-K1-D12
                  BLASTX
                  g1628583
                  499
                  1.0e-50
                  120
                  81
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147409
                  LIB3168-089-P1-K1-D2
                  BLASTX
                  g1628583
                  496
                  3.0e-50
                  131
                  76
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147410
                  LIB3168-089-P1-K1-D3
                  BLASTX
```

Seq. No.

Seq. ID

Method NCBI GI q2129657 BLAST score 445 E value 3.0e-44Match length 125 74 % identity

NCBI Description oleosin isoform - Arabidopsis thaliana

>gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis thaliana]  $\overline{>}gi_{987016_{emb}_{CAA90878_{emb}_{CAA90878_{emb}_{CAA90878_{emb}_{emb}_{CAA90878_{emb}_{emb}_{emb}_{emb}_{emb}_{emb}_{emb}}$ 

[Arabidopsis thaliana]

Seq. No. 147411

LIB3168-089-P1-K1-D6 Seq. ID

Method BLASTX

```
NCBI GI
                  q112739
BLAST score
                  414
E value
                  1.0e-40
Match length
                  138
% identity
                  62
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) > gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147412
Seq. No.
                  LIB3168-089-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  562
                  6.0e-58
E value
Match length
                  111
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147413
Seq. ID
                  LIB3168-089-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  613
E value
                  6.0e-64
Match length
                  127
% identity
                  97
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147414
                  LIB3168-089-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  602
E value
                  1.0e-62
Match length
                  120
% identity
                  97
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147415
                  LIB3168-089-P1-K1-E2
Seq. ID
                  BLASTN
Method
                  g1279569
NCBI GI
BLAST score
                  86
E value
                  2.0e-40
                  260
Match length
```

% identity

```
NCBI Description Nicotiana acuminata chloroplast JLA region, 1-1028bp
                  147416
Seq. No.
                  LIB3168-089-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  387
                  2.0e-37
E value
Match length
                  86
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147417
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  568
E value
                  1.0e-58
Match length
                  120
                  91
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147418
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  g2494106
BLAST score
                  99
                  2.0e-48
E value
Match length
                  166
                  90
% identity
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
```

Seq. No. 147419

Seq. ID LIB3168-089-P1-K1-E6

Method BLASTX
NCBI GI g1628583
BLAST score 408
E value 7.0e-40
Match length 109
% identity 74

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147420

Seq. ID LIB3168-089-P1-K1-E7

Method BLASTX
NCBI GI g1526424
BLAST score 350
E value 3.0e-33
Match length 110
% identity 68

```
NCBI Description (D64140) LEA protein in group 3 [Arabidopsis thaliana]
                  147421
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1 E8-
Method
                  BLASTX
NCBI GI
                  q2129577
BLAST score
                  408
E value
                   4.0e-40
Match length
                  81
% identity
NCBI Description
                  DnaJ homolog protein - Arabidopsis thaliana >qi 727357
                   (U22340) DnaJ homolog [Arabidopsis thaliana]
Seq. No.
                  147422
Seq. ID
                  LIB3168-089-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  48
E value
                  3.0e-23
Match length
                  117
% identity
                  54
NCBI Description
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi_4490713_emb_CAB38847.1_ (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
                  147423
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  92
E value
                  3.0e-51
Match length
                  131
                  78
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  tha\overline{1}iana] >gi_808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147424
Seq. ID
                  LIB3168-089-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  469
E value
                  4.0e-47
Match length
                  121
% identity
                  78
```

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi\_808936 emb\_CAA32493\_ (X14312) 12S seed

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

storage protein [Arabidopsis thaliana]

```
Seq. No.
                   147425
Seq. ID
                  LIB3168-089-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  618
E value
                  2.0e-64
Match length
                  120
% identity
                  98
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147426
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-F2
Method
                  BLASTN
NCBI GI
                  g2924729
BLAST score
                  307
E value
                  1.0e-172
Match length
                  407
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNA5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147427
Seq. ID
                  LIB3168-089-P1-K1-F3
Method
                  BLASTN
NCBI GI
                  g4006815
BLAST score
                  286
E value
                  1.0e-160
Match length
                  364
                  95
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T6P5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147428
Seq. ID
                  LIB3168-089-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  623
E value
                  5.0e-65
Match length
                  154
                  78
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147429
Seq. ID
                  LIB3168-089-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  573
E value
                  3.0e-59
Match length
                  115
```

```
% identity
                  93
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir_ $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147430
                  LIB3168-089-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  636
                  1.0e-66
E value
Match length
                  126
% identity
                  95
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147431
Seq. ID
                  LIB3168-089-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q1107501
BLAST score
                  182
E value
                  2.0e-13
Match length
                  94
% identity
                  47
NCBI Description
                  (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb AA394824 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  147432
                  LIB3168-089-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q21106
BLAST score
                  265
E value
                  4.0e-23
Match length
                  105
% identity
                  50
                  (X59802) cruciferin [Raphanus sativus]
NCBI Description
Seq. No.
                  147433
```

Seq. ID LIB3168-089-P1-K1-F9

Method BLASTX NCBI GI q112741 BLAST score 677 E value 2.0e-71 Match length 137 % identity 91

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

```
>gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147434
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  267
                  2.0e-23
E value
                  75
Match length
                  79
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147435
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-G10
Method
                  BLASTX
                  g1361983
NCBI GI
BLAST score
                  621
E value
                  7.0e-65
                  123
Match length
                  98
% identity
                  ARP protein - Arabidopsis thaliana >gi 886434 emb CAA89858
NCBI Description
                   (Z49776) ARP protein [Arabidopsis thaliana]
                  147436
Seq. No.
                  LIB3168-089-P1-K1-G11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4512656
BLAST score
                  161
                  3.0e-85
E value
Match length
                  426
                  89
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
                  147437
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g1628583
                  80
BLAST score
E value
                  7.0e-39
Match length
                  98
                  82
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147438
                  LIB3168-089-P1-K1-G2
Seq. ID
                  BLASTX
Method
                  g21114
NCBI GI
BLAST score
                  \bar{1}31
E value
                  1.0e-19
Match length
                  66
                  72
% identity
```

```
NCBI Description (X59806) cruciferin [Raphanus sativus]
                  147439
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-G3
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  350
E value.
                  4.0e-33
                  89
Match length
                  78
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147440
Seq. No.
                  LIB3168-089-P1-K1-G6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4567259
BLAST score
                  317
E value
                  1.0e-178
Match length
                  389
% identity
                  95
                  Arabidopsis thaliana chromosome II BAC F3K23 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  147441
                  LIB3168-089-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  720
E value
                  2.0e-76
Match length
                  148
% identity
                  96
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147442
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-G8
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  55
E value
                  6.0e-52
Match length
                  113
% identity
                  96
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147443
Seq. ID
                  LIB3168-089-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g3859610
BLAST score
                  144
E value
                  2.0e-75
```

```
Match length
% identity
                  94
NCBI Description
                  Arabidopsis thaliana BAC T9E19
Seq. No.
                  147444
Seq. ID
                  LIB3168-089-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  584
                  1.0e-60
E value
                  113
Match length
                  95
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147445
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q3935151
BLAST score
                  712
                  2.0e-75
E value
Match length
                  133
                  98
% identity
                  (AC005106) T25N20.15 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  147446
                  LIB3168-089-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129641
BLAST score
                  600
E value
                  2.0e-62
Match length
                  110
% identity
                  major latex protein type 1 - Arabidopsis thaliana
NCBI Description
                  >gi 1107493 emb CAA63026 (X91960) major latex protein
                  typel [Arabidopsis thaliana]
```

Seq. No. 147447

Seq. ID LIB3168-089-P1-K1-H3

Method BLASTX
NCBI GI g112682
BLAST score 603
E value 1.0e-62
Match length 147
% identity 79

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147448

```
LIB3168-089-P1-K1-H4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3449314
BLAST score
                   334
                   0.0e+00
E value
                   414
Match length
                   86
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K22F20, complete sequence [Arabidopsis thaliana]
                   147449
Seq. No.
Seq. ID
                   LIB3168-089-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q2134962
BLAST score
                   376
                   4.0e-36
E value
                   129
Match length
% identity
NCBI Description
                   cyclophilin-like protein CyP-60 - human >gi 1199598
                   (U37219) cyclophilin-like protein CyP-60 [Homo sapiens]
                   >gi 1587642 prf 2207180A cyclophilin:ISOTYPE=CyP-60 [Homo
                   sapiens]
Seq. No.
                   147450
Seq. ID
                   LIB3168-089-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g2781394
BLAST score
                   496
E value
                   3.0e-50
Match length
                   107
% identity
                   95
NCBI Description
                   (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
                   147451
Seq. No.
Seq. ID
                  LIB3168-089-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   542
E value
                   3.0e-58
Match length
                   128
% identity
                   88
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   147452
Seq. ID
                   LIB3168-089-P1-K1-H8
Method
                  BLASTX
NCBI GI
                   q112739
BLAST score
                   300
E value
                   2.0e-27
Match length
                   102
% identity
                   63
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68854 pir__NWMU2 2S albumin 2 precursor -
```

Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi\_4490711\_emb\_CAB38845.1\_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 147453

Seq. ID LIB3168-089-P1-K1-H9

Method BLASTX
NCBI GI g3335169
BLAST score 684
E value 2.0e-73
Match length 147
% identity 89

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi\_4455197\_emb\_CAB36520.1\_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 147454

Seq. ID LIB3168-090-P1-K1-A1

Method BLASTX
NCBI GI g3929364
BLAST score 701
E value 3.0e-74
Match length 137
% identity 99

NCBI Description NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (COMPLEX I-23KD) (CI-23KD) >gi 1076356 pir S52380 NADH

dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi\_666977\_emb\_CAA59061\_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi\_3152573 (AC002986) Match to NADH:ubiquinone oxidoreductase gb\_X84318 from A.thaliana. ESTs gb\_Z27005, gb\_T04711, gb\_T45078 and gb\_Z28689 come

from this gene. [Arabidopsis thaliana]

Seq. No. 147455

Seq. ID LIB3168-090-P1-K1-A11

Method BLASTN
NCBI GI g166609
BLAST score 113
E value 6.0e-57
Match length 226
% identity 86

NCBI Description A.thaliana at 2S1 gene encoding albumin 2S subunit 1,

complete cds

Seq. No. 147456

Seq. ID LIB3168-090-P1-K1-A2

Method BLASTN
NCBI GI g3869073
BLAST score 258
E value 1.0e-143
Match length 383
% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MKN22, complete sequence [Arabidopsis thaliana]

NCBI GI

```
Seq. No.
                  147457
Seq. ID
                  LIB3168-090-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  g4335711
BLAST score
                  90
                  4.0e-43
E value
                  256
Match length
                  82
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F9013 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147458
                  LIB3168-090-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  45
E value
                  2.0e-57
Match length
                  120
% identity
                  93
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147459
Seq. ID
                  LIB3168-090-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  457
E value
                  9.0e-46
Match length
                  98
                  88
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147460
Seq. ID
                  LIB3168-090-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  596
E value
                  6.0e-62
Match length
                  124
                  96
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                - 147461
Seq. ID
                  LIB3168-090-P1-K1-A9
Method
                  BLASTX
```

18566

g3757514

```
BLAST score
                  641
                  3.0e-67
E value
Match length
                  123
                  99
% identity
NCBI Description
                  (AC005167) putative plasma membrane intrinsic protein
                  [Arabidopsis thaliana]
                  >gi_4581129_gb_AAD24619.1_AC005825_26 (AC005825) putative
                  plasma membrane intrinsic protein [Arabidopsis thaliana]
Seq. No.
                  147462
                  LIB3168-090-P1-K1-B11
Seq. ID
                  BLASTN
Method
NCBI GI
                  q16131
                  35
BLAST score
                  2.0e-10
E value
Match length
                  146
% identity
                  84
                  Arabidopsis thaliana genes for 5.8S rRNA and 25S rRNA with
NCBI Description
                  18S rRNA fragment
Seq. No.
                  147463
Seq. ID
                  LIB3168-090-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g82214
BLAST score
                  423
E value
                  1.0e-41
Match length
                  129
% identity
NCBI Description
                  hypothetical protein 350 - common tobacco chloroplast
                  >gi_4388761_emb_CAA77394_ (Z00044) hypothetical protein
                  [Nicotiana tabacum]
Seq. No.
                  147464
                  LIB3168-090-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g114335
BLAST score
                  665
E value
                  5.0e-70
                  141
Match length
                  94
% identity
NCBI Description
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
                  >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                  type 2, plasma membrane - Arabidopsis thaliana >gi 166629
                  (J05570) H+-ATPase [Arabidopsis thaliana]
Seq. No.
                  147465
Seq. ID
                  LIB3168-090-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  q2924257
BLAST score
                  59
E value
                  2.0e-24
Match length
                  83
% identity
                  93
NCBI Description
                  Tobacco chloroplast genome DNA
                  147466
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-B8
```

NCBI Description

thaliana]

```
BLASTX
Method
NCBI GI
                   g1169598
BLAST score
                   475
                   7.0e-75
E value
                   142
Match length
                   94
% identity
                   OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                   desaturase [Arabidopsis thaliana]
Seq. No.
                   147467
                   LIB3168-090-P1-K1-C1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   611
E value
                   1.0e-63
Match length
                   120
                   98
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147468
Seq. ID
                   LIB3168-090-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   403
E value
                   1.0e-39
Match length
                   89
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147469
Seq. ID
                   LIB3168-090-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   g16231
BLAST score
                   49
E value
                   1.0e-18
Match length
                   133
% identity
                   83
NCBI Description
                   Arabidopsis CRA1 gene for 12S seed storage protein
                   >gi_166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage
                  protein CRA1 gene, exons 1-4
Seq. No.
                   147470
                   LIB3168-090-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3176874
BLAST score
                   623
E value
                   4.0e-65
Match length
                   121
% identity
                   99
```

(AF065639) cucumisin-like serine protease [Arabidopsis

```
147471
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-C3
                  BLASTX
Method
NCBI GI
                  g112681
BLAST score
                  560
                  9.0e-58
E value
                  131
Match length
% identity
                  83
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147472
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-C4
                  BLASTX
Method
NCBI GI
                  g2129659
                  45
BLAST score
                  7.0e-39
E value
Match length
                  109
% identity
                  83
                  oleosin, isoform 21K - Arabidopsis thaliana >gi 725260
NCBI Description
                  (L40954) oleosin [Arabidopsis thaliana]
                  147473
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-C5
                  BLASTX
Method
NCBI GI
                  g2583125
BLAST score
                  46
                  1.0e-26
E value
                  126
Match length
% identity
                   (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                  thaliana]
                  147474
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g2264311
BLAST score
                  43
                  3.0e-15
E value
                  100
Match length
                  92
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLN1, complete sequence [Arabidopsis thaliana]
                  147475
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-C9
                  BLASTN
Method
                  g2842474
NCBI GI
BLAST score
                  71
                  7.0e-32
E value
                  193
Match length
                  85
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                  (ESSAII project)
```

```
147476
Seq. No.
                  LIB3168-090-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112739
                  469
BLAST score
                  5.0e-47
E value
Match length
                  131
                  73
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147477
Seq. No.
                  LIB3168-090-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  387
                  1.0e-37
E value
Match length
                  113
% identity
                  73
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                  >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb_CAA90878_ (Z54165) oleosin
                  [Arabidopsis thaliana]
                  147478
Seq. No.
                  LIB3168-090-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3924598
BLAST score
                  213
E value
                  1.0e-17
                  41
Match length
% identity
NCBI Description (AF069442) putative oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  147479
                  LIB3168-090-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  607
E value
                  3.0e-63
                  127
Match length
                  92
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147480
Seq. No.
                  LIB3168-090-P1-K1-D5
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2828184
```

187

BLAST score

1.0e-101 E value 383 Match length 70 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MSN9, complete sequence [Arabidopsis thaliana] 147481 Seq. No. LIB3168-090-P1-K1-D6 Seq. ID Method BLASTX NCBI GI q1628583 441 BLAST score E value 6.0e-44 Match length 98 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147482 Seq. ID LIB3168-090-P1-K1-D7 Method BLASTX NCBI GI g3024434 BLAST score 483 E value 1.0e-48 Match length 117 85 % identity 26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING NCBI Description PROTEIN HOMOLOG 1) (TBP-1) >gi 2564337 dbj BAA22951 (D88663) Tat binding protein 1 [Brassica rapa] 147483 Seq. No. LIB3168-090-P1-K1-D8 Seq. ID Method BLASTN NCBI GI g2842474 BLAST score 61 1.0e-25 E value Match length 184 65 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No. 147484

LIB3168-090-P1-K1-D9 Seq. ID

Method BLASTX NCBI GI g1345973 BLAST score 728 E value 2.0e-77 139 Match length 95 % identity

NCBI Description

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM >gi 541882 pir JQ2335 omega-3 fatty acid desaturase (EC 1.14.99.-) CF3 - Arabidopsis thaliana >gi\_408483 (L22931) omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi\_471091\_dbj\_BAA04505\_ (D17579) fatty acid desaturase [Arabidopsis thaliana] >gi\_1197795\_dbj\_BAA05514\_ (D26508) microsomal omega-3 fatty acid desaturase [Arabidopsis thaliana] >gi 3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana] 147485 Seq. No. Seq. ID LIB3168-090-P1-K1-E11 Method BLASTN NCBI GI g4512690 BLAST score 111 E value 2.0e-55 Match length 401 95 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic sequence, complete sequence Seq. No. 147486 LIB3168-090-P1-K1-E3 Seq. ID Method BLASTX NCBI GI g112741 BLAST score 574 E value 2.0e-59 Match length 107 98 % identity 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] Seq. No. 147487 Seq. ID LIB3168-090-P1-K1-E5 Method BLASTX NCBI GI g4204298 BLAST score 470 3.0e-47 E value Match length 119 % identity 81 NCBI Description (AC003027) lcl prt seq No definition line found [Arabidopsis thaliana] Seq. No. 147488 LIB3168-090-P1-K1-E6 Seq. ID Method BLASTN NCBI GI g2924652 BLAST score 163 E value 2.0e-86 Match length 345 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9L2, complete sequence [Arabidopsis thaliana] Seq. No.

147489

LIB3168-090-P1-K1-E7

Method BLASTX NCBI GI g2506938 BLAST score 527 E value 7.0e-54

Seq. ID





Match length 122 8 identity 84

NCBI Description NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4, CHLOROPLAST

Seq. No. 147490

Seq. ID LIB3168-090-P1-K1-E8

Method BLASTN
NCBI GI g2570187
BLAST score 35
E value 1.0e-10
Match length 93
% identity 88

NCBI Description Arabidopsis thaliana DNA for alcohol dehydrogenase,

complete cds >gi\_2570191\_dbj\_D63462\_D63462 Arabidopsis
thaliana DNA for alcohol dehydrogenase, complete cds

Seq. No. 147491

Seq. ID LIB3168-090-P1-K1-E9

Method BLASTX
NCBI GI g112737
BLAST score 573
E value 3.0e-59
Match length 122
% identity 89

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147492

Seq. ID LIB3168-090-P1-K1-F1

Method BLASTX
NCBI GI g112681
BLAST score 348
E value 7.0e-33
Match length 113
% identity 68

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147493

Seq. ID LIB3168-090-P1-K1-F11

Method BLASTN
NCBI GI g2264367
BLAST score 219
E value 1.0e-120
Match length 370
% identity 95

NCBI Description Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm,

complete sequence [Arabidopsis thaliana]

```
147494
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-F3
                  BLASTN
Method
NCBI GI
                   g2618683
                   180
BLAST score
                   1.0e-96
E value
                   421
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  147495
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                   407
                   5.0e-40
E value
                  80
Match length
% identity
                   95
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147496
Seq. ID
                  LIB3168-090-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  595
E value
                  7.0e-62
Match length
                  120
% identity
                  94
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147497
Seq. No.
                  LIB3168-090-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2997591
BLAST score
                  159
                  1.0e-10
E value
Match length
                  82
% identity
                  51
NCBI Description
                   (AF020814) glucose-6-phosphate/phosphate-translocator
                  precursor [Pisum sativum]
Seq. No.
                  147498
Seq. ID
                  LIB3168-090-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  497
E value
                  2.0e-50
Match length
                  99
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
```

BLAST score

Match length

E value

377

1.0e-36 76

```
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   147499
Seq. No.
Seq. ID
                   LIB3168-090-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g114335
BLAST score
                   473
E value
                   2.0e-47
Match length
                   126
% identity
                   74
                   PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                   >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
type 2, plasma membrane - Arabidopsis thaliana >gi_166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
                   147500
Seq. No.
                   LIB3168-090-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1336804
                   206
BLAST score
                   3.0e-16
E value
                   46
Match length
                   91
% identity
                   vacuolar H(+)-ATPase subunit B [Mesembryanthemum
NCBI Description
                   crystallinum, leaf, Peptide Partial, 170 aa]
                   147501
Seq. No.
Seq. ID
                   LIB3168-090-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q2160146
                   430
BLAST score
                   2.0e-42
E value
                   127
Match length
% identity
                   69
NCBI Description
                   (AC000375) Strong similarity to Arabidopsis
                   gb X91953,F21M12.3,F21M12.1. EST gb H36326 comes from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   147502
Seq. ID
                   LIB3168-090-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   q3449328
BLAST score
                   173
E value
                   2.0e-92
                   370
Match length
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCI2, complete sequence [Arabidopsis thaliana]
Seq. No.
                   147503
                   LIB3168-090-P1-K1-G5
Seq. ID
Method
                   BLASTX
                   g2961390
NCBI GI
```

Seq. ID

```
% identity
NCBI Description
                   (AL022141) beta-galactosidase like protein [Arabidopsis
                  thaliana]
                  147504
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q2252866
BLAST score
                  192
E value
                  1.0e-14
Match length
                  58
% identity
NCBI Description
                   (AF013294) contains region of similarity to SYT
                   [Arabidopsis thaliana]
                  147505
Seq. No.
                  LIB3168-090-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
                  715
BLAST score
E value
                  7.0e-76
Match length
                  143
                  94
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147506
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  a112681
                  712
BLAST score
E value
                  1.0e-75
                  143
Match length
                  94
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147507
Seq. No.
Seq. ID
                  LIB3168-090-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1628583
                  431
BLAST score
E value
                  7.0e-43
                  95
Match length
                  91
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147508
Seq. No.
```

18576

LIB3168-090-P1-K1-H1

```
Method
                   BLASTX
                   q1628583
NCBI GI
                   515
BLAST score
                   2.0e-52
E value
                   120
Match length
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147509
Seq. ID
                   LIB3168-090-P1-K1-H11
Method
                   BLASTX
                   g112741
NCBI GI
BLAST score
                   330
E value
                   6.0e-31
                   114
Match length
                   38
% identity
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                   Arabidopsis \overline{\text{thaliana}} > \overline{\text{gi}}_{166616} (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
                   147510
Seq. No.
Seq. ID
                   LIB3168-090-P1-K1-H3
Method
                   BLASTX
                   g112682
NCBI GI
                   619
BLAST score
                   1.0e-64
E value
                   132
Match length
% identity
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   147511
                   LIB3168-091-P1-K1-A1
Seq. ID
                   BLASTN
Method
NCBI GI
                   q2160155
BLAST score
                   48
                   7.0e-18
E value
                   132
Match length
                   91
% identity
```

Seq. No. 147512

NCBI Description

Seq. ID LIB3168-091-P1-K1-A6

Method BLASTX
NCBI GI g1628583
BLAST score 507
E value 2.0e-51

1, complete sequence [Arabidopsis thaliana]

Sequence of BAC F21M12 from Arabidopsis thaliana chromosome

```
Match length
% identity
                  69
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147513
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  59
E value
                  2.0e-61
Match length
                  142
                  86
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147514
Seq. ID
                  LIB3168-091-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q395203
BLAST score
                  121
                  1.0e-61
E value
Match length
                  278
% identity
NCBI Description A.thaliana 2S albumin gene isoforms 1 and 2, complete CDS's
Seq. No.
                  147515
Seq. ID
                  LIB3168-091-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g4097693
BLAST score
                  44
E value
                  8.0e-16
Match length
                  103
% identity
NCBI Description
                  Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete
                  cds
Seq. No.
                  147516
                  LIB3168-091-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  328
E value
                  2.0e-30
Match length
                  145
```

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor -

56

% identity

Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi\_4490711\_emb\_CAB38845.1\_ (AL035680) NWMU2-2S albumin 2

NCBI GI

BLAST score



## precursor [Arabidopsis thaliana]

```
147517
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g3335169
BLAST score
                  781
E value
                  1.0e-83
Match length
                  146
% identity
                  (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]
NCBI Description
                  >gi 4455197 emb_CAB36520.1_ (AL035440) embryo-specific
                  protein 1 (ATS1) [Arabidopsis thaliana]
Seq. No.
                  147518
                  LIB3168-091-P1-K1-B4
Seq. ID
Method
                  BLASTX
                  q112682
NCBI GI
BLAST score
                  718
                  3.0e-76
E value
Match length
                  157
                  89
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147519
                  LIB3168-091-P1-K1-B6
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  576
                  1.0e-59
E value
                  135
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147520
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2129767
                  434
BLAST score
                  4.0e-43
E value
Match length
                  84
% identity
NCBI Description
                  vacuolar processing enzyme (EC 3.4.22.-) isozyme beta
                  precursor - Arabidopsis thaliana >gi 1805364 dbj BAA09615
                  (D61394) beta-VPE [Arabidopsis thaliana]
Seq. No.
                  147521
                  LIB3168-091-P1-K1-B8
Seq. ID
Method
                  BLASTN
```

q2252823

```
E value
                  2.0e-30
Match length
                  179
                  73
% identity
NCBI Description
                  Arabidopsis thaliana BAC IG005I10
Seq. No.
                  147522
Seq. ID
                  LIB3168-091-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g2618677
BLAST score
                  301
E value
                  1.0e-169
                  339
Match length
                  98
% identity
                  Arabidopsis thaliana BAC F21B7 chromosome 1, complete
NCBI Description
                  sequence [Arabidopsis thaliana]
                  147523
Seq. No.
                  LIB3168-091-P1-K1-C1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
                  49
BLAST score
                  1.0e-37
E value
Match length
                  81
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147524
Seq. ID
                  LIB3168-091-P1-K1-C11
Method
                  BLASTX
                  g1170373
NCBI GI
                  339
BLAST score
                  1.0e-39
E value
Match length
                  92
% identity
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >qi 1072473 pir S46302
NCBI Description
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
                  >qi 397482 emb CAA52684 (X74604) heat shock protein 70
                  cognate [Arabidopsis thaliana]
Seq. No.
                  147525
                  LIB3168-091-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3264759
BLAST score
                  541
                  2.0e-55
E value
                  138
Match length
                  78
% identity
                  (AF071889) 40S ribosomal protein S8 [Prunus armeniaca]
NCBI Description
                  147526
Seq. No.
                  LIB3168-091-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  519
```

7.0e-53

E value

Seq. ID

```
Match length
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                   (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147527
Seq. ID
                  LIB3168-091-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  533
E value
                  1.0e-54
                  112
Match length
                  90
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147528
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  141
E value
                  3.0e-09
Match length
                  49
% identity
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  147529
Seq. ID
                  LIB3168-091-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g2656032
BLAST score
                  82
E value
                  4.0e-38
Match length
                  266
% identity
                  87
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MZF18
                  147530
Seq. No.
                  LIB3168-091-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4263704
BLAST score
                  254
E value
                  8.0e-22
Match length
                  84
% identity
NCBI Description
                   (AC006223) putative sugar starvation-induced protein
                  [Arabidopsis thaliana]
                  147531
Seq. No.
```

LIB3168-091-P1-K1-D1

```
BLASTX
Method
                  g112681
NCBI GI
                  617
BLAST score
                  2.0e-64
E value
Match length
                  128
                  95
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir_ S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147532
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-D11
                  BLASTN
Method
                  g1785673
NCBI GI
                  36
BLAST score
                  6.0e-11
E value
Match length
                  115
% identity
                  83
                  A.thaliana mitochondrial genome, part A
NCBI Description
                  147533
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-D12
Method
                  BLASTN
                  q4079614
NCBI GI
                  40
BLAST score
                  9.0e-14
E value
Match length
                  81
% identity
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147534
                  LIB3168-091-P1-K1-D2
Seq. ID
Method
                  BLASTX
                  g112681
NCBI GI
BLAST score
                  630
E value
                  7.0e-66
                  130
Match length
                  96
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir_S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147535
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-D3
                  BLASTX
Method
NCBI GI
                  q1352347
BLAST score
                  472
E value
                  2.0e-47
Match length
                  93
                  100
% identity
                  ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)
NCBI Description
                  >gi 480620 pir_S37103 translation elongation factor eEF-1
```

```
beta-Al chain - Arabidopsis thaliana (cv. Colombia)
                   >gi 398608_emb CAA52751 (X74733) elongation factor-1 beta
                   Al [Arabidopsis thaliana]
                   147536
Seq. No.
Seq. ID
                   LIB3168-091-P1-K1-D4
Method
                   BLASTN
NCBI GI
                   g3228389
BLAST score
                   345
E value
                   0.0e + 00
Match length
                   375
% identity
NCBI Description
                   Genomic sequence for Arabidopsis thaliana BAC F17L21,
                   complete sequence [Arabidopsis thaliana]
                   147537
Seq. No.
Seq. ID
                   LIB3168-091-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   g2244950
BLAST score
                   205
E value
                   1.0e-111
Match length
                   294
% identity
                   96
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   147538
Seq. No.
Seq. ID
                   LIB3168-091-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   g16236
BLAST score
                   63
                   7.0e-27
E value
Match length
                   122
                   86
% identity
NCBI Description
                   Arabidopsis CRB gene for 12S seed storage protein
                   >gi 166677 gb M37248 ATHCRBAA A.thaliana 12S storage
                   protein CRA1 gene, exons 1-4
Seq. No.
                   147539
Seq. ID
                   LIB3168-091-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q1345592
BLAST score
                   503
E value
                   5.0e-51
Match length
                   106
% identity
NCBI Description
                   14-3-3-LIKE PROTEIN GF14 EPSILON >gi 1022778 (U36446) GF14
                   epsilon isoform [Arabidopsis thaliana]
Seq. No.
                   147540
Seq. ID
                  LIB3168-091-P1-K1-D8
Method
                  BLASTN
NCBI GI
                   g4734011
BLAST score
                   67
E value
                   3.0e-29
Match length
                  206
                  70
% identity
```

```
NCBI Description Arabidopsis thaliana chromosome II BAC F24C20 genomic
                  sequence, complete sequence
Seq. No.
                  147541
                  LIB3168-091-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  547
                  3.0e-56
E value
Match length
                  118
                  87
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147542
Seq. ID
                  LIB3168-091-P1-K1-E1
Method
                  BLASTX
                  g112737
NCBI GI
BLAST score
                  668
E value
                  2.0e-70
Match length
                  141
                  90
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >qi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147543
                  LIB3168-091-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4079614
BLAST score
                  57
E value
                  3.0e-23
                  143
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147544
                  LIB3168-091-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  689 ...
                  8.0e-73
E value
Match length
                  128
                  99
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
```

```
3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
```

>gi\_4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 147545
Seq. ID LIB3168-091-P1-K1-E2

Method BLASTX
NCBI GI g112682
BLAST score 598
E value 3.0e-62
Match length 138
% identity 82

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147546

Seq. ID LIB3168-091-P1-K1-E3

Method BLASTX
NCBI GI g1531762
BLAST score 195
E value 6.0e-15
Match length 51
% identity 75

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 147547

Seq. ID LIB3168-091-P1-K1-E4

Method BLASTX
NCBI GI g112739
BLAST score 510
E value 8.0e-52
Match length 142
% identity 73

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711\_emb\_CAB38845.1\_ (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 147548

Seq. ID LIB3168-091-P1-K1-E5

Method BLASTX
NCBI GI g112737
BLAST score 684
E value 3.0e-72
Match length 147
% identity 88

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit

```
(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147549
Seq. ID
                  LIB3168-091-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q2924505
BLAST score
                  214
                  1.0e-117
E value
                  427
Match length
                  96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13
NCBI Description
                  (ESSAII project)
                  147550
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-E7
                  BLASTX
Method
NCBI GI
                  g4544473
                  731
BLAST score
                  9.0e-78
E value
                  136
Match length
% identity
                  (AC006580) putative mei2 protein [Arabidopsis thaliana]
NCBI Description
                  147551
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g112682
                  62
BLAST score
                  6.0e-66
E value
                  138
Match length
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147552
                  LIB3168-091-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1772309
BLAST score
                  171
                  4.0e-12
E value
                  79
Match length
                  94
% identity
                 (D34631) acetyl-CoA carboxylase [Arabidopsis thaliana]
NCBI Description
                  147553
Seq. No.
                  LIB3168-091-P1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3985932
BLAST score
                  269
E value
                  1.0e-149
Match length
                  463
```

1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

18586

NCBI Description

```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K22J17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147554
                  LIB3168-091-P1-K1-F11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  227
E value
                  6.0e-19
                  96
Match length
                  54
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147555
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  q461841
BLAST score
                  185
                  7.0e-14
E value
                  80
Match length
% identity
                  CRUCIFERIN CRU4 PRECURSOR (11S GLOBULIN) (12S STORAGE
NCBI Description
                  PROTEIN)
Seq. No.
                  147556
Seq. ID
                  LIB3168-091-P1-K1-F2
Method
                  BLASTX
                  g112743
NCBI GI
                  731
BLAST score
                  1.0e-77
E value
Match length
                  152
                  90
% identity
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68856_pir__NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi_166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb_CAA80869_
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi_4490713 emb CAB38847.1_ (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147557
                  LIB3168-091-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  684
E value
                  3.0e-72
Match length
                  143
% identity
                  90
```

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

E value Match length



## precursor [Arabidopsis thaliana]

```
147558
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g112737
                  546
BLAST score
                  4.0e-56
E value
Match length
                  121
% identity
                  85
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147559
                  LIB3168-091-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1673426
                  171
BLAST score
E value
                  1.0e-12
                  71
Match length
% identity
                  (X99979) factor 1-alpha [Forsythia x intermedia]
NCBI Description
Seq. No.
                  147560
Seq. ID
                  LIB3168-091-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g21913
BLAST score
                  188
E value
                  4.0e-14
Match length
                  84
% identity
                  43
                  (X62626) vicilin [Theobroma cacao]
NCBI Description
Seq. No.
                  147561
                  LIB3168-091-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  45
E value
                  5.0e-15
Match length
                  76
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147562
                  LIB3168-091-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  596
```

5.0e~62

Seq. ID

```
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   147563
Seq. No.
                   LIB3168-091-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   688
                   1.0e-72
E value
Match length
                   134
                   97
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147564
Seq. ID
                   LIB3168-091-P1-K1-G1
Method
                   BLASTX
                   g112681
NCBI GI
BLAST score
                   661
                   1.0e-69
E value
Match length
                   135
                   93
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   147565
                   LIB3168-091-P1-K1-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g166611
BLAST score
                   45
                   3.0e-16
E value
Match length
                   106
% identity
                   84
                   A.thaliana at2S3 gene encoding albumin 2S subunit 3,
NCBI Description
                   complete cds
Seq. No.
                   147566
Seq. ID
                   LIB3168-091-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   g2129657
BLAST score
                   299
E value
                   4.0e-27
Match length
                   111
% identity
                   oleosin isoform - Arabidopsis thaliana
NCBI Description
                   >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
thaliana] >gi_987016_emb_CAA90878_ (Z54165) oleosin
                   [Arabidopsis thaliana]
Seq. No.
                   147567
```

LIB3168-091-P1-K1-G12

```
BLASTX
Method
NCBI GI
                  g133938
BLAST score
                  515
                  1.0e-52
E value
                  121
Match length
                  83
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70866 pir R3SP3
NCBI Description
                  ribosomal protein S3 - spinach chloroplast
                  >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3
                  [Spinacia oleracea]
                  147568
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-G2
Method
                  BLASTX
                  g112739
NCBI GI
BLAST score
                  335
E value
                  2.0e-31
                  105
Match length
% identity
                  66
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) > gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147569
Seq. ID
                  LIB3168-091-P1-K1-G3
                  BLASTX
Method
                  q1628583
NCBI GI
                  304
BLAST score
E value
                  6.0e-28
                  95
Match length
                  66
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147570
Seq. No.
                  LIB3168-091-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  594
E value
                  1.0e-61
Match length
                  123
% identity
                  93
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147571
Seq. ID
                  LIB3168-091-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  344
E value
                  3.0e - 32
```

```
122
Match length
% identity
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                  >gi_987014_emb_CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878 (254165) oleosin
                  [Arabidopsis thaliana]
Seq. No.
                  147572
Seq. ID
                  LIB3168-091-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  651
                  2.0e-68
E value
Match length
                  123
                  98
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147573
Seq. ID
                  LIB3168-091-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  59
E value
                  1.0e-56
                  153
Match length
                  76
% identity
                 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147574
Seq. ID
                  LIB3168-091-P1-K1-G8
                  BLASTX
Method
NCBI GI
                  q112681
BLAST score
                  177
E value
                  4.0e-13
                  67
Match length
                  57
% identity
                 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
```

Seq. No. 147575

Seq. ID LIB3168-091-P1-K1-G9

Method BLASTX NCBI GI g529353 BLAST score 378 E value 2.0e-36

```
Match length
% identity
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
                  147576
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  671
                  1.0e-70
E value
                  151
Match length
                  85
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147577
Seq. ID
                  LIB3168-091-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  261
E value
                  5.0e-23
                  74
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147578
                  LIB3168-091-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  443
BLAST score
                  5.0e-44
E value
                  104
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147579
                  LIB3168-091-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  625
E value
                  3.0e-65
Match length
                  138
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
```

Seq. No. 147580

```
Seq. ID
                  LIB3168-091-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  694
                  2.0e-73
E value
                  151
Match length
                  86
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  147581
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-H4
                  BLASTX
Method
NCBI GI
                  q112741
BLAST score
                  711
                  2.0e-75
E value
                  141
Match length
                  94
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147582
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-H5
Method
                  BLASTX
                  g112741
NCBI GI
BLAST score
                  659
E value
                  3.0e-69
Match length
                  124
                  98
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147583
Seq. ID
                  LIB3168-091-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  406
E value
                  5.0e-40
Match length
                  88
% identity
                  89
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

NCBI GI

```
cruciferin seed storage protein [Arabidopsis thaliana]
                  147584
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-H7
                  BLASTX
Method
                  g1628583
NCBI GI
                  544
BLAST score
E value
                  8.0e-56
                  119
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147585
Seq. No.
Seq. ID
                  LIB3168-091-P1-K1-H8
                  BLASTX
Method
NCBI GI
                  q112681
BLAST score
                  667
                  3.0e-70
E value
                  150
Match length
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147586
                  LIB3168-091-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  566
                  2.0e-58
E value
                  119
Match length
                  92
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147587
                  LIB3168-093-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4204303
BLAST score
                  346
E value
                  5.0e-33
Match length
                  82
% identity
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  147588
                  LIB3168-093-P1-K1-A10
Seq. ID
Method
                  BLASTN
```

18594

g2264311



BLAST score 2.0e-24 E value Match length 87 % identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MLN1, complete sequence [Arabidopsis thaliana]

Seq. No. 147589

LIB3168-093-P1-K1-A12 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 649 E value 3.0e-68 Match length 127 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147590

Seq. ID LIB3168-093-P1-K1-A3

Method BLASTN NCBI GI q4455168 BLAST score 67 4.0e-30 E value Match length 67 % identity 100

Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 NCBI Description

(ESSAII project)

Seq. No. 147591

LIB3168-093-P1-K1-A4 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 601 1.0e-62 E value 125 Match length % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi 2842495\_emb\_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147592

Seq. ID LIB3168-093-P1-K1-A5

Method BLASTX NCBI GI g112681 BLAST score 80 1.0e-58 E value Match length 126 % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \_S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi\_808936\_emb\_CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

147593 Seq. No.

```
LIB3168-093-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  101
                  6.0e-04
E value
                  77
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147594
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-A7
Method
                  BLASTN
                  g2828278
NCBI GI
BLAST score
                  166
                  2.0e-88
E value
Match length
                  242
                  97
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
                  (ESSAII project)
                  147595
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  376
E value
                  1.0e-36
Match length
                  81
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147596
Seq. ID
                  LIB3168-093-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q3822223
BLAST score
                  151
E value
                  8.0e-10
Match length
                  104
% identity
NCBI Description
                  (AF077955) branched-chain alpha keto-acid dehydrogenase El
                  alpha subunit [Arabidopsis thaliana]
Seq. No.
                  147597
Seq. ID
                  LIB3168-093-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  q4589437
BLAST score
                  239
E value
                  1.0e-132
Match length
                  306
% identity
                  98
```

```
Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MPN9, complete sequence
                  147598
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-B2
                  BLASTN
Method
                  q4584531
NCBI GI
BLAST score
                  32
E value
                  1.0e-08
                  96
Match length
                  83
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8
NCBI Description
                  (ESSA project)
                  147599
Seq. No.
                  LIB3168-093-P1-K1-B3
Seq. ID
                  BLASTX
Method
                  g267055
NCBI GI
BLAST score
                  305
E value
                  2.0e-28
                  69
Match length
                  90
% identity
                  SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE)
NCBI Description
                  >gi 66572 pir YUMU sucrose synthase (EC 2.4.1.13)
                  Arabidopsis thaliana >gi 16526 emb CAA43303 (X60987)
                  sucrose synthase [Arabidopsis thaliana]
                  147600
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  608
E value
                  2.0e-63
Match length
                  119
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147601
Seq. No.
                  LIB3168-093-P1-K1-B5
Seq. ID
Method
                  BLASTX
                  g112739
NCBI GI
BLAST score
                  211
E value
                  2.0e-24
Match length
                  100
                  61
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-25 albumin 2
                  precursor [Arabidopsis thaliana]
```

Seq. No. 147602
Seq. ID LIB3168-093-P1-K1-B6

NCBI GI

BLAST score

```
Method
                   BLASTX
NCBI GI
                   g1628583
BLAST score
                   364
E value
                   8.0e-35
Match length
                   78
                   95
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   147603
Seq. No.
Seq. ID
                   LIB3168-093-P1-K1-B8
Method
                   BLASTX
NCBI GI
                   g1109699
BLAST score
                   497
E value
                   2.0e-50
Match length
                   95
% identity
                   100
                   (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   147604
                   LIB3168-093-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2335106
BLAST score
                   161
E value
                   6.0e-11
Match length
                   133
% identity
                   (AC002339) salt inducible protein-like [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   147605
Seq. ID
                   LIB3168-093-P1-K1-C1
Method
                   BLASTN
                   g2252823
NCBI GI
BLAST score
                   75
E value
                   3.0e - 34
                   183
Match length
                   85
% identity
NCBI Description
                  Arabidopsis thaliana BAC IG005I10
Seq. No.
                   147606
Seq. ID
                   LIB3168-093-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   g4589969
BLAST score
                   347
E value
                   0.0e + 00
Match length
                   421
                   95
% identity
                  Arabidopsis thaliana chromosome II BAC F1P15 genomic
NCBI Description
                   sequence, complete sequence
                   147607
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-C11
Method
                  BLASTX
```

18598

g1628583

```
E value
                   3.0e-25
Match length
                   71
% identity
                   86
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147608
                  LIB3168-093-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                  q136251
BLAST score
                   452
E value
                   3.0e-45
                   113
Match length
                   78
% identity
                  TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR
NCBI Description
                  >gi 99767 pir A31393 tryptophan synthase (EC 4.2.1.20)
                  beta chain - Arabidopsis thaliana >gi 166892 (M23872)
                  tryptophan synthase beta subunit [Arabidopsis thaliana]
Seq. No.
                  147609
                  LIB3168-093-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                   484
                   5.0e-49
E value
Match length
                  106
% identity
                  88
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147610
Seq. ID
                  LIB3168-093-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q3776023
BLAST score
                  324
E value
                   4.0e-30
Match length
                  73
% identity
NCBI Description
                   (AJ010473) RNA helicase [Arabidopsis thaliana]
Seq. No.
                  147611
Seq. ID
                  LIB3168-093-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g3869062
BLAST score
                  61
E value
                  9.0e-26
Match length
                  117
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K11I1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147612
Seq. ID
                  LIB3168-093-P1-K1-C8
```



Method BLASTX
NCBI GI g112737
BLAST score 557
E value 2.0e-57
Match length 137
% identity 60

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir\_NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147613

Seq. ID LIB3168-093-P1-K1-C9

Method BLASTX
NCBI GI g881615
BLAST score 628
E value 9.0e-66
Match length 123
% identity 98

NCBI Description (U29142) fatty acid elongase 1 [Arabidopsis thaliana]

>gi\_3096921\_emb\_CAA18831.1\_ (AL023094) fatty acid elongase

1 [Arabidopsis thaliana]

Seq. No. 147614

Seq. ID LIB3168-093-P1-K1-D1

Method BLASTX
NCBI GI g112737
BLAST score 593
E value 1.0e-61
Match length 130
% identity 87

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi\_4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147615

Seq. ID LIB3168-093-P1-K1-D10

Method BLASTX
NCBI GI g3335169
BLAST score 563
E value 4.0e-58
Match length 135
% identity 77

NCBI Description (AF067857) embryo-specific protein 1 [Arabidopsis thaliana]

>gi\_4455197\_emb\_CAB36520.1\_ (AL035440) embryo-specific

protein 1 (ATS1) [Arabidopsis thaliana]

Seq. No. 147616

Seq. ID LIB3168-093-P1-K1-D11

Method BLASTX

```
NCBI ĞI
                  g112741
BLAST score
                  705
E value
                  9.0e-75
Match length
                  132
% identity
                  99
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) > gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >qi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147617
Seq. ID
                  LIB3168-093-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  612
E value
                  8.0e-64
Match length
                  141
% identity
                  87
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147618
Seq. ID
                  LIB3168-093-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g2760172
BLAST score
                  361
E value
                  0.0e + 00
Match length
                  384
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147619
                  LIB3168-093-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  a112737
BLAST score
                  573
E value
                  3.0e-59
Match length
                  122
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147620
Seq. ID
                  LIB3168-093-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  340
```

```
5.0e-32
E value
                  110
Match length
                  65
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir_NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1_{-} (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147621
Seq. ID
                  LIB3168-093-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g267083
                  613
BLAST score
E value
                  6.0e-64
                  136
Match length
% identity
                  83
                  TUBULIN BETA-9 CHAIN >qi 320190 pir JQ1593 tubulin beta-9
NCBI Description
                  chain - Arabidopsis thaliana >gi 166910 (M84706) beta-9
                  tubulin [Arabidopsis thaliana]
Seq. No.
                  147622
                  LIB3168-093-P1-K1-E11
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  619
E value
                  1.0e-64
Match length
                  120
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147623
Seq. ID
                  LIB3168-093-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  580
E value
                  4.0e-60
Match length
                  135
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__$08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147624
                  LIB3168-093-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2842474
BLAST score
                  91
E value
                  2.0e-43
Match length
                  194
                  43
% identity
```

```
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
                  (ESSAII project)
Seq. No.
                  147625
Seq. ID
                  LIB3168-093-P1-K1-E5
Method
                  BLASTX
                  g2129657
NCBI GI
BLAST score
                  354
E value
                  1.0e-33
Match length
                  101
                  75
% identity
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                  >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016_emb_CAA90878_ (Z54165) oleosin
                  [Arabidopsis thaliana]
Seq. No.
                  147626
                  LIB3168-093-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  455
E value
                  2.0e-45
Match length
                  142
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147627
                  LIB3168-093-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  475
                  8.0e-71
E value
Match length
                  137
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147628
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g625977
BLAST score
                  586
E value
                  8.0e-61
Match length
                  116
% identity
                  97
                  p40 protein homolog - Arabidopsis thaliana >gi 402904
NCBI Description
                  (U01955) laminin receptor-like protein [Arabidopsis
```

thaliana]

Seq. No.

Seq. ID LIB3168-093-P1-K1-E9

147629

Method BLASTX NCBI GI g112682 BLAST score 543 Section

```
7.0e-56
E value
                  117
Match length
                  87
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147630
Seq. No.
                  LIB3168-093-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
                  392
BLAST score
                  2.0e-38
E value
                  82
Match length
% identity
                  93
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147631
Seq. ID
                  LIB3168-093-P1-K1-F10
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  52
                  9.0e-60
E value
Match length
                  121
                  99
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147632
Seq. No.
                  LIB3168-093-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4406816
BLAST score
                  521
E value
                  3.0e-53
Match length
                  105
% identity
                  93
NCBI Description
                  (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
                  147633
Seq. No.
                  LIB3168-093-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2253010
BLAST score
                  122
E value
                  4.0e-20
Match length
                  69
% identity
NCBI Description
                  (Y14199) MAP3K delta-1 protein kinase [Arabidopsis
                  thaliana]
                  147634
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-F5
Method
                  BLASTX
```

```
NCBI GI
                  g418908
BLAST score
                  182
                  2.0e-13
E value
                  75
Match length
% identity
NCBI Description vicilin precursor - cacao
                  147635
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1864017
BLAST score
                  513
                  3.0e-52
E value
                  110
Match length
                  90
% identity
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
                  147636
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-F7
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  595
E value
                  7.0e-62
                  120
Match length
                  96
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147637
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                   621
                   6.0e-65
E value
Match length
                  118
                  98
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147638
                  LIB3168-093-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  191
E value
                  2.0e-14
Match length
                  121
                   34
% identity
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
NCBI Description
                   [Nicotiana tabacum]
Seq. No.
                  147639
                  LIB3168-093-P1-K1-G10
Seq. ID
Method
                  BLASTX
```

```
NCBI GI
                   g112739
BLAST score
                   439
                  1.0e-43
E value
                  126
Match length
                  71
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854 pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871
                   (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147640
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-G11
                  BLASTX
Method
NCBI GI
                  g2129657
BLAST score
                  320
E value
                  1.0e-29
Match length
                  96
                  72
% identity
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                  >gi_987014_emb_CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] \overline{>}gi \overline{9}87016 emb CAA90878 (Z54165) oleosin
                   [Arabidopsis thaliana]
                  147641
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q3242709
BLAST score
                  259
                  2.0e-22
E value
                  70
Match length
% identity
                   (AC003040) putative guanine nucleotide-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  147642
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  530
E value
                  1.0e-57
Match length
                  127
                  92
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147643
                  LIB3168-093-P1-K1-G4
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4567193
BLAST score
                  404
E value
                  0.0e + 00
Match length
                  424
% identity
                  99
```

```
NCBI Description Arabidopsis thaliana chromosome II BAC T26C19 genomic
                  sequence, complete sequence
                  147644
                  LIB3168-093-P1-K1-G5
```

Seq. ID BLASTX Method NCBI GI q112681 535 BLAST score 8.0e-55 E value 138 Match length 78 % identity

Seq. No.

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

147645 Seq. No.

LIB3168-093-P1-K1-G6 Seq. ID

Method BLASTN NCBI GI g4757413 77 BLAST score E value 3.0e-35 Match length 289 90 % identity

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MXO21, complete sequence

Seq. No. 147646

LIB3168-093-P1-K1-G7 Seq. ID

Method BLASTX NCBI GI g4678285 259 BLAST score E value 2.0e-22 72 Match length

% identity 61

NCBI Description (AL049660) putative protein [Arabidopsis thaliana]

Seq. No. 147647

Seq. ID LIB3168-093-P1-K1-G8

Method BLASTN NCBI GI g2623294 BLAST score 202 E value 1.0e-110 Match length 362 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T20B5 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 147648

Seq. ID LIB3168-093-P1-K1-G9

Method BLASTX NCBI GI g3128170 BLAST score 736 E value 2.0e-78 Match length 139 97 % identity

NCBI GI

E value

BLAST score

Match length

g1345973

1.0e-52

516

106

```
NCBI Description
                  (AC004521) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  147649
Seq. ID
                  LIB3168-093-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g4220510
BLAST score
                  171
                  3.0e-91
E value
Match length
                  426
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                   (ESSAII project)
                  147650
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g4415928
BLAST score
                  110
E value
                  5.0e-55
Match length
                  182
                  91
% identity
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147651
Seq. ID
                  LIB3168-093-P1-K1-H5
                  BLASTX
Method
NCBI GI
                  q112682
BLAST score
                  474
E value
                  3.0e-55
Match length
                  131
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147652
Seq. ID
                  LIB3168-093-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  563
E value
                  4.0e-58
Match length
                  141
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147653
Seq. No.
Seq. ID
                  LIB3168-093-P1-K1-H7
Method
                  BLASTX
```

```
% identity
NCBI Description
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi 408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >gi 471091 dbj BAA04505 (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >qi 1197795 dbj BAA05514 (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >qi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  147654
                  LIB3168-093-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3169175
BLAST score
                  421
E value
                  2.0e-41
Match length
                  135
% identity
                  56
                  (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                  thaliana]
                  147655
Seq. No.
                  LIB3168-093-P1-K1-H9
Seq. ID
Method
                  BLASTX
                                                                      NCBI GI
                  g1628583
BLAST score
                  500
                  6.0e-51
E value
                  98
Match length
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147656
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  240
                  1.0e-20
E value
Match length
                  52
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
```

Seq. No. 147657

Seq. ID LIB3168-094-P1-K1-A10

Method BLASTX
NCBI GI g1628583
BLAST score 650
E value 2.0e-68
Match length 125
% identity 99

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

```
cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147658
Seq. ID
                  LIB3168-094-P1-K1-A11
                  BLASTX
Method
                  g1628583
NCBI GI
BLAST score
                  398
E value
                  7.0e-39
Match length
                  99
                  80
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147659
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-A12
                  BLASTX
Method
NCBI GI
                  q2271477
BLAST score
                  433
                  7.0e-43
E value
Match length
                  101
                  83
% identity
NCBI Description
                  (AF009631) AP47/50p [Arabidopsis thaliana]
Seq. No.
                  147660
                  LIB3168-094-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  528
                  5.0e-54
E value
Match length
                  119
                  85
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147661
Seq. ID
                  LIB3168-094-P1-K1-A3
Method
                  BLASTN
                  g1628582
NCBI GI
BLAST score
                  37
E value
                  2.0e-11
                  73
Match length
% identity
                  89
                  Arabidopsis thaliana 12S cruciferin seed storage protein
NCBI Description
                  (ATCRU3) gene, complete cds
Seq. No.
                  147662
Seq. ID
                  LIB3168-094-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  704
                  1.0e-74
E value
Match length
                  140
% identity
                  99
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
```

thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S

```
thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
```

```
Seq. No.
                  147663
Seq. ID
                  LIB3168-094-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  356
E value
                  8.0e - 34
Match length
                  114
% identity
                  64
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  147664
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  261
                  9.0e-23
E value
Match length
                  86
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147665
Seq. ID
                  LIB3168-094-P1-K1-A7
Method
                  BLASTX
                  g4204299
NCBI GI
BLAST score
                  321
                  2.0e-30
E value
Match length
                  64
% identity
NCBI Description
                  (AC003027) 1cl prt seq No definition line found
                  [Arabidopsis thaliana]
                  147666
Seq. No.
                  LIB3168-094-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  102
                  4.0e-04
E value
Match length
                  113
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

147667

Seq. No.

```
LIB3168-094-P1-K1-B12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g114649
BLAST score
                  220
E value
                  7.0e-18
Match length
                  46
                  100
% identity
NCBI Description
                  ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
                  >gi 67899 pir LWLVA H+-transporting ATP synthase (EC
                  3.6.1.34) lipid-binding protein - liverwort (Marchantia
                  polymorpha) chloroplast >gi 11653_emb CAA28066 (X04465)
                  atpH [Marchantia polymorpha]
                  147668
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  324
E value
                  3.0e-30
Match length
                  91
                  71
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147669
Seq. ID
                  LIB3168-094-P1-K1-B3
Method
                  BLASTX
                  g2642158
NCBI GI
BLAST score
                  457
E value
                  1.0e-45
Match length
                  117
                  71
% identity
NCBI Description
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
                  147670
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q4584110
BLAST score
                  328
E value
                  1.0e-30
Match length
                  129
                  50
% identity
NCBI Description
                  (AJ133639) SAH7 protein [Arabidopsis thaliana]
Seq. No.
                  147671
Seq. ID
                  LIB3168-094-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g4584110
BLAST score
                  161
E value
                  6.0e-11
                  87
Match length
% identity
                  40
NCBI Description
                  (AJ133639) SAH7 protein [Arabidopsis thaliana]
Seq. No.
                  147672
Seq. ID
                  LIB3168-094-P1-K1-B6
```

% identity

```
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  622
E value
                  5.0e-65
Match length
                  120
                  99
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147673
                  LIB3168-094-P1-K1-B7
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
BLAST score
                  383
                  2.0e-37
E value
Match length
                  78
% identity
                  95
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147674
Seq. ID
                  LIB3168-094-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  426
E value
                  3.0e-42
Match length
                  93
% identity
                  89
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >qi 68853 pir NWMUl 2S albumin 1 precursor -
                  Arabidopsis thaliana >qi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >qi 395204 emb CAA80870
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147675
Seq. ID
                  LIB3168-094-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g3941412
BLAST score
                  178
E value
                  5.0e-13
Match length
                  38
% identity
NCBI Description
                  (AF062860) putative transcription factor [Arabidopsis
                  thaliana]
Seq. No.
                  147676
                  LIB3168-094-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  618
E value
                  1.0e-64
Match length
                  120
```



NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147677

Seq. ID LIB3168-094-P1-K1-C11

Method BLASTX
NCBI GI g1628583
BLAST score 619
E value 1.0e-64
Match length 120

% identity 99
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147678

Seq. ID LIB3168-094-P1-K1-C12

Method BLASTN
NCBI GI 94159712
BLAST score 361
E value 0.0e+00
Match length 408
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 147679

Seq. ID LIB3168-094-P1-K1-C3

Method BLASTX
NCBI GI g112737
BLAST score 580
E value 5.0e-60
Match length 141
% identity 80

NCBI Description 2S

on 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710 emb\_CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147680

Seq. ID LIB3168-094-P1-K1-C4

Method BLASTX
NCBI GI 94204299
BLAST score 618
E value 1.0e-64
Match length 139
% identity 87

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 147681

Seq. ID LIB3168-094-P1-K1-C5

Method BLASTX

% identity

```
NCBI GI
                  q4204298
BLAST score
                  640
E value
                  4.0e-67
                  138
Match length
                  90
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  147682
                  LIB3168-094-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129657
BLAST score
                  301
                  2.0e-27
E value
                  90
Match length
                  72
% identity
                  oleosin isoform - Arabidopsis thaliana
NCBI Description
                  >gi 987014 emb CAA90877 (Z54164) oleosin [Arabidopsis
                  thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                   [Arabidopsis thaliana]
                  147683
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                   480
                   2.0e-48
E value
Match length
                  98
                   92
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201 emb_CAA80868
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147684
Seq. ID
                  LIB3168-094-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                   384
E value
                   2.0e-37
Match length
                  86
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                   147685
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  622
E value
                  5.0e-65
Match length
                  120
                  99
```

34

```
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147686
                  LIB3168-094-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
                  613
BLAST score
                  6.0e-64
E value
                  120
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147687
                  LIB3168-094-P1-K1-D11
Seq. ID
                  BLASTX
Method
                  g3047082
NCBI GI
BLAST score
                  154
E value
                  4.0e-10
                  41
Match length
% identity
                  (AF058914) similar to Vigna radiata pectinacetylesterase
NCBI Description
                  precursor (GB:X99348) [Arabidopsis thaliana]
                  147688
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g99698
BLAST score
                  481
E value
                  2.0e-48
                  94
Match length
                  99
% identity
NCBI Description
                  glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone
                  lambdaAtgskb6) - Arabidopsis thaliana
Seq. No.
                  147689
Seq. ID
                  LIB3168-094-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  443
                  5.0e-44
E value
                  143
Match length
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
```

Seq. No. 147690

Seq. ID LIB3168-094-P1-K1-D3

Method BLASTN
NCBI GI g1592685
BLAST score 53
E value 4.0e-21
Match length 227

cruciferin seed storage protein [Arabidopsis thaliana]

BLAST score

```
% identity
NCBI Description A.thaliana mRNA for oleosin type4 protein
                   147691
Seq. No.
Seq. ID
                   LIB3168-094-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g112681
BLAST score
                   567
                   1.0e-58
E value
                   131
Match length
                   84
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   147692
Seq. ID
                   LIB3168-094-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g2129657
BLAST score
                   422
E value
                   1.0e-41
                   115
Match length
                   77
% identity
NCBI Description
                   oleosin isoform - Arabidopsis thaliana
                   >gi_987014_emb_CAA90877_ (Z54164) oleosin [Arabidopsis
                   thaliana] >gi 987016 emb CAA90878 (Z54165) oleosin
                   [Arabidopsis thaliana]
                   147693
Seq. No.
Seq. ID
                   LIB3168-094-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g1890281
BLAST score
                   351
E value
                   3.0e-33
Match length
                   114
% identity
NCBI Description
                   (U89984) transformation-sensitive protein homolog
                   [Acanthamoeba castellanii]
Seq. No.
                   147694
Seq. ID
                   LIB3168-094-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g2160151
BLAST score
                   540
E value
                   2.0e-55
Match length
                   111
% identity
                   96
NCBI Description
                   (AC000375) Strong similarity to Brassica aspartic protease
                   (gb X77260). [Arabidopsis thaliana]
                   147695
Seq. No.
Seq. ID
                   LIB3168-094-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g1592677
```

NCBI Description

```
E value
                  3.0e-17
Match length
                  113
% identity
                  43
NCBI Description
                  (X91912) LEA76 homologue type2 [Arabidopsis thaliana]
Seq. No.
                  147696
Seq. ID
                  LIB3168-094-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  628
                  1.0e-65
E value
                  132
Match length
                  89
% identity
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >qi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147697
Seq. ID
                  LIB3168-094-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  572
E value
                  4.0e-59
Match length
                  140
                  81
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147698
Seq. ID
                  LIB3168-094-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  417
E value
                  7.0e-41
Match length
                  79
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147699
Seq. ID
                  LIB3168-094-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q2088654
BLAST score
                  552
E value
                  8.0e-57
Match length
                  121
                  91
% identity
```

[Arabidopsis thaliana]

(AF002109) 60S acidic ribosomal protein PO isolog

Seq. ID

```
147700
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  550
                  1.0e-56
E value
Match length
                  133
                  80
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  147701
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  728
                  2.0e-77
E value
Match length
                  141
                  99
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147702
Seq. ID
                  LIB3168-094-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  447
                  2.0e-44
E value
                  119
Match length
                  76
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147703
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  701
E value
                  3.0e-74
Match length
                  137
% identity
                  96
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147704
```

18619

LIB3168-094-P1-K1-F12

```
Method
                   BLASTN
NCBI GI
                   q3228389
BLAST score
                   364
                   0.0e + 00
E value
Match length
                   403
% identity
                   98
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
                   complete sequence [Arabidopsis thaliana]
                   147705
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-F5
                  {\tt BLASTX}
Method
NCBI GI
                   q4584110
BLAST score
                   289
                   6.0e-26
E value
Match length
                   106
                   54
% identity
NCBI Description
                   (AJ133639) SAH7 protein [Arabidopsis thaliana]
Seq. No.
                  147706
Seq. ID
                  LIB3168-094-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                   637
                   9.0e-67
E value
                   136
Match length
                   90
% identity
                   2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853 pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147707
Seq. ID
                  LIB3168-094-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  518
                  8.0e-53
E value
Match length
                  139
% identity
                  78
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147708
Seq. ID
                  LIB3168-094-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q4204298
BLAST score
                  550
E value
                  1.0e-56
Match length
                  133
% identity
                  80
```

```
(AC003027) lcl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  147709
Seq. No.
                  LIB3168-094-P1-K1-G10
Seq. ID
Method
                  BLASTX
                  q4406780
NCBI GI
BLAST score
                  590
E value
                  3.0e-61
                  138
Match length
                  84
% identity
                   (AC006532) putative multispanning membrane protein
NCBI Description
                   [Arabidopsis thaliana]
                  147710
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-G11
Method
                  BLASTN
                  q3036791
NCBI GI
BLAST score
                  413
                  0.0e + 00
E value
                  417
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T19K4
NCBI Description
                   (ESSAII project)
Seq. No.
                  147711
                  LIB3168-094-P1-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618683
BLAST score
                  379
                  0.0e+00
E value
Match length
                  427
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T32G6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147712
Seq. ID
                  LIB3168-094-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g3808062
BLAST score
                  166
E value
                  1.0e-11
Match length
                  70
                   44
% identity
                   (AB019195) PV100 [Cucurbita maxima]
NCBI Description
Seq. No.
                  147713
Seq. ID
                  LIB3168-094-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q135535
BLAST score
                  375
E value
                  3.0e - 36
Match length
                  76
% identity
                  99
                  T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
NCBI Description
                   (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide
                  Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955
```

Method

NCBI GI

BLASTN

q3176695

```
(D11351) t-complex polypeptide 1 homologue [Arabidopsis
                  thaliana] >gi 2326265 dbj BAA21772 (D11352) CCT
                  alpha/TCP-1 [Arabidopsis thaliana]
                  147714
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-G5
                  BLASTN
Method
NCBI GI
                  q4589428
BLAST score
                  158
                  1.0e<sub>-83</sub>
E value
Match length
                  216
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFH8, complete sequence
                  147715
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  a112681
BLAST score
                  700
                  4.0e-74
E value
                  140
Match length
                  99
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147716
Seq. No.
                  LIB3168-094-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4734005
BLAST score
                  244
E value
                  1.0e-20
                  77
Match length
                  58
% identity
NCBI Description
                  (AC007178) hypothetical protein [Arabidopsis thaliana]
                  147717
Seq. No.
                  LIB3168-094-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  702
                  2.0e-74
E value
Match length
                  133
% identity
                  98
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147718
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-G9
```

BLAST score

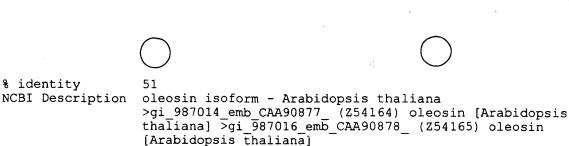
E value

362

1.0e-34

```
BLAST score
E value
                  9.0e-79
Match length
                  338
% identity
                  86
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F14J9 genomic
                  sequence contains phyA marker, complete sequence
                  [Arabidopsis thaliana]
Seq. No.
                  147719
Seq. ID
                  LIB3168-094-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  554
E value
                  5.0e-57
Match length
                  134
% identity
                  81
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  147720
Seq. No.
Seq. ID
                  LIB3168-094-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  501
                  7.0e-51
E value
Match length
                  125
% identity
NCBI Description
                  (AC003027) 1cl prt seq No definition line found
                  [Arabidopsis thaliana]
Seq. No.
                  147721
Seq. ID
                  LIB3168-094-P1-K1-H11
Method
                  BLASTX
NCBI GI
                 ·q112741
BLAST score
                  619
E value
                  9.0e-65
Match length
                  117
% identity
                  99
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) > gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >qi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147722
Seq. ID
                  LIB3168-094-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q112739
```

```
Match length
% identity
                  68
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147723
Seq. No.
                  LIB3168-094-P1-K1-H2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112737
BLAST score
                  573
                  3.0e-59
E value
                  123
Match length
                  89
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147724
                  LIB3168-094-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  69
                  8.0e-60
E value
                  127
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147725
Seq. ID
                  LIB3168-094-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  622
E value
                  5.0e-65
                  120
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147726
Seq. No.
                  LIB3168-094-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129657
                  194
BLAST score
                  8.0e-15
E value
                  93
Match length
```



147727 Seq. No. Seq. ID LIB3168-094-P1-K1-H7 Method BLASTX NCBI GI q112681 BLAST score 690 5.0e-73 E value Match length 139

% identity

% identity 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147728 LIB3168-094-P1-K1-H8 Seq. ID Method BLASTX NCBI GI q1628583 663

BLAST score E value 8.0e-70 Match length 137 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

147729 Seq. No. Seq. ID LIB3168-094-P1-K1-H9

Method BLASTX NCBI GI q2129657 BLAST score 366 E value 5.0e-35 Match length 104 % identity

NCBI Description oleosin isoform - Arabidopsis thaliana

 $>gi_987014$  emb\_CAA90877\_ (Z54164) oleosin [Arabidopsis thaliana]  $>gi_987016$  emb\_CAA90878\_ (Z54165) oleosin

[Arabidopsis thaliana]

Seq. No. 147730

Seq. ID LIB3168-095-P1-K1-A1

Method BLASTX NCBI GI q1628583 BLAST score 521 E value 3.0e-53 Match length 110 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

```
147731
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g112682
                  560
BLAST score
                  9.0e-58
E value
Match length
                  133
                  80
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147732
Seq. ID
                  LIB3168-095-P1-K1-A11
Method
                  BLASTX
                  g112741
NCBI GI
BLAST score
                  871
E value
                  4.0e-94
Match length
                  164
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147733
                  LIB3168-095-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204299
BLAST score
                  651
                  2.0e-68. ...
E value
Match length
                  126
% identity
NCBI Description
                  (AC003027) lcl prt seq No definition line found
                  [Arabidopsis thaliana]
                  147734
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  93
E value
                  2.0e-58
Match length
                  120
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147735
                  LIB3168-095-P1-K1-A3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
```

E value

Match length

1.0e-149

```
BLAST score
                    433
 E value
                    9.0e-43
 Match length
                    147
 % identity
                    64
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
 NCBI Description
                    thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
 Seq. No.
                   147736
 Seq. ID
                   LIB3168-095-P1-K1-A5
 Method
                   BLASTX
 NCBI GI
                   q1628583
 BLAST score
                   642
 E value
                   3.0e-67
 Match length
                   123
 % identity
                   100
 NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
 Seq. No.
                   147737
 Seq. ID
                   LIB3168-095-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   g112682
BLAST score
                   660
E value
                   2.0e-69
Match length
                   150
% identity
                   83
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__$08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                   thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   147738
Seq. ID
                   LIB3168-095-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g112741
BLAST score
                   680
E value
                   7.0e-72
Match length
                  126
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147739
Seq. ID
                  LIB3168-095-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g2828181
BLAST score
                  269
```

```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLE8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147740
Seq. ID
                  LIB3168-095-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  191
                  4.0e-15
E value
Match length
                  70
% identity
                  61
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147741
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-B1
                  BLASTX
Method
NCBI GI
                  q1592670
                  457
BLAST score
                  3.0e-46
E value
                  132
Match length
% identity
NCBI Description
                  (X91920) dehydrin [Arabidopsis thaliana]
                  >gi 4567280 gb AAD23693.1 AC006841 21 (AC006841) putative
                  dehydrin [Arabidopsis thaliana]
                  147742
Seq. No.
                  LIB3168-095-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q21913
BLAST score
                  201
                  1.0e-15
E value
Match length
                  83
% identity
                  (X62626) vicilin [Theobroma cacao]
NCBI Description
                  147743
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  609
                  2.0e-63
E value
                  163
Match length
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
```

Seq. No. 147744

18628

precursor [Arabidopsis thaliana]

```
Seq. ID
                  LIB3168-095-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  717
E value
                  5.0e-76
Match length
                  172
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147745
Seq. ID
                  LIB3168-095-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  628
E value
                  1.0e-65
Match length
                  123
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147746
                  LIB3168-095-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  664
E value
                  8.0e-70
Match length
                  169
% identity
                  78
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147747
                  LIB3168-095-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  383
E value
                  4.0e-37
Match length
                  102
% identity
                  71
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147748
                  LIB3168-095-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  628
E value
                  1.0e-65
Match length
                  120
% identity
                  100
```

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147749 LIB3168-095-P1-K1-B6 Seq. ID Method BLASTX NCBI GI q112681 BLAST score 212 4.0e-17 E value Match length 42 % identity 100 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] 147750 Seq. No. LIB3168-095-P1-K1-B7 Seq. ID Method BLASTX NCBI GI g1628583 136 BLAST score 1.0e-32 E value Match length 78 80 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 147751 Seq. No. LIB3168-095-P1-K1-B8 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 682 E value 7.0e-72 Match length 167 % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147752 Seq. ID LIB3168-095-P1-K1-B9 Method BLASTX NCBI GI g3738257 BLAST score 504 E value 1.0e-61 Match length 143 % identity (AB018410) cytosolic phosphoglycerate kinase 1 [Populus NCBI Description nigra] 147753 Seq. No. Seq. ID LIB3168-095-P1-K1-C10 Method BLASTN NCBI GI q4512656

```
BLAST score
E value
                   1.0e-81
Match length
                   499
% identity
                   83
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                   sequence, complete sequence
Seq. No.
                   147754
Seq. ID
                  LIB3168-095-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g4249382
BLAST score
                   505
                   4.0e-51
E value
                   126
Match length
% identity
                   78
NCBI Description
                   (AC005966) Strong similarity to gi 3337350 F13P17.3
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
                  147755
Seq. No.
                  LIB3168-095-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1628583
BLAST score
                   479
E value
                   2.0e-48
Match length
                  101
% identity
                   91
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147756
Seq. ID
                  LIB3168-095-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  665
E value
                   6.0e-70
Match length
                  158
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147757
Seq. ID
                  LIB3168-095-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  633
E value
                  4.0e-66
Match length
                  170
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
```

Seq. No. 147758

Seq. ID LIB3168-095-P1-K1-C4

Seq. ID

Method

NCBI GI

```
BLASTX
Method
NCBI GI
                  g1345973
BLAST score
                  332
                  3.0e-31
E value
                  62
Match length
                  100
% identity
                  OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
                  1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                  omega-3 fatty acid desaturase [Arabidopsis thaliana]
                  >qi 471091 dbj BAA04505 (D17579) fatty acid desaturase
                  [Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                  microsomal omega-3 fatty acid desaturase [Arabidopsis
                  thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  147759
Seq. ID
                  LIB3168-095-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  935
E value
                  1.0e-101
Match length
                  178
                  98
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147760
                  LIB3168-095-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  607
E value
                  3.0e-63
Match length
                  120
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147761
Seq. No.
                  LIB3168-095-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4539292
BLAST score
                  463
E value
                  3.0e-46
Match length
                  88
% identity
NCBI Description
                  (ALO49480) putative ribosomal protein S10 [Arabidopsis
                  thaliana]
Seq. No.
                  147762
```

LIB3168-095-P1-K1-C8

BLASTX

g3273743

Seq. No.

Seq. ID Method

```
620
BLAST score
E value
                   1.0e-64
Match length
                   118
% identity
                   100
                   (AF057357) lipid transfer protein 2 precursor [Arabidopsis
NCBI Description
                   thaliana] >gi_3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
                   147763
Seq. No.
                  LIB3168-095-P1-K1-C9
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1628583
                   619
BLAST score
                   9.0e-65
E value
                   120
Match length
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   147764
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   g3176695
                   218
BLAST score
                   1.0e-119
E value
                   270
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F14J9 genomic
                   sequence contains phyA marker, complete sequence
                   [Arabidopsis thaliana]
Seq. No.
                   147765
Seq. ID
                   LIB3168-095-P1-K1-D11
Method
                   BLASTN
                   g4490701
NCBI GI
                   39
BLAST score
                   6.0e-13
E value
Match length
                   180
% identity
                   56
                   Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18
NCBI Description
                   (ESSA project)
Seq. No.
                   147766
                  LIB3168-095-P1-K1-D12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3985954
BLAST score
                   219
E value
                   1.0e-120
Match length
                   342
                   92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRG21, complete sequence [Arabidopsis thaliana]
                   147767
```

18633

LIB3168-095-P1-K1-D2

BLASTX

N NCBI GI g112737 BLAST score 647 E value 7.0e-68 Match length 163 % identity 81 NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >qi 395204 emb CAA80870 (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana] Seq. No. 147768 Seq. ID LIB3168-095-P1-K1-D3 Method BLASTX g1628583 NCBI GI BLAST score 642

3.0e-67 E value Match length 123 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147769 Seq. ID LIB3168-095-P1-K1-D5 Method BLASTX g119143

NCBI GI BLAST score 396 E value 1.0e-47 Match length 103 % identity 97

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

> >qi 81606 pir S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453 (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi 1369927 emb CAA34454 (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455 (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana] >qi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana] >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]

Seq. No. 147770 Seq. ID LIB3168-095-P1-K1-D6 Method BLASTX

NCBI GI g112741 BLAST score 846 E value 4.0e-91 Match length 157 % identity

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868 (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

Seq. No.

147775

```
precursor [Arabidopsis thaliana]
Seq. No.
                  147771
Seq. ID
                  LIB3168-095-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  693
E value
                  3.0e-73
Match length
                  166
                  81
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147772
Seq. ID
                  LIB3168-095-P1-K1-D8
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  625
E value
                  3.0e-65
Match length
                  120
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495 emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147773
                  LIB3168-095-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3287694
BLAST score
                  151
E value
                  2.0e-86
Match length
                  160
                  99
% identity
NCBI Description
                  (AC003979) Similar to myb-related transcription factor
                  (THM27) gb X95296 from Solanum lycopersicum. ESTs
                  gb_T42000, gb_T04118, gb_AA598042, gb_AA394757 and
                  gb AA598046 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  147774
Seq. ID
                  LIB3168-095-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g112737...
BLAST score
                  684
E value
                  4.0e-72
Match length
                  145
% identity
                  88
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
```

>qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

```
Seq. ID
                  LIB3168-095-P1-K1-E12
Method
                  BLASTX
                  q112681
NCBI GI
                  892
BLAST score
E value
                  2.0e-96
Match length
                  171
                  98
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147776
Seq. No.
                  LIB3168-095-P1-K1-E2
Seq. ID
                  BLASTX
Method
                  g112681
NCBI GI
                  391
BLAST score
                  3.0e-46
E value
Match length
                  139
                  77
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147777
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-E4
Method
                  BLASTN
NCBI GI
                  q2864607
BLAST score
                  202
E value
                  1.0e-110
Match length
                  254
                  95
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
NCBI Description
                  (ESSAII project)
Seq. No.
                  147778
                  LIB3168-095-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  827
                  7.0e-89
E value
Match length
                  180
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147779
                  LIB3168-095-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  102
```

BLAST score

```
E value
                   2.0e-60
Match length
                   120
% identity
                   96
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147780
Seq. ID
                   LIB3168-095-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q683553
BLAST score
                   144
                   7.0e-09
E value
Match length
                   117
                   30
% identity
NCBI Description
                   (Z48450) oleosin-like protein [Citrus sinensis]
                   >gi_1582679_prf__2119230A oleosin homolog [Citrus sinensis]
                   147781
Seq. No.
Seq. ID
                   LIB3168-095-P1-K1-E9
Method
                   BLASTX
                   g1628583
NCBI GI
BLAST score
                   651
E value
                   2.0e-68
Match length
                   139
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147782
Seq. ID
                   LIB3168-095-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q2702364
BLAST score
                   212
E value
                   6.0e-17
Match length
                   102
% identity
NCBI Description
                   (AF036706) No definition line found [Caenorhabditis
                   elegans]
                   147783
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   g3869073
BLAST score
                   230
E value
                   1.0e-126
Match length
                   483
                   93
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MKN22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147784
                  LIB3168-095-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
```

```
E value
Match length
                  180
% identity
                  82
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147785
Seq. ID
                  LIB3168-095-P1-K1-F12
Method
                  BLASTN
                  g4589445
NCBI GI
BLAST score
                  226
E value
                  1.0e-124
Match length
                  409
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MWL2, complete sequence
                  147786
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  631
                  4.0e-66
E value
Match length
                  117
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  147787
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g119143
BLAST score
                  735
E value
                  5.0e-83
Match length
                  158
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi 81606 pir S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453
                  (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1369927 emb CAA34454 (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                  >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                  147788
Seq. ID
                  LIB3168-095-P1-K1-F4
```

```
BLASTN
Method
NCBI GI
                   g4199934
BLAST score
                   152
E value
                   4.0e-80
                   196
Match length
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                   complete sequence [Arabidopsis thaliana]
                   147789
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   g112741
BLAST score
                   849
E value
                   2.0e-91
Match length
                  160
                   98
% identity
NCBI Description
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >qi 166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                   147790
Seq. ID
                  LIB3168-095-P1-K1-F7
Method
                  BLASTX
NCBI GI
                   g4406780
BLAST score
                   603
E value
                   9.0e-63
Match length
                   142
% identity
                   83
NCBI Description
                   (AC006532) putative multispanning membrane protein
                   [Arabidopsis thaliana]
Seq. No.
                  147791
Seq. ID
                  LIB3168-095-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                   655
E value
                  8.0e-69
Match length
                  150
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147792
Seq. ID
                  LIB3168-095-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g2864607
BLAST score
                  389
E value
                  0.0e+00
Match length
                  420
```

```
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6
                   (ESSAII project)
Seq. No.
                   147793
                   LIB3168-095-P1-K1-G11
Seq. ID
Method
                   BLASTN
NCBI GI
                  g2924257
BLAST score
                   49
                   2.0e-18
E value
Match length
                  89
                   89
% identity
NCBI Description
                  Tobacco chloroplast genome DNA
Seq. No.
                   147794
Seq. ID
                  LIB3168-095-P1-K1-G12
Method
                  BLASTN
NCBI GI
                   q4732166
BLAST score
                   476
E value
                   0.0e+00
Match length
                   519
% identity
                   98
NCBI Description
                  Arabidopsis thaliana BAC F21I2
Seq. No.
                   147795
Seq. ID
                  LIB3168-095-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                   625
                   3.0e-65
E value
                  120
Match length
                   100
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147796
                  LIB3168-095-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                   427
E value
                   4.0e-42
Match length
                  90
% identity
```

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi\_4490710\_emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147797

Seq. ID LIB3168-095-P1-K1-G5

Method BLASTX NCBI GI g112739 BLAST score 62

% identity

```
E value
                  8.0e-34
Match length
                  116
% identity
                  70
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147798
Seq. No.
Seq. ID
                  LIB3168-095-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g1107501
BLAST score
                  369
E value
                  3.0e - 35
Match length
                  91
% identity
NCBI Description
                  (X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
                  Match to gb X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  147799
Seq. ID
                  LIB3168-095-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g4529972
BLAST score
                  682
E value
                  5.0e-72
Match length
                  149
% identity
                  91
NCBI Description
                  (AC002330) putative chloroplast outer envelope 86-like
                  protein [Arabidopsis thaliana]
                  147800
Seq. No.
                  LIB3168-095-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  44
E value
                  2.0e-69
Match length
                  160
% identity
                  83
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147801
Seq. ID
                  LIB3168-095-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q131378
BLAST score
                  220
E value
                  6.0e-18
Match length
                  43
```



NCBI Description PHOTOSYSTEM II REACTION CENTRE N PROTEIN

>gi\_2924272\_emb\_CAA77424\_ (Z00044) PSII N-protein

[Nicotiana tabacum]

Seq. No. 147802

Seq. ID LIB3168-095-P1-K1-H1

Method BLASTX
NCBI GI g2920587
BLAST score 349
E value 4.0e-33
Match length 177

% identity

NCBI Description (AF038362) TBP-associated factor 172 [Homo sapiens]

>gi 2995136\_emb\_CAA04475\_ (AJ001017) TAFII170 [Homo

sapiens]

Seq. No. 147803

Seq. ID LIB3168-095-P1-K1-H10

Method BLASTX
NCBI GI g112737
BLAST score 340
E value 2.0e-32
Match length 81
% identity 83

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor -

Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710\_emb\_CAB38844.1\_ (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147804

Seq. ID LIB3168-095-P1-K1-H12

Method BLASTX
NCBI GI g112681
BLAST score 227
E value 5.0e-19
Match length 89
% identity 55

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana]  $>gi_808936_emb_CAA32493_ (X14312) 12S seed$ 

storage protein [Arabidopsis thaliana]

Seq. No. 147805

Seq. ID LIB3168-095-P1-K1-H2

Method BLASTX
NCBI GI g112681
BLAST score 536
E value 6.0e-55
Match length 144
% identity 78

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

 Seq. No.
 147806

 Seq. ID
 LIB3168-095-P1-K1-H6

 Method
 BLASTN

 NCBI GI
 q4539331

BLAST score 33 E value 9.0e-10 Match length 61 % identity 89

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13

(ESSA project)

Seq. No. 147807

Seq. ID LIB3168-095-P1-K1-H7

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147808

Seq. ID LIB3168-095-P1-K1-H8

Method BLASTX
NCBI GI g1628583
BLAST score 548
E value 3.0e-56
Match length 157
% identity 75

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147809

Seq. ID LIB3168-096-P1-K1-A1

Method BLASTX
NCBI GI g2160189
BLAST score 241
E value 2.0e-20
Match length 101
% identity 7

NCBI Description (AC000132) Similar to A. thaliana receptor-like protein

kinase (gb\_RLK5\_ARATH). ESTs gb\_ATTS0475,gb\_ATTS4362 come

from this gene. [Arabidopsis thaliana]

Seq. No. 147810

Seq. ID LIB3168-096-P1-K1-A10

Method BLASTX
NCBI GI g3169180
BLAST score 568
E value 1.0e-58
Match length 131

```
% identity
NCBI Description
                  (AC004401) putative casein kinase II catalytic subunit
                  [Arabidopsis thaliana]
Seq. No.
                  147811
Seq. ID
                  LIB3168-096-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  681
                  8.0e-72
E value
Match length
                  136
                  99
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147812
Seq. ID
                  LIB3168-096-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  102
E value
                  2.0e-62
Match length
                  123
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147813
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  821
                  3.0e-88
E value
Match length
                  152
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147814
                  LIB3168-096-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2288981
BLAST score
                  396
E value
                  2.0e-38
                  80
Match length
% identity
                  (AC002335) calcium binding protein isolog [Arabidopsis
NCBI Description
```

Seq. No. 147815

protein [Arabidopsis thaliana]

thaliana] >gi 3763938 (AC004450) putative calcium binding

BLAST score

```
LIB3168-096-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  129
                  4.0e-16
E value
Match length
                  82
% identity
                  66
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147816
Seq. ID
                  LIB3168-096-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  187
E value
                  2.0e-14
                  37
Match length
                  100
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147817
Seq. ID
                  LIB3168-096-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  193
E value
                  1.0e-14
Match length
                  133
                  82
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147818
                  LIB3168-096-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g166611
BLAST score
                  41
E value
                  7.0e-14
Match length
                  105
% identity
                  87
NCBI Description
                  A.thaliana at 2S3 gene encoding albumin 2S subunit 3,
                  complete cds
Seq. No.
                  147819
Seq. ID
                  LIB3168-096-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g137465
```

Seq. ID

```
9.0e-51
E value
Match length
                   102
                   98
% identity
                  VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT)
NCBI Description
                   (V-ATPASE 57 KD SUBUNIT) >gi_81637_pir__A31886
                   H+-transporting ATPase (EC 3.6.1.3\overline{5}) 57\overline{K} chain -
                   Arabidopsis thaliana >qi 166627 (J04185) nucleotide-binding
                   subunit of vacuolar ATPase [Arabidopsis thaliana]
                   147820
Seq. No.
                  LIB3168-096-P1-K1-A9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4204299
                   500
BLAST score
E value
                   1.0e-50
                   104
Match length
% identity
                   94
                   (AC003027) lcl prt seg No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   147821
                   LIB3168-096-P1-K1-B1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3805849
BLAST score
                   908
                   2.0e-98
E value
Match length
                   177
% identity
                   (AL031986) cytoplasmatic aconitate hydratase (citrate
NCBI Description
                   hydro-lyase) (aconitase) (EC 4.2.1.3) [Arabidopsis thaliana]
                   147822
Seq. No.
                   LIB3168-096-P1-K1-B10
Seq. ID
                   BLASTX
Method
                   g1652577
NCBI GI
BLAST score
                   64
E value
                   2.0e-10
Match length
                   60
                   63
% identity
                   (D90906) carboxyl-terminal protease [Synechocystis sp.]
NCBI Description
                   147823
Seq. No.
                   LIB3168-096-P1-K1-B11
Seq. ID
Method
                   BLASTX
                   g112681
NCBI GI
BLAST score
                   67
E value
                   3.0e-52
Match length
                   131
% identity
                   81
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   147824
```

18646

LIB3168-096-P1-K1-B2

```
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   717
E value
                   5.0e-76
                   175
Match length
% identity
                   82
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   147825
Seq. No.
                  LIB3168-096-P1-K1-B4
Seq. ID
                  BLASTX
Method
                   g112681
NCBI GI
                   795
BLAST score
                   4.0e-85
E value
                   171
Match length
                   92
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir_s08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   tha\overline{\text{liana}} >qi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   147826
                  LIB3168-096-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GÍ
                   q112682
BLAST score
                   781
E value
                   2.0e-83
Match length
                   173
% identity
NCBI Description
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                   cruciferin precursor (CRB) - Arabidopsis thaliana
                   >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                   tha\overline{\text{liana}} >gi 808937 emb CAA32494 (X14313) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   147827
                   LIB3168-096-P1-K1-B6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204298
BLAST score
                   675
                   4.0e-71
E value
                   171
Match length
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   147828
                  LIB3168-096-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2462931
BLAST score
                   287
E value
                   1.0e-25
Match length
                   70
% identity
                   96
```

```
(Z83833) UDP-glucose:sterol glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   147829
Seq. ID
                   LIB3168-096-P1-K1-B8
Method
                   BLASTN
NCBI GI
                   q3449334
BLAST score
                   282
                   1.0e-157
E value
                   471
Match length
                   98
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MYH9, complete sequence [Arabidopsis thaliana]
                   147830
Seq. No.
                   LIB3168-096-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q112681
BLAST score
                   135
E value
                   4.0e-86
Match length
                   168
% identity
                   99
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   147831
Seq. No.
                   LIB3168-096-P1-K1-C1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4079614
BLAST score
                   390
E value
                   0.0e + 00
Match length
                   485
% identity
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F21M11 genomic
                   sequence, complete sequence [Arabidopsis thaliana].
                   147832
Seq. No.
Seq. ID
                   LIB3168-096-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g112741
BLAST score
                   831
E value
                   2.0e-89
Match length
                   162
% identity
                   95
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
```

Seq. No. 147833

Seq. ID LIB3168-096-P1-K1-C11

18648

precursor [Arabidopsis thaliana]

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

NCBI GI

g112682

```
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  546
                  6.0e-56
E value
Match length
                  120
                  88
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147834
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-C12
                  BLASTX
Method
NCBI GI
                  g1628583
                  940
BLAST score
                  1.0e-102
E value
                  187
Match length
                  97
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147835
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-C2
Method
                  BLASTX
                  g339878
NCBI GI
BLAST score
                  339
                  1.0e-31
E value
Match length
                  154
% identity
                  (M55169) tripeptidyl peptidase II [Homo sapiens]
NCBI Description
Seq. No.
                  147836
Seq. ID
                  LIB3168-096-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g4204298
BLAST score
                  845
                  5.0e-91
E value
Match length
                  176
% identity
                  92
NCBI Description
                   (AC003027) lcl prt seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                  147837
                  LIB3168-096-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3805763
BLAST score
                  251
E value
                  2.0e-21
Match length
                  181
% identity
                  38
NCBI Description
                  (AC005693) hypothetical protein [Arabidopsis thaliana]
                  147838
Seq. No.
                  LIB3168-096-P1-K1-C5
Seq. ID
Method
                  BLASTX
```

Method

NCBI GI

BLAST score

BLASTX

930

g1628583

BLAST score 848 2.0e-91 E value Match length 174 % identity 93 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] 147839 Seq. No. Seq. ID LIB3168-096-P1-K1-C6 Method BLASTX NCBI GI g112741 BLAST score 840 2.0e-90 E value Match length 157 % identity 99 NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >qi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868 (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] Seq. No. 147840 Seq. ID LIB3168-096-P1-K1-C7 Method BLASTX NCBI GI q112681 806 BLAST score 2.0e-86 E value Match length 176 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 147841 Seq. ID LIB3168-096-P1-K1-C8 Method BLASTX NCBI GI q1628583 BLAST score 634 3.0e-66 E value Match length 123 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147842 Seq. ID LIB3168-096-P1-K1-D1

```
E value
                   1.0e-101
Match length
                   178
% identity
                   100
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495 emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                   147843
Seq. ID
                   LIB3168-096-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   q1419390
                   847
BLAST score
E value
                   3.0e-91
                   180
Match length
                   91
% identity
                   (X98926) thylakoid-bound ascorbate peroxidase [Arabidopsis
NCBI Description
                   thaliana]
                   147844
Seq. No.
Seq. ID
                   LIB3168-096-P1-K1-D11
Method
                  BLASTX
NCBI GI
                   g4204299
BLAST score
                   720
E value
                   2.0e-76
Match length
                   141
% identity
NCBI Description
                   (AC003027) lcl_prt_seq No definition line found
                   [Arabidopsis thaliana]
Seq. No.
                   147845
Seq. ID
                   LIB3168-096-P1-K1-D12
Method
                  BLASTX
NCBI GI
                   q3915961
BLAST score
                   805
E value
                   2.0e-86
Match length
                  167
                   92
% identity
NCBI Description
                  HYPOTHETICAL 267 KD PROTEIN (ORF 2280)
                  >gi_2924274_emb_CAA77427_ (Z00044) Ycf2 protein [Nicotiana
                  tabacum] >gi 2924285 emb CAA77438 (Z00044) hypothetical
                  protein [Nicotiana tabacum]
Seq. No.
                  147846
                  LIB3168-096-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827524
BLAST score
                  459
E value
                  9.0e-46
Match length
                  81
% identity
NCBI Description
                  (AL021633) predicted protein [Arabidopsis thaliana]
Seq. No.
                  147847
```

Seq. ID LIB3168-096-P1-K1-D3

Method BLASTX NCBI GI g112681 BLAST score 733



E value 7.0e-78 Match length 180 % identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147848

Seq. ID LIB3168-096-P1-K1-D5

Method BLASTX
NCBI GI g112681
BLAST score 831
E value 2.0e-89
Match length 181
% identity 88

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147849

Seq. ID LIB3168-096-P1-K1-D6

Method BLASTX
NCBI GI g112681
BLAST score 87
E value 5.0e-51
Match length 153

% identity 75

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147850

Seq. ID LIB3168-096-P1-K1-D7

Method BLASTX
NCBI GI g112681
BLAST score 810
E value 6.0e-87
Match length 162
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147851

Seq. ID LIB3168-096-P1-K1-D8

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 578

 E value
 1.0e-59

.

```
Match length
                  153
% identity
                  75
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147852
                  LIB3168-096-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  730
E value
                  2.0e-77
Match length
                  144
                  99
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  tha\overline{liana} >gi_808936_emb_CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147853
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  q3128138
BLAST score
                  354
                  0.0e+00
E value
                  450
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFO20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147854
Seq. ID
                  LIB3168-096-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  846
E value
                  4.0e-91
Match length
                  157
% identity
                  100
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712_emb_CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
```

Seq. No. 147855

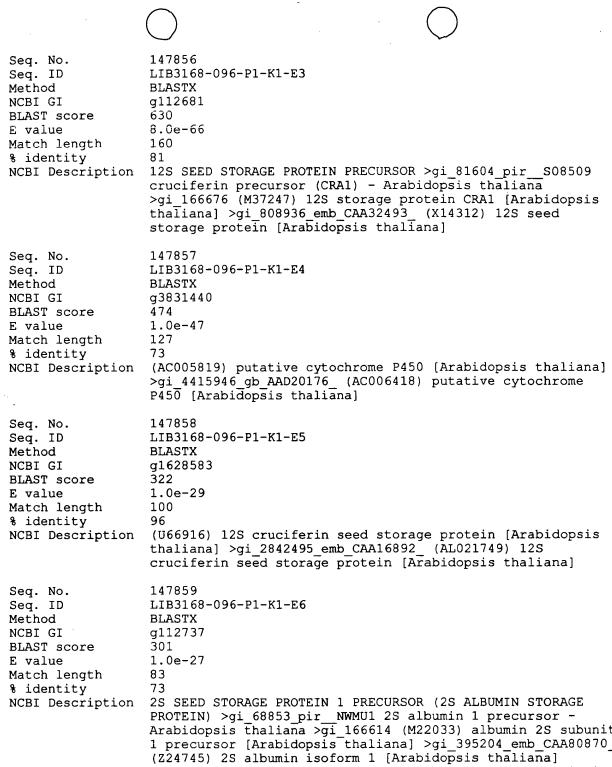
Seq. ID LIB3168-096-P1-K1-E2

75

Method BLASTX
NCBI GI g3522958
BLAST score 622
E value 7.0e-65
Match length 169

% identity

NCBI Description (AC004411) putative pectinesterase [Arabidopsis thaliana]



Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147860

LIB3168-096-P1-K1-E7 Seq. ID

Method BLASTN

```
NCBI GI
                  g4199934
BLAST score
                  269
                  1.0e-150
E value
Match length
                  318
% identity
                  99
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  147861
Seq. ID
                  LIB3168-096-P1-K1-E8
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                  360
                  3.0e - 34
E value
Match length
                  147
                  55
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147862
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q4235150
BLAST score
                  267
E value
                  1.0e-148
                  358
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T25B24 genomic
                  sequence, complete sequence
Seq. No.
                  147863
Seq. ID
                  LIB3168-096-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  721
                  2.0e-76
E value
Match length
                  143
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147864
                  LIB3168-096-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  607
E value
                  4.0e-63
Match length
                  111
                  100
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
```

>gi\_4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3



## precursor [Arabidopsis thaliana]

```
      Seq. No.
      147865

      Seq. ID
      LIB3168-096-P1-K1-F11

      Method
      BLASTX

      NCBI GI
      g4263791

      BLAST score
      801

      E value
      8.0e-86

      Match length
      181
```

% identity 87
NCBI Description (AC006068) putative receptor protein kinase [Arabidopsis

thaliana]

 Seq. No.
 147866

 Seq. ID
 LIB3168-096-P1-K1-F12

 Method
 BLASTX

 NCBI GI
 g112681

NCBI GI g112681
BLAST score 978
E value 1.0e-106
Match length 184
% identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147867

Seq. ID LIB3168-096-P1-K1-F2

Method BLASTN
NCBI GI g4097693
BLAST score 37
E value 2.0e-11
Match length 65
% identity 94

NCBI Description Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete

cds

Seq. No. 147868

Seg. ID LIB3168-096-P1-K1-F3

Method BLASTX
NCBI GI g135406
BLAST score 647
E value 8.0e-68
Match length 122
% identity 99

NCBI Description TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi\_99768\_pir\_\_A32712 tubulin

alpha-5 chain - Arabidopsis thaliana >gi\_166912 (M17189) alpha-tubulin [Arabidopsis thaliana] >gi\_166918 (M84698)

alpha-5 tubulin [Arabidopsis thaliana]

Seq. No. 147869

Seq. ID LIB3168-096-P1-K1-F4

Method BLASTX
NCBI GI g112682
BLAST score 728
E value 2.0e-77

```
Match length
                  159
% identity
                  87
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147870
Seq. No.
                  LIB3168-096-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
                  3.0e-65
E value
Match length
                  120
                  100
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147871
Seq. No.
                  LIB3168-096-P1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3738275
BLAST score
                  438
                  0.0e + 00
E value
Match length
                  551
% identity
                  Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147872
                  LIB3168-096-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  624
E value
                  4.0e-65
Match length
                  119
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147873
```

Seq. ID LIB3168-096-P1-K1-F8 Method BLASTX

NCBI GI g112681 BLAST score 729 E value 2.0e-77 Match length 177 % identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

```
147874
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  g2618599
BLAST score
                  106
                   4.0e-53
E value
                  122
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBD2, complete sequence [Arabidopsis thaliana]
                  147875
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  546
E value
                   4.0e-56
Match length
                  118
% identity
                  87
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >qi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                   3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147876
                  LIB3168-096-P1-K1-G10
Seq. ID
Method
                  BLASTX
                  g4204299
NCBI GI
BLAST score
                  816
                  1.0e-87
E value
Match length
                  174
                   90
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  147877
                  LIB3168-096-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455223
BLAST score
                  505
                   4.0e-51
E value
Match length
                  165
% identity
NCBI Description
                   (AL035440) putative DNA binding protein [Arabidopsis
                  thaliana]
Seq. No.
                  147878
                  LIB3168-096-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1107501
BLAST score
                  404
                  3.0e-39
E value
Match length
                  99
% identity
                  82
```

Match length

NCBI Description

% identity

166 81

```
(X91954) orf [Arabidopsis thaliana] >gi 3367530 (AC004392)
NCBI Description
                  Match to gb_X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                  this gene. [Arabidopsis thaliana]
                  147879
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q1628583
                  642
BLAST score
                  3.0e-67
E value
                  123
Match length
                  100
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147880
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-G3
Method
                  BLASTX
                  q112739
NCBI GI
                  505
BLAST score
                  3.0e-51
E value
Match length
                  139
                  74
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >qi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147881
Seq. No.
                  LIB3168-096-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  78
E value
                  9.0e-44
Match length
                  118
                  83
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147882
Seq. ID
                  LIB3168-096-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  677
E value
                  2.0e-71
```

18659

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana



>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

147883 Seq. No.

Seq. ID LIB3168-096-P1-K1-G6

Method BLASTX NCBI GI q1628583 BLAST score 562 E value 5.0e-58 Match length 120 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147884

Seq. ID LIB3168-096-P1-K1-G7

Method BLASTX NCBI GI q112737 BLAST score 727 E value 4.0e-77 Match length 164 % identity

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

> PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 147885

Seq. ID LIB3168-096-P1-K1-G8

Method BLASTX NCBI GI q1628583 BLAST score 420 E value 3.0e-41Match length 79 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147886

Seq. ID LIB3168-096-P1-K1-G9

Method BLASTX NCBI GI q112681 BLAST score 657 E value 4.0e-69 Match length 130 % identity 99

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir \$08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

```
Seq. No.
                  147887
Seq. ID
                  LIB3168-096-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  637
E value
                  1.0e-66
Match length
                  122
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147888
Seq. ID
                  LIB3168-096-P1-K1-H10
                  BLASTX
Method
NCBI GI
                  g112681
BLAST score
                  799
                  1.0e-85
E value
Match length
                  176
                  87
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir_S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147889
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  625
E value
                  3.0e-65
Match length
                  120
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147890
Seq. ID
                  LIB3168-096-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q2499236
BLAST score
                  546
                  5.0e-56
E value
Match length
                  128
% identity
                  88
NCBI Description
                  NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST
                  >gi_1419474_emb_CAA66944_ (X98298) ndhA [Arabidopsis
                  thaliana]
                147891
Seq. No.
Seq. ID
                  LIB3168-096-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1173103
BLAST score
                  745
E value
                  3.0e-79
```



Match length 133 99 % identity

RIBONUCLEASE 1 PRECURSOR >gi\_561998 (U05206) ribonuclease NCBI Description

[Arabidopsis thaliana] >gi 3461823 (AC004138) ribonuclease,

RNS1 [Arabidopsis thaliana]

147892 Seq. No.

Seq. ID LIB3168-096-P1-K1-H3

Method BLASTX NCBI GI g112682 BLAST score 643 2.0e-67 E value Match length 160 % identity 76

12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_ \$08510 NCBI Description

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

147893 Seq. No.

LIB3168-096-P1-K1-H4 Seq. ID

Method BLASTN NCBI GI g4510360 BLAST score 349 E value 0.0e+00Match length 462 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F11F19 genomic

sequence, complete sequence

Seq. No. 147894

Seq. ID LIB3168-096-P1-K1-H6

Method BLASTX NCBI GI g112739 BLAST score 521 E value 5.0e-53 Match length 146 72 % identity

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871 (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

Seq. No. 147895

Seq. ID LIB3168-096-P1-K1-H7

Method BLASTX NCBI GI q1628583 BLAST score 660 E value 2.0e-69 Match length 158 % identity 82

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S



## cruciferin seed storage protein [Arabidopsis thaliana]

147896 Seq. No. Seq. ID LIB3168-096-P1-K1-H8 Method BLASTX NCBI GI g112741 BLAST score 78 E value 5.0e-88 Match length 164 % identity 97 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi\_4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana] Seq. No. 147897 LIB3168-096-P1-K1-H9 Seq. ID Method BLASTX NCBI GI q112682 788 BLAST score E value 2.0e-84 176 Match length % identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81605 pir \$08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 147898 Seq. ID LIB3168-098-P1-K1-A1 Method BLASTX NCBI GI g4006897 BLAST score 95 E value 1.0e-43 Match length 119 % identity NCBI Description (Z99708) globulin-like protein [Arabidopsis thaliana] Seq. No. 147899 Seq. ID LIB3168-098-P1-K1-A10 Method BLASTX NCBI GI g2642443

BLAST score 578 E value 8.0e-60 Match length 134 % identity

(AC002391) putative cytochrome P450 [Arabidopsis thaliana] NCBI Description

Seq. No. 147900

Seq. ID LIB3168-098-P1-K1-A2

Method BLASTX NCBI GI g112739 BLAST score 295

Seq. ID

```
1.0e-26
E value
                  115
Match length
                  44
% identity
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68854 pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb CAA80871
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147901
Seq. ID
                  LIB3168-098-P1-K1-A3
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  619
E value
                  1.0e-64
                  129
Match length
% identity
                  95
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147902
Seq. ID
                  LIB3168-098-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  467
E value
                  7.0e-47
Match length
                  116
% identity
                  78
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  147903
                  LIB3168-098-P1-K1-A5
Seq. ID
Method
                  BLASTN
                  q2673901
NCBI GI
BLAST score
                  100
E value
                  6.0e-49
                  386
Match length
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC T24P15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  147904
Seq. No.
                  LIB3168-098-P1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4678291
BLAST score
                  233
E value
                  1.0e-128
                  261
Match length
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10
                  (ESSA project)
                  147905
Seq. No.
```

LIB3168-098-P1-K1-A7

NCBI GI

E value

BLAST score

g112682

4.0e-62

597

Method BLASTX NCBI GI g1628583 BLAST score 444 E value 2.0e-44 Match length 100 85 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147906 Seq. ID LIB3168-098-P1-K1-A8 Method BLASTX NCBI GI q112739 BLAST score 431 E value 1.0e-42 130 Match length 69 % identity 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871 (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana] >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2 precursor [Arabidopsis thaliana] 147907 Seq. No. Seq. ID LIB3168-098-P1-K1-A9 Method BLASTX NCBI GI g1628583 BLAST score 393 3.0e-38 E value Match length 81 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] 147908 Seq. No. Seq. ID LIB3168-098-P1-K1-B10 Method BLASTX NCBI GI g2661422 BLAST score 399 E value 3.0e-40 Match length 97 % identity NCBI Description (AJ001342) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] >gi 3096936 emb CAA18846.1 (AL023094) Putative S-phase-specific ribosomal protein [Arabidopsis thaliana] Seq. No. 147909 Seq. ID LIB3168-098-P1-K1-B11 Method BLASTX

Match length 126 % identity 89 NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis tha $\overline{l}$ iana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed storage protein [Arabidopsis thaliana] 147910 Seq. No. Seq. ID LIB3168-098-P1-K1-B12 Method BLASTX NCBI GI q112682 BLAST score 344 8.0e-33 E value Match length 66 95 % identity 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir \_S08510 NCBI Description cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] 147911 Seq. No. LIB3168-098-P1-K1-B2 Seq. ID Method BLASTX NCBI GI q1628583 BLAST score 422 5.0e-42 E value Match length 86 % identity 94 (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147912 LIB3168-098-P1-K1-B3 Seq. ID Method BLASTN NCBI GI q3293260 BLAST score 90 E value 5.0e-43178 Match length % identity NCBI Description Arabidopsis thaliana cystathionine gamma-synthase precursor (CGS1) gene, nuclear gene encoding chloroplast protein, complete cds

Seq. No. 147913

Seq. ID LIB3168-098-P1-K1-B4

Method BLASTX
NCBI GI g112741
BLAST score 516
E value 1.0e-52
Match length 113
% identity 86

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit

3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868 (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. No. 147914

Seq. ID LIB3168-098-P1-K1-B5

Method BLASTX NCBI GI g1628583 BLAST score 409 4.0e-40 E value Match length 120 68 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495 emb\_CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147915

Seq. ID LIB3168-098-P1-K1-B6

Method BLASTN NCBI GI q4539378 BLAST score 187 1.0e-101 E value Match length 208 97 % identity

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21

(ESSA project)

Seq. No. 147916

Seq. ID LIB3168-098-P1-K1-B7

Method BLASTX NCBI GI q1628583 BLAST score 257 3.0e-22 E value 69 Match length 76 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

147917 Seq. No.

Seq. ID LIB3168-098-P1-K1-C1

Method BLASTX NCBI GI g1628583 BLAST score 118 6.0e-06 E value Match length 68 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147918

LIB3168-098-P1-K1-C10 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 557

```
2.0e-57
E value
                  147
Match length
                  76
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147919
Seq. No.
                  LIB3168-098-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  329
E value
                  4.0e-31
                  73
Match length
% identity
                  88
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147920
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g2262155
BLAST score
                  188
E value
                  1.0e-101
Match length
                  393
                  97
% identity
NCBI Description
                  DNA sequence of Arabidopsis thaliana BAC F5J6 from
                  chromosome IV, complete sequence [Arabidopsis thaliana]
                  147921
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-C2
Method
                  BLASTX
                  g3193310
NCBI GI
                  580
BLAST score
                  4.0e-60
E value
                  141
Match length
% identity
NCBI Description
                   (AF069300) contains similarity to Nicotiana tabacum hinl
                   (GB:Y07563) [Arabidopsis thaliana]
                  147922
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-C3
                  BLASTX
Method
NCBI GI
                  g99735
BLAST score
                  461
E value
                  3.0e-46
Match length
                  106
% identity
                  86
                  L-ascorbate peroxidase (EC 1.11.1.11) precursor -
NCBI Description
                  Arabidopsis thaliana (fragment)
Seq. No.
                  147923
                  LIB3168-098-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2961390
BLAST score
```

18668

162

NCBI Description

```
1.0e-11
E value
Match length
                  31
                  97
% identity
NCBI Description
                  (AL022141) beta-galactosidase like protein [Arabidopsis
                  thaliana]
                  147924
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-C9
Method
                  BLASTX
                  g112681
NCBI GI
BLAST score
                  221
                  2.0e-18
E value
Match length
                  73
% identity
                  63
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147925
                  LIB3168-098-P1-K1-D1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g166609
BLAST score
                  227
                  1.0e-125
E value
                  243
Match length
% identity
NCBI Description
                  A.thaliana at 2S1 gene encoding albumin 2S subunit 1,
                  complete cds
                  147926
Seq. No.
                  LIB3168-098-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  460
E value
                  5.0e-46
Match length
                  142
% identity
                  66
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147927
Seq. ID
                  LIB3168-098-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g4581084
BLAST score
                  212
E value
                  1.0e-116
                  351
Match length
                  97
% identity
```

sequence, complete sequence

Arabidopsis thaliana chromosome I BAC T30F21 genomic

```
Seq. No.
                   147928
Seq. ID
                  LIB3168-098-P1-K1-D12
Method
                  BLASTX
NCBI GI
                   q112681
BLAST score
                   584
E value
                   2.0e-60
Match length
                   147
% identity
                   80
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                  147929
                  LIB3168-098-P1-K1-D2
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
                   527
BLAST score
                   5.0e-54
E value
Match length
                  104
                   98
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147930
                  LIB3168-098-P1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2815404
BLAST score
                  38
E value
                   7.0e-12
                  90
Match length
% identity
                  86
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMG4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147931
Seq. ID
                  LIB3168-098-P1-K1-D8
Method
                  BLASTN
NCBI GI
                  g1769896
BLAST score
                  330
E value
                  0.0e+00
Match length
                  386
% identity
                  46
NCBI Description A.thaliana lectin receptor kinase gene
Seq. No.
                  147932
Seq. ID
                  LIB3168-098-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  319
E value
                  1.0e-29
                  66
Match length
% identity
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis
```

thalianal Nai 2042405 amb GRA16002 (A)

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147933

Seq. ID LIB3168-098-P1-K1-E1

Method BLASTX
NCBI GI g112682
BLAST score 512
E value 3.0e-52
Match length 117

% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147934

Seq. ID LIB3168-098-P1-K1-E11

Method BLASTX
NCBI GI g1345973
BLAST score 179
E value 2.0e-13
Match length 49
% identity 73

NCBI Description

OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

>gi\_541882\_pir\_\_JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi\_408483 (L22931)

omega-3 fatty acid desaturase [Arabidopsis thaliana]

>gi\_471091\_dbj\_BAA04505\_ (D17579) fatty acid desaturase

[Arabidopsis thaliana] >gi\_1197795\_dbj\_BAA05514\_ (D26508)

microsomal omega-3 fatty acid desaturase [Arabidopsis
thaliana] >gi\_3420053 (AC004680) omega-3 fatty acid

desaturase [Arabidopsis thaliana]

Seq. No. 147935

Seq. ID LIB3168-098-P1-K1-E12

Method BLASTX
NCBI GI g112681
BLAST score 203
E value 3.0e-16
Match length 50
% identity 78

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147936

Seq. ID LIB3168-098-P1-K1-E3

Method BLASTX
NCBI GI g1628583
BLAST score 225
E value 4.0e-19
Match length 64
% identity 73

18671

1 - . 1.

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147937 LIB3168-098-P1-K1-E6 Seq. ID BLASTX Method NCBI GI q112681 BLAST score 373 3.0e-37 E value 113 Match length % identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir \$08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 147938 LIB3168-098-P1-K1-E9 Seq. ID Method BLASTX NCBI GI g112682 BLAST score 231 1.0e-23 E value 72 Match length 83 % identity NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] 147939 Seq. No. LIB3168-098-P1-K1-F1 Seq. ID Method BLASTX NCBI GI g1628583 BLAST score 59 E value 2.0e-26 95 Match length % identity (U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 147940 Seq. ID LIB3168-098-P1-K1-F10 Method BLASTX NCBI GI g112681 BLAST score 480 2.0e-60 E value Match length 145 % identity 84 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana

storage protein [Arabidopsis thaliana]

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

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147941
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  386
                  2.0e-37
E value
Match length
                  116
% identity
                  69
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68854 pir NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
                  147942
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-F12
                  BLASTN
Method
                  q4314354
NCBI GI
BLAST score
                  309
                  1.0e-173
E value
Match length
                  450
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T9I22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147943
                  LIB3168-098-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  47
                  3.0e - 30
E value
                  106
Match length
                  70
% identity
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147944
                  LIB3168-098-P1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159705
BLAST score
                  278
E value
                  1.0e-155
Match length
                  407
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGD8, complete sequence
                  147945
Seq. No.
                  LIB3168-098-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
```

```
BLAST score
                  540
E value
                  2.0e-55
                  134
Match length
                  78
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147946
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  420
                  2.0e-41
E value
Match length
                  82
% identity
                  94
NCBI Description
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
                  147947
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q4204298
                  437
BLAST score
                  2.0e-43
E value
Match length
                  86
                  97
% identity
                  (AC003027) lcl_prt_seq No definition line found
NCBI Description
                  [Arabidopsis thataliana]
Seq. No.
                  147948
                  LIB3168-098-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2584827
BLAST score
                  58
E value
                  2.0e-24
Match length
                  78
                  94
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  147949
Seq. ID
                  LIB3168-098-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1174805
BLAST score
                  224
                  2.0e-18
E value
                  140
Match length
% identity
                  41
NCBI Description
                  TRNA PSEUDOURIDINE SYNTHASE B (TRNA PSEUDOURIDINE 55
```

SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE) >gi 1074717 pir B64170 hypothetical protein HI1289 - Haemophilus influenzae (strain Rd KW20) >gi\_1574748 (U32809) tRNA pseudouridine 55 synthase (truB) [Haemophilus influenzae Rd]

147950 Seq. No.

Seq. ID LIB3168-098-P1-K1-G1

Method BLASTX NCBI GI q3947690 BLAST score 249 E value 3.0e-21Match length 146 % identity

NCBI Description (AJ131245) Sec24B protein [Homo sapiens]

Seq. No. 147951

LIB3168-098-P1-K1-G10 Seq. ID

Method BLASTX NCBI GI q1628583 BLAST score 408 E value 4.0e-40 Match length 100 % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 147952

Seq. ID LIB3168-098-P1-K1-G11

Method BLASTX NCBI GI q4204299 BLAST score 606 3.0e-63 E value 125 Match length

% identity

NCBI Description (AC003027) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

147953 Seq. No.

LIB3168-098-P1-K1-G2 Seq. ID

Method BLASTX NCBI GI q82051 BLAST score 320 E value 1.0e-29 Match length 125 % identity 50

NCBI Description lipid body-associated membrane protein - carrot

>gi\_259453\_bbs\_117620 (S47635) lipid body membrane

protein=DC 59 [Daucus carota=carrots, var Juwarot, Peptide,

180 aa] [Daucus carota]

Seq. No. 147954

Seq. ID LIB3168-098-P1-K1-G4

Method BLASTN NCBI GI g4159712

BLAST score 67



E value 1.0e-29 Match length 138 % identity 88

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MWI23, complete sequence

Seq. No. 147955

Seq. ID LIB3168-098-P1-K1-G5

Method BLASTX
NCBI GI g112681
BLAST score 187
E value 2.0e-14
Match length 36
% identity 100

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147956

Seq. ID LIB3168-098-P1-K1-G8

Method BLASTX
NCBI GI g112681
BLAST score 459
E value 4.0e-46
Match length 101
% identity 93

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147957

Seq. ID LIB3168-098-P1-K1-G9

Method BLASTX
NCBI GI g112682
BLAST score 322
E value 3.0e-34
Match length 110
% identity 72

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir\_\_ \$08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147958

Seq. ID LIB3168-098-P1-K1-H1

Method BLASTN
NCBI GI g3128142
BLAST score 211
E value 1.0e-115
Match length 438
% identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

% identity

78



## MQN23, complete sequence [Arabidopsis thaliana]

```
147959
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g112681
                  247
BLAST score
                  2.0e-26
E value
Match length
                  89
                  74
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  147960
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g4159704
                  357
BLAST score
                  0.0e+00
E value
                  400
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
NCBI Description
                  MCB17, complete sequence
Seq. No.
                  147961
Seq. ID
                  LIB3168-098-P1-K1-H2
Method
                  BLASTX
                  q1346831
NCBI GI
BLAST score
                  154
E value
                  9.0e-11
Match length
                  32
% identity
                  94
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I)
                  >gi_984310 (U26948) photosystem I component [Glycine max]
Seq. No.
                  147962
                  LIB3168-098-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3004557
BLAST score
                  496
E value
                  2.0e-50
                  98
Match length
% identity
NCBI Description
                   (AC003673) plasma membrane proton pump H+ ATPase, PMA1
                  [Arabidopsis thaliana]
Seq. No.
                  147963
Seq. ID
                  LIB3168-098-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  a1628583
BLAST score
                  540
                  2.0e-55
E value
Match length
                  138
```

Method

NCBI GI

BLASTX

g112737

```
NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147964
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  q4455339
BLAST score
                  38
                  2.0e-12
E value
Match length
                  114
                  83
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
NCBI Description
                  (ESSAII project)
                  147965
Seq. No.
Seq. ID
                  LIB3168-098-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  g725259
BLAST score
                  105
E value
                  2.0e-52
                  132
Match length
                  95
% identity
NCBI Description Arabidopsis thaliana oleosin mRNA, complete cds
                  147966
Seq. No.
                  LIB3168-099-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  335
E value
                  1.0e-42
Match length
                  124
% identity
                  75
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147967
Seq. No.
Seq. ID
                  LIB3168-099-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  744
E value
                  3.0e-79
Match length
                  143
% identity
                  97
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir_ NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147968
Seq. ID
                  LIB3168-099-P1-K1-A11
```

18678

,671. a 1

```
BLAST score
E value
                  3.0e-65
Match length
                  148
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147969
Seq. ID
                  LIB3168-099-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  q4263038
BLAST score
                  359
                  0.0e+00
E value
Match length
                  383
% identity
                  82
                  Arabidopsis thaliana BAC T5L23 from chromosome IV, near 19
NCBI Description
                  cM, complete sequence [Arabidopsis thaliana]
                  147970
Seq. No.
                  LIB3168-099-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  525
E value
                  1.0e-53
Match length
                  111
                  91
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147971
Seq. No.
Seq. ID
                  LIB3168-099-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  q4589419
BLAST score
                  181
E value
                  2.0e-97
Match length
                  261
% identity
                  69
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2I5, complete sequence
Seq. No.
                  147972
Seq. ID
                  LIB3168-099-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  q226120
BLAST score
                  248
E value
                  4.0e-21
Match length
                  123
% identity
                  40
NCBI Description
                  vicilin gene B [Saguinus oedipus]
Seq. No.
```

147973

```
Seq. ID
                  LIB3168-099-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  769
E value
                  3.0e-82
Match length
                  153
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147974
                  LIB3168-099-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  165
E value
                  1.0e-11
Match length
                  36
% identity
                  89
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147975
                  LIB3168-099-P1-K1-A8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1628583
BLAST score
                  536
                  5.0e-55
E value
                  107
Match length
                  97
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147976
Seq. ID
                  LIB3168-099-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  a2739359
BLAST score
                  88
E value
                  1.0e-41
Match length
                  215
                  91
% identity
                  Arabidopsis thaliana chromosome II BAC T9J22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  147977
Seq. ID
                  LIB3168-099-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  693
E value
                  3.0e-73
Match length
                  148
% identity
                  91
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
```



thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed storage protein [Arabidopsis thaliana]

 Seq. No.
 147978

 Seq. ID
 LIB3168-099-P1-K1-B11

 Method
 BLASTX

 NCBI GI
 g3157944

 BLAST score
 751

 E value
 4.0e-80

E value 4.0e-Match length 145 % identity 99

NCBI Description (AC002131) Very strong similarity to aminomethyltransferase

precursor gb\_U79769 from Mesembryanthemum crystallinum.

ESTs gb\_T43167, gb\_T21076, gb\_H36999, gb\_T22773,

 $gb_N380\overline{3}8$ ,  $gb_T137\overline{4}2$ ,  $gb_Z265\overline{4}5$ ,  $gb_T2075\overline{3}$  and  $gb_W43123$ 

come from this ge

Seq. No. 147979

Seq. ID LIB3168-099-P1-K1-B2

Method BLASTX
NCBI GI g881615
BLAST score 655
E value 6.0e-69
Match length 128
% identity 99

NCBI Description (U29142) fatty acid elongase 1 [Arabidopsis thaliana]

>gi 3096921 emb\_CAA18831.1\_ (AL023094) fatty acid elongase

1 [Arabidopsis thaliana]

Seq. No. 147980

Seq. ID LIB3168-099-P1-K1-B3

Method BLASTX
NCBI GI g112681
BLAST score 533
E value 1.0e-54
Match length 126
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 147981

Seq. ID LIB3168-099-P1-K1-B4

Method BLASTX
NCBI GI g4454042
BLAST score 297
E value 6.0e-27
Match length 97
% identity 53

NCBI Description (AL035394) putative protein [Arabidopsis thaliana]

Seq. No. 147982

Seq. ID LIB3168-099-P1-K1-B5

Method BLASTX NCBI GI g1628583

Seq. No.

Seq. ID

Method

147987

BLASTX

LIB3168-099-P1-K1-C1

```
BLAST score
                   54
                   8.0e-79
E value
Match length
                   153
% identity
                   91
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147983
                  LIB3168-099-P1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4567259
BLAST score
                  335
                  0.0e + 00
E value
Match length
                   413
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3K23 genomic
                  sequence, complete sequence
                  147984
Seq. No.
Seq. ID
                  LIB3168-099-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q4678226
BLAST score
                  546
E value
                   4.0e-56
Match length
                  131
% identity
                  86
NCBI Description
                   (AC007135) putative 40S ribosomal protein S14 [Arabidopsis
Seq. No.
                  147985
                  LIB3168-099-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2828296
BLAST score
                  593
E value
                  1.0e-61
Match length
                  117
% identity
                  96
NCBI Description
                  (AL021687) RNase L inhibitor [Arabidopsis thaliana]
                  147986
Seq. No.
Seq. ID
                  LIB3168-099-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  589
E value
                  4.0e-61
Match length
                  138
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                  cruciferin precursor (CRB) - Arabidopsīs thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
```

```
NCBI GI
                  g1628583
BLAST score
                  435
E value
                  4.0e-43
                  114
Match length
                  76
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147988
Seq. No.
                  LIB3168-099-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
                  643
BLAST score
                  2.0e-67
E value
                  150
Match length
% identity
                  84
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana | >qi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147989
Seq. ID
                  LIB3168-099-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  g3738088
BLAST score
                  41
E value
                  1.0e-13
                  507
Match length
                  38
% identity
                  Arabidopsis thaliana chromosome II BAC T30L20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  147990
Seq. No.
                  LIB3168-099-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  587.
BLAST score
E value
                  5.0e-61
Match length
                  121
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147991
Seq. ID
                  LIB3168-099-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  q2656029
BLAST score
                  296
                  1.0e-166
E value
Match length
                  430
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

MQB2

Seq. ID Method

```
Seq. No.
                  147992
Seq. ID
                  LIB3168-099-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  655
                  9.0e-69
É value
                  128
Match length
                  97
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir $08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >qi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >qi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  147993
Seq. ID
                  LIB3168-099-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  607
E value
                  3.0e-63
                  120
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147994
Seq. No.
                  LIB3168-099-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  617
                  2.0e-64
E value
Match length
                  152
                  78
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  147995
                  LIB3168-099-P1-K1-C6
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
                  558
BLAST score
E value
                  2.0e-57
                  119
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  147996
Seq. No.
```

LIB3168-099-P1-K1-C7

BLASTN

```
g2656030
NCBI GI
BLAST score
                  223
E value
                  1.0e-122
Match length
                  414
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  147997
Seq. No.
Seq. ID
                  LIB3168-099-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g4263540
BLAST score
                  37
E value
                  3.0e-11
Match length
                  49
                  94
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T6A13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  147998
Seq. No.
                  LIB3168-099-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  671
BLAST score
                  1.0e-70
E value
Match length
                  132
                  96
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  147999
                  LIB3168-099-P1-K1-D1
Seq. ID
Method
                  BLASTX
                  g3935148
NCBI GI
BLAST score
                  568
                  1.0e-58
E value
Match length
                  131
% identity
                  85
                   (AC005106) T25N20.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148000
Seq. ID
                  LIB3168-099-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q4512684
BLAST score
                   677
```

E value 2.0e-71 Match length 136 % identity 100

(AC006931) unknown protein [Arabidopsis thaliana] NCBI Description

>qi 4559324 gb AAD22986.1 AC007087 5 (AC007087) unknown

protein [Arabidopsis thaliana]

Seq. No. 148001

Seq. ID LIB3168-099-P1-K1-D12

Method BLASTX NCBI GI g112682

Match length

% identity

95

94

BLAST score 646 E value 9.0e-68 Match length 147 % identity 83 NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 148002 Seq. ID LIB3168-099-P1-K1-D2 Method BLASTX NCBI GI g1628583 BLAST score 423 E value 6.0e-42 Match length 95 % identity 87 NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 148003 LIB3168-099-P1-K1-D5 Seq. ID Method BLASTX NCBI GI g112682 BLAST score 653 1.0e-68 E value Match length 134 % identity 91 NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510 cruciferin precursor (CRB) - Arabidopsis thaliana >gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis thaliana] >gi\_808937\_emb\_CAA32494\_ (X14313) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 148004 Seq. ID LIB3168-099-P1-K1-D6 Method BLASTX NCBI GI q1628583 BLAST score 603 E value 1.0e-62 Match length 120 % identity NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana] Seq. No. 148005 Seq. ID LIB3168-099-P1-K1-D8 Method BLASTN NCBI GI g4580400 BLAST score 50 E value 9.0e-20

NCBI Description Arabidopsis thaliana chromosome II BAC T16I21 genomic

```
sequence, complete sequence
                  148006
                  LIB3168-099-P1-K1-E1
                  BLASTX
                  g1592670
                  370
                  1.0e-35
                  99
                  71
                  (X91920) dehydrin [Arabidopsis thaliana]
NCBI Description
                  >qi 4567280 gb AAD23693.1 AC006841 21 (AC006841) putative
                  dehydrin [Arabidopsis thaliana]
                  148007
                  LIB3168-099-P1-K1-E10
                  BLASTN
                  q3241920
                  183
                  2.0e-98
                  400
```

```
Seq. No.
Seq. ID
Method
NCBI GI
BLAST score
E value
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```

MAE1, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   148008
                   LIB3168-099-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455338
                   831
BLAST score
                   2.0e-89
E value
Match length
                   148
```

100 % identity

Seq. No. Seq. ID

Method

NCBI GI BLAST score

E value

Match length

% identity

(AL035525) putative protein [Arabidopsis thaliana] NCBI Description

```
148009
Seq. No.
Seq. ID
                   LIB3168-099-P1-K1-E2
Method
                   BLASTN
NCBI GI
                   q3746057
BLAST score
                   449
                   0.0e + 00
```

E value Match length 460 100 % identity

Arabidopsis thaliana chromosome II BAC T16B12 genomic NCBI Description sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 148010

Seq. ID LIB3168-099-P1-K1-E3

Method BLASTX NCBI GI q1628583 BLAST score 634 E value 2.0e-66 Match length 123 % identity

(U66916) 12S cruciferin seed storage protein [Arabidopsis NCBI Description thaliana] >gi 2842495 emb CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. ID

```
Seq. No.
                  148011
Seq. ID
                  LIB3168-099-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  731
E value
                  1.0e-77
Match length
                  139
% identity
                  99
NCBI Description
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >qi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201 emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  148012
Seq. ID
                  LIB3168-099-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g1723958
BLAST score
                  235
                  1.0e-19
E value
Match length
                  96
                  49
% identity
                  PUTATIVE KINESIN-LIKE PROTEIN YGL216W
NCBI Description
                  >gi_2131622_pir__S64238 hypothetical protein YGL216w -
                  yeast (Saccharomyces cerevisiae) >gi 1322862 emb CAA96933
                  (Z72739) ORF YGL216w [Saccharomyces cerevisiae]
                  148013
Seq. No.
Seq. ID
                  LIB3168-099-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  608
E value
                  2.0e-63
Match length
                  144
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir $08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  148014
Seq. ID
                  LIB3168-099-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g4589437
BLAST score
                  253
E value
                  1.0e-140
Match length
                  368
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MPN9, complete sequence
Seq. No.
                  148015
```

18688

LIB3168-099-P1-K1-E8

Method

BLASTX

```
BLASTX
Method
                   g1628583
NCBI GI
BLAST score
                   541
E value
                   1.0e-55
                   117
Match length
                   91
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   148016
Seq. No.
Seq. ID
                   LIB3168-099-P1-K1-E9
                   BLASTN
Method
NCBI GI
                   g16472
BLAST score
                   42
                   2.0e-14
E value
Match length
                   138
% identity
                   83
                   A.thaliana rRNA repeat unit, most frequent IGR type
NCBI Description
                   148017
Seq. No.
Seq. ID
                   LIB3168-099-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g4455192
BLAST score
                   374
E value
                   7.0e-36
Match length
                   134
% identity
                   58
NCBI Description
                   (AL035440) putative protein [Arabidopsis thaliana]
                   148018
Seq. No.
Seq. ID
                   LIB3168-099-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g2129657
BLAST score
                   309
                   9.0e-37
E value
Match length
                   119
% identity
                   72
                   oleosin isoform - Arabidopsis thaliana
NCBI Description
                   >gi_987014\_emb\_CAA90877\_ (Z54164) oleosin [Arabidopsis thaliana] >gi_987016\_emb\_CAA90878\_ (Z54165) oleosin
                   [Arabidopsis thaliana]
                   148019
Seq. No.
Seq. ID
                   LIB3168-099-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   g2264312
BLAST score
                   309
E value
                   1.0e-173
Match length
                   443
% identity
                   93
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MOK16, complete sequence [Arabidopsis thaliana]
                   148020
Seq. No.
                   LIB3168-099-P1-K1-F3
Seq. ID
```

18689

\_

```
g112741
NCBI GI
BLAST score
                  430
E value
                  8.0e-43
                  86
Match length
                  94
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855 pir_NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  148021
                  LIB3168-099-P1-K1-F5
Seq. ID
Method
                  BLASTX
                  q2244906
NCBI GI
                  460
BLAST score
E value
                  5.0e-46
                  88
Match length
                  99
% identity
NCBI Description
                   (Z97339) indole-3-acetate beta-glucosyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                  148022
                  LIB3168-099-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  450
                   6.0e-45
E value
                  117
Match length
% identity
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  148023
Seq. ID
                  LIB3168-099-P1-K1-F7
Method
                  BLASTN
                  g4079614
NCBI GI
BLAST score
                  372
E value
                  0.0e + 00
                   393
Match length
% identity
                  Arabidopsis thaliana chromosome I BAC F21M11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148024
Seq. ID
                  LIB3168-099-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  q3402747
BLAST score
                  415
E value
                  0.0e + 00
                  444
Match length
% identity
                  98
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22
NCBI Description
                   (ESSAII project)
```

NCBI Description

```
Seq. No.
                  148025
Seq. ID
                  LIB3168-099-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  182
                  4.0e-47
E value
Match length
                  137
                  74
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >qi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  148026
Seq. ID
                  LIB3168-099-P1-K1-G11
Method
                  BLASTX
                  g112743
NCBI GI
BLAST score
                  778
E value
                  3.0e-83
                  151
Match length
                  97
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi_395202_emb_CAA80869_
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  148027
                  LIB3168-099-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q135535
BLAST score
                  501
E value
                  9.0e-51
Match length
                  106
% identity
                  96
NCBI Description
                  T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA)
                  (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide
                  Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955
                  (D11351) t-complex polypeptide 1 homologue [Arabidopsis
                  thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT
                  alpha/TCP-1 [Arabidopsis thaliana]
Seq. No.
                  148028
Seq. ID
                  LIB3168-099-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  608
E value
                  2.0e-63
Match length
                  114
                  98
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
```

PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_ (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

Seq. ID LIB3168-099-P1-K1-G4 BLASTX Method NCBI GI g4204308 BLAST score 425 7.0e-42 E value Match length 85 % identity 84

148029

NCBI Description (AC003027) lcl prt seq No definition line found

[Arabidopsis thaliana]

Seq. No. 148030

Seq. No.

LIB3168-099-P1-K1-G5 Seq. ID

Method BLASTN NCBI GI g304110 BLAST score 309 E value 1.0e-173 346 Match length 99 % identity

NCBI Description Arabidopsis thaliana signal recognition particle 54 kDa

subunit (Srp54-1) gene, complete cds

Seq. No. 148031

Seq. ID LIB3168-099-P1-K1-G6

Method BLASTX NCBI GI g3264805 BLAST score 705 E value 9.0e-75 Match length 136 97 % identity

NCBI Description (AF071788) phosphoenolpyruvate carboxylase [Arabidopsis

thaliana] >gi\_4079630\_emb\_CAA10486 (AJ131710) phospho

enole pyruvate carboxylase [Arabidopsis thaliana]

Seq. No. 148032

Seq. ID LIB3168-099-P1-K1-G8

Method BLASTX NCBI GI g1628583 BLAST score 499 E value 2.0e-50 Match length 101 % identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

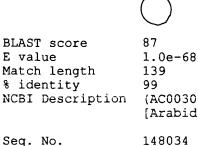
thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 148033

Seq. ID LIB3168-099-P1-K1-G9

Method BLASTX NCBI GI q4204299



(AC003027) lcl\_prt\_seq No definition line found

[Arabidopsis thaliana]

Seq. No. Seq. ID

LIB3168-099-P1-K1-H1

Method BLASTX
NCBI GI g112682
BLAST score 590
E value 3.0e-61

Match length 117 % identity 96

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No.

148035

Seq. ID LIB3168-099-P1-K1-H10

Method BLASTN
NCBI GI g2583106
BLAST score 168
E value 1.0e-89
Match length 241
% identity 93

NCBI Description Arabidopsis thaliana chromosome II BAC F4L23 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No.

148036

Seq. ID LIB3168-099-P1-K1-H12

Method BLASTX
NCBI GI g112681
BLAST score 663
E value 9.0e-70
Match length 150
% identity 85

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 148037

Seq. ID LIB3168-099-P1-K1-H2

Method BLASTX
NCBI GI g1628583
BLAST score 642
E value 3.0e-67
Match length 123
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                    148038
  Seq. ID
                    LIB3168-099-P1-K1-H3
 Method
                    BLASTX
 NCBI GI
                    g112682
 BLAST score
                    696
 E value
                    1.0e-73
 Match length
                    157
 % identity
                    83
 NCBI Description
                    12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__s08510
                    cruciferin precursor (CRB) - Arabidopsis thaliana
                    >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                    thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
                    storage protein [Arabidopsis thaliana]
 Seq. No.
                    148039
 Seq. ID
                    LIB3168-099-P1-K1-H4
 Method
                    BLASTX
 NCBI GI
                    g1628583
 BLAST score
                    314
 E value
                    4.0e-29
 Match length
                    69
 % identity
                    87
 NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
 Seq. No.
                   148040
 Seq. ID
                   LIB3168-099-P1-K1-H5
 Method
                   BLASTN
 NCBI GI
                   q4097693
 BLAST score
                   79
 E value
                   5.0e-37
Match length
                   95
 % identity
NCBI Description
                   Arabidopsis thaliana prohibitin 1 (Atphb1) gene, complete
Seq. No.
                   148041
Seq. ID
                   LIB3168-099-P1-K1-H7
Method
                   BLASTN
NCBI GI
                   g4580454
BLAST score
                   383
E value
                   0.0e + 00
Match length
                   419
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T2G17 genomic
                   sequence, complete sequence
Seq. No.
                  148042
Seq. ID
                  LIB3168-099-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  811
E value
                  4.0e-87
Match length
                  156
% identity
                  99
```

```
(U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]
```

Seq. No. 148043 Seq. ID LIB3168-100-P1-K1-A1 Method BLASTX q112739 NCBI GI BLAST score 337 2.0e-51 E value Match length 131 82 % identity

NCBI Description 2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE

NCBI Description

PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor - Arabidopsis thaliana >gi\_166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi\_395205\_emb\_CAA80871\_ (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

 Seq. No.
 148044

 Seq. ID
 LIB3168-100-P1-K1-A10

 Method
 BLASTN

 NCBI GI
 g4510338

 BLAST score
 433

E value 0.0e+00
Match length 441
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F2H17 genomic

sequence, complete sequence

Seq. No. 148045 Seq. ID LIB3168-100-P1-K1-A11

Method BLASTX
NCBI GI g112682
BLAST score 639
E value 6.0e-67

E value 6.0e
Match length 146
% identity 83

NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81605\_pir\_\_S08510

cruciferin precursor (CRB) - Arabidopsis thaliana

>gi\_166678 (M37248) 12S storage protein CRB [Arabidopsis
thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed

storage protein [Arabidopsis thaliana]

Seq. No. 148046

Seq. ID LIB3168-100-P1-K1-A12

Method BLASTX
NCBI GI g1628583
BLAST score 599
E value 2.0e-62
Match length 126
% identity 92

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

```
Seq. No.
                   148047
Seq. ID
                  LIB3168-100-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                   626
E value
                   2.0e-65
Match length
                   123
% identity
                   98
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                   thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                   148048
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-A3
                  BLASTN
Method
NCBI GI
                  g4586098
                  244
BLAST score
                  1.0e-135
E value
Match length
                   437
                   97
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16J13
                   (ESSA project)
                  148049
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-A4
                  BLASTX
Method
NCBI GI
                   g1170505
BLAST score
                   531
E value
                   3.0e-54
Match length
                   105
                   97
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2)
NCBI Description
                   >gi 322504 pir JC1453 translation initiation factor
                   eIF-4A2 - Arabidopsis thaliana >qi 16556 emb CAA46189
                   (X65053) eukaryotic translation initiation factor 4A-2
                   [Arabidopsis thaliana] >gi 4585969 gb AAD25605.1 AC005287 7
                   (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis
                   thaliana]
Seq. No.
                   148050
Seq. ID
                  LIB3168-100-P1-K1-A6
Method
                  BLASTX
NCBI GI
                   g2505876
BLAST score
                  332
                   5.0e-31
E value
                  72
Match length
                  86
% identity
NCBI Description
                   (Y12776) MYB-related protein [Arabidopsis thaliana]
                  148051
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  433
E value
                  8.0e-43
Match length
                  144
% identity
                   61
```



NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509 cruciferin precursor (CRA1) - Arabidopsis thaliana >gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed storage protein [Arabidopsis thaliana]

 Seq. No.
 148052

 Seq. ID
 LIB3168-100-P1-K1-A8

 Method
 BLASTN

 NCBI GI
 g2564049

 BLAST score
 305

E value 1.0e-171
Match length 372
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLE2, complete sequence [Arabidopsis thaliana]

Seq. No. 148053

Seq. ID LIB3168-100-P1-K1-A9

Method BLASTX
NCBI GI g1628583
BLAST score 529
E value 5.0e-54
Match length 120
% identity 85

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 148054

Seq. ID LIB3168-100-P1-K1-B1

Method BLASTX
NCBI GI g112737
BLAST score 600
E value 2.0e-62
Match length 143
% identity 81

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 148055

Seq. ID LIB3168-100-P1-K1-B11

Method BLASTX
NCBI GI g67842
BLAST score 225
E value 1.0e-18
Match length 80
% identity 60

NCBI Description H+-transporting ATP synthase (EC 3.6.1.34) beta chain - spinach chloroplast >gi\_343355 (J01441) ATPase beta subunit

[Spinacia oleracea] >gi\_223530\_prf\_\_0811259A ATPase beta

[Spinacia oleracea]

```
148056
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-B12
Method
                  BLASTX
NCBI GI
                   g112681
BLAST score
                   737
                   2.0e-78
E value
Match length
                  140
% identity
                   99
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
Seq. No.
                   148057
Seq. ID
                  LIB3168-100-P1-K1-B2
                  BLASTX
Method
                  g1628583
NCBI GI
BLAST score
                   404
E value
                   2.0e-39
                  112
Match length
                   73
% identity
                   (U66916) 12S cruciferin seed storage protein (Arabidopsis
NCBI Description
                   thaliana] >gi_2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                   148058
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-B3
Method
                   BLASTX
                   q542157
NCBI GI
BLAST score
                   585
                   1.0e-60
E value
Match length
                   136
% identity
                   81
                  ribosomal 5S RNA-binding protein - Rice
NCBI Description
Seq. No.
                   148059
Seq. ID
                  LIB3168-100-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g3269286
BLAST score
                   453
                   9.0e-57
E value
Match length
                   141
                   90
% identity
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
                  148060
Seq. No.
                  LIB3168-100-P1-K1-B7
Seq. ID
Method
                   BLASTN
NCBI GI
                   a3046852
BLAST score
                   268
E value
                   1.0e-149
Match length
                   433
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQJ16, complete sequence [Arabidopsis thaliana]
```

```
148061
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  3.0e-65
Match length
                  120
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  148062
Seq. ID
                  LIB3168-100-P1-K1-C1
Method
                  BLASTN
                  g2564049
NCBI GI
                  171
BLAST score
                  1.0e-91
E value
Match length
                  171
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148063
                  LIB3168-100-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  752
E value
                  3.0e-80
                  145
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  148064
                  LIB3168-100-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112741
                  771
BLAST score
                  2.0e-82
E value
                  143
Match length
                  100
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  148065
                  LIB3168-100-P1-K1-C12
Seq. ID
Method
                  BLASTN
                  q4753195
NCBI GI
BLAST score
                  227
```

E value 1.0e-124 Match length 416 % identity 100 NCBI Description Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5 cM, complete sequence 148066 Seq. No. Seq. ID LIB3168-100-P1-K1-C2 Method BLASTX NCBI GI q112737 BLAST score 598 4.0e-62 E value Match length 124 % identity 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi\_68853\_pir NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_ (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >qi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1 precursor [Arabidopsis thaliana] 148067 Seq. No. Seq. ID LIB3168-100-P1-K1-C3 Method BLASTX NCBI GI q1169598 BLAST score 629 9.0e-66 E value Match length 126 % identity OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM NCBI Description (DELTA-12 DESATURASE) >qi 438451 (L26296) delta-12 desaturase [Arabidopsis thaliana] 148068 Seq. No. LIB3168-100-P1-K1-C6 Seq. ID Method BLASTX NCBI GI q112681 BLAST score 646 E value 9.0e-68 Match length 148 % identity 12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir \$08509 NCBI Description cruciferin precursor (CRA1) - Arabidopsis thaliana >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed storage protein [Arabidopsis thaliana] Seq. No. 148069 LIB3168-100-P1-K1-C7 Seq. ID Method BLASTN g16231 NCBI GI BLAST score 112 E value 4.0e-56 176 Match length

18700

NCBI Description Arabidopsis CRA1 gene for 12S seed storage protein

95

% identity

NCBI Description

Seq. No.

```
>gi 166675_gb_M37247_ATHCRA1AA A.thaliana 12S storage
                  protein CRA1 gene, exons 1-4
                  148070
Seq. No.
                  LIB3168-100-P1-K1-C8
Seq. ID
                  BLASTX
Method
                  q112741
NCBI GI
                  764
BLAST score
                  1.0e-81
E value
                  145
Match length
                  99
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >qi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  148071
Seq. No.
                  LIB3168-100-P1-K1-C9
Seq. ID
                  BLASTX
Method
                  g1628583
NCBI GI
                  441
BLAST score
                  9.0e-44
E value
                  149
Match length
                  62
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  148072
Seq. No.
                  LIB3168-100-P1-K1-D1
Seq. ID
                  BLASTX
Method
NCBI GI
                  g112682
BLAST score
                  555
                  3.0e-57
E value
Match length
                  126
                  89
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >qi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
                  148073
Seq. No.
                  LIB3168-100-P1-K1-D10
Seq. ID
                  BLASTN
Method
                  g4733991
NCBI GI
                  38
BLAST score
                  7.0e-12
E value
Match length
                  82
                  87
% identity
```

18701

sequence, complete sequence

148074

Arabidopsis thaliana chromosome II BAC T4D8 genomic

```
LIB3168-100-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  631
                  5.0e-66
E value
Match length
                  144
% identity
                  85
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir__S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  148075
Seq. No.
                  LIB3168-100-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  650
                  3.0e-68
E value
                  136
Match length
                  92
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  148076
Seq. ID
                  LIB3168-100-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g112737
BLAST score
                  624
                  3.0e-65
E value
                  146
Match length
                  82
% identity
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
Seq. No.
                  148077
                  LIB3168-100-P1-K1-D3
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  153
                  5.0e-10
E value
                  81
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  148078
                  LIB3168-100-P1-K1-D4
Seq. ID
```

18702

```
Method
                  BLASTX
NCBI GI
                  q112737
BLAST score
                  605
E value
                  5.0e-63
Match length
                  143
                  82
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi_4490710_emb_CAB38844.1_ (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  148079
Seq. No.
                  LIB3168-100-P1-K1-D5
Seq. ID
Method
                  BLASTX
                  q1628583
NCBI GI
                  625
BLAST score
                  3.0e-65
E value
                  120
Match length
% identity
                  100
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  148080
                  LIB3168-100-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2288981
                  312
BLAST score
E value
                  1.0e-28
                  64
Match length
% identity
                  52
                  (AC002335) calcium binding protein isolog [Arabidopsis
NCBI Description
                  thaliana] >gi 3763938 (AC004450) putative calcium binding
                  protein [Arabidopsis thaliana]
                  148081
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-D7
Method
                  BLASTN
                  g4490701
NCBI GI
BLAST score
                  147
E value
                  4.0e-77
                  147
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T24A18
NCBI Description
                  (ESSA project)
                  148082
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q2827621
BLAST score
                  312
E value
                  1.0e-28
Match length
                  136
% identity
                  45
```

```
(AL021636) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148083
                  LIB3168-100-P1-K1-D9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4455262
BLAST score
                  316
                  1.0e-178
E value
Match length
                  436
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                  (ESSAII project)
                  148084
Seq. No.
                  LIB3168-100-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  467
                  6.0e-47
E value
                  100
Match length
% identity
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  148085
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  669
E value
                  2.0e-70
Match length
                  148
% identity
                  88
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  148086
                  LIB3168-100-P1-K1-E11
Seq. ID
Method-
                  BLASTN
NCBI GI
                  g4584351
BLAST score
                  75
E value
                  5.0e-34
Match length
                  299
% identity
                  89
                  Arabidopsis thaliana chromosome II BAC T12H3 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  148087
Seq. ID
                  LIB3168-100-P1-K1-E12
Method
                  BLASTX
                  g112741
NCBI GI
```

Method BLASTX
NCBI GI g112741
BLAST score 750
E value 6.0e-80
Match length 141
% identity 99

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE



PROTEIN) >gi\_68855\_pir\_\_NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi\_4490712\_emb\_CAB38846.1\_ (AL035680) NWMU3-2S albumin 3 precursor [Arabidopsis thaliana]

 Seq. No.
 148088

 Seq. ID
 LIB3168-100-P1-K1-E2

 Method
 BLASTX

 NCBI GI
 g112681

 BLAST score
 648

 E value
 5.0e-68

 Match length
 147

% identity 85
NCBI Description 12S SEED STORAGE PROTEIN PRECURSOR >gi\_81604\_pir\_\_S08509

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed

storage protein [Arabidopsis thaliana]

 Seq. No.
 148089

 Seq. ID
 LIB3168-100-P1-K1-E3

 Method
 BLASTX

 NCBI GI
 g1628583

 BLAST score
 557

 E value
 2.0e-57

 Match length
 119

E value 2.00 Match length 119 % identity 90

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 148090

Seq. ID LIB3168-100-P1-K1-E4

Method BLASTX
NCBI GI g112737
BLAST score 517
E value 4.0e-59
Match length 147
% identity 80

NCBI Description 2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor - Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi\_395204\_emb\_CAA80870\_(Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]

>gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

precursor [Arabidopsis thaliana]

Seq. No. 148091

Seq. ID LIB3168-100-P1-K1-E5

Method BLASTX
NCBI GI g2462749
BLAST score 231
E value 4.0e-19
Match length 117
% identity 38

Method

NCBI GI

E value

BLAST score

BLASTX

g112741

4.0e-69

50

```
NCBI Description
                  (AC002292) Putative Serine/Threonine protein kinase
                   [Arabidopsis thaliana]
Seq. No.
                  148092
Seq. ID
                  LIB3168-100-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q3327922
BLAST score
                  146
                  3.0e-76
E value
Match length
                  424
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T31E10 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  148093
Seq. No.
                  LIB3168-100-P1-K1-E8
Seq. ID
Method
                  BLASTX
                  g112737
NCBI GI
BLAST score
                  619
E value
                  1.0e-64
Match length
                  146
% identity
                  82
NCBI Description
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68853_pir__NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi_166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi_395204_emb_CAA80870_
                   (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  148094
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q3935148
                  736
BLAST score
                  2.0e-78
E value
Match length
                  147
% identity
                  97
                   (AC005106) T25N20.12 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148095
Seq. ID
                  LIB3168-100-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1531762
BLAST score
                  195
E value
                  7.0e-15
                  51
Match length
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148096
Seq. ID
                  LIB3168-100-P1-K1-F12
```

Match length 135 % identity 94

NCBI Description

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -

Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb\_CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 148097

Seq. ID LIB3168-100-P1-K1-F4

BLASTX Method g112739 NCBI GI BLAST score 398 9.0e-39 E value 119 Match length 69 % identity

2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE NCBI Description

PROTEIN) >gi\_68854\_pir\_\_NWMU2 2S albumin 2 precursor -Arabidopsis thaliana >gi 166615 (M22033) albumin 2S subunit 2 precursor [Arabidopsis thaliana] >gi 395205 emb CAA80871

(Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]

>gi 4490711 emb CAB38845.1 (AL035680) NWMU2-2S albumin 2

precursor [Arabidopsis thaliana]

148098 Seq. No.

LIB3168-100-P1-K1-F5 Seq. ID

Method BLASTX NCBI GI g112741 BLAST score 572 2.0e-73 E value 136 Match length % identity 95

NCBI Description

2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -Arabidopsis thaliana >gi 166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]

>qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 148099

LIB3168-100-P1-K1-F6 Seq. ID

Method BLASTX NCBI GI g1628583 BLAST score 430 9.0e-43 E value 96 Match length % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

> thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S cruciferin seed storage protein [Arabidopsis thaliana]

148100 Seq. No.

LIB3168-100-P1-K1-F7 Seq. ID

Method BLASTX

```
g1628583
NCBI GI
BLAST score
                  625
                  2.0e-65
E value
Match length
                  120
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  148101
Seq. No.
                  LIB3168-100-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1628583
                  699
BLAST score
                  5.0e-74
E value
                  136
Match length
                  97
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  148102
                  LIB3168-100-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1724100
                  319
BLAST score
E value
                  2.0e-29
                  149
Match length
                  41
% identity
                   (U79765) porin [Mesembryanthemum crystallinum]
NCBI Description
                  148103
Seq. No.
                  LIB3168-100-P1-K1-G1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1628583
BLAST score
                   595
E value
                   8.0e-62
Match length
                  146
% identity
                   80
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  148104
Seq. No.
                  LIB3168-100-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                   q1628583
BLAST score
                   622
                   6.0e-65
E value
Match length
                   120
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   148105
Seq. No.
                  LIB3168-100-P1-K1-G11
Seq. ID
```

```
Method
                    BLASTX
  NCBI GI
                    q1628583
  BLAST score
                     621
  E value
                    7.0e-65
  Match length
                     120
                     99
  % identity
  NCBI Description
                     (U66916) 12S cruciferin seed storage protein [Arabidopsis
                     thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                    cruciferin seed storage protein [Arabidopsis thaliana]
  Seq. No.
                     148106
                    LIB3168-100-P1-K1-G12
  Seq. ID
  Method
                    BLASTX
                    g1628583
  NCBI GI
  BLAST score
                     763
  E value
                     2.0e-81
                     151
  Match length
                     100
  % identity
                     (U66916) 12S cruciferin seed storage protein [Arabidopsis
  NCBI Description
                     thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                    cruciferin seed storage protein [Arabidopsis thaliana]
                    148107
  Seq. No.
                    LIB3168-100-P1-K1-G3
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                     g1628583
BLAST score
                     605
                     6.0e-63
  E value
                     120
  Match length
  % identity
                     (U66916) 12S cruciferin seed storage protein [Arabidopsis
  NCBI Description
                     thaliana] >qi 2842495 emb CAA16892 (AL021749) 12S
                     cruciferin seed storage protein [Arabidopsis thaliana]
  Seq. No.
                     148108
                     LIB3168-100-P1-K1-G4
  Seq. ID
  Method
                     BLASTN
  NCBI GI
                     g511598
  BLAST score
                     129
  E value
                     2.0e-66
  Match length
                     241
  % identity
                    Arabidopsis thaliana cell wall protein (APTR-1) gene,
  NCBI Description
                     complete cds
                     148109
  Seq. No.
                    LIB3168-100-P1-K1-G5
  Seq. ID
                    BLASTX
  Method
  NCBI GI
                     q1628583
  BLAST score
                     485
                     5.0e-49
  E value
  Match length
                    128
                     76
  % identity
  NCBI Description
                    (U66916) 12S cruciferin seed storage protein [Arabidopsis
                     thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
```

cruciferin seed storage protein [Arabidopsis thaliana]

```
148110
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-G6
Method
                  BLASTX
                  q3935137
NCBI GI
BLAST score
                  243
E value
                  1.0e-20
Match length
                  48
% identity
                  98
NCBI Description
                  (AC005106) T25N20.1 [Arabidopsis thaliana]
                  148111
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  a4678327
BLAST score
                  437
                  2.0e-43
E value
Match length
                  90
% identity
NCBI Description
                  (AL049658) putative cyclic nucleotide-gated channel
                  [Arabidopsis thaliana]
Seq. No.
                  148112
Seq. ID
                  LIB3168-100-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  680
                  8.0e-72
E value
Match length
                  141
                  91
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  148113
                  LIB3168-100-P1-K1-G9
Seq. ID
Method
                  BLASTX
                  g2352921
NCBI GI
BLAST score
                  269
                  1.0e-23
E value
Match length
                  94
                  79
% identity
NCBI Description
                  (AF012862) cytosolic glucose-6-phosphate dehydrogenase 1
                  [Petroselinum crispum]
Seq. No.
                  148114
                  LIB3168-100-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  643
                  2.0e-67
E value
                  148
Match length
                  84
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
```

18710

-design

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score

Match length % identity

BLAST score

Match length

% identity

```
thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  148115
                  LIB3168-100-P1-K1-H10
                  BLASTX
                  g112737
                  605
                  5.0e-63
                  143
                  82
                  2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68853 pir NWMU1 2S albumin 1 precursor -
                  Arabidopsis thaliana >gi 166614 (M22033) albumin 2S subunit
                  1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870
                  (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana]
                  >gi 4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1
                  precursor [Arabidopsis thaliana]
                  148116
                  LIB3168-100-P1-K1-H12
                  BLASTX
                  q1628583
                  227
                  6.0e-19
                  48
                  92
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  148117
                  LIB3168-100-P1-K1-H2
                  BLASTX
                  g1628583
                  788
                  2.0e-84
                  151
                  99
```

Seq. No. Seq. ID Method NCBI GI BLAST score E value Match length % identity

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 148118 LIB3168-100-P1-K1-H4 Seq. ID Method BLASTX NCBI GI g112737

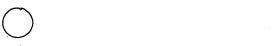
BLAST score 617 2.0e-64 E value Match length 128 91 % identity

· Line

2S SEED STORAGE PROTEIN 1 PRECURSOR (2S ALBUMIN STORAGE NCBI Description PROTEIN) >gi\_68853\_pir\_\_NWMU1 2S albumin 1 precursor -Arabidopsis thaliana >gi\_166614 (M22033) albumin 2S subunit 1 precursor [Arabidopsis thaliana] >gi 395204 emb CAA80870

> (Z24745) 2S albumin isoform 1 [Arabidopsis thaliana] >gi\_4490710 emb CAB38844.1 (AL035680) NWMU1-2S albumin 1

> > 18711



## precursor [Arabidopsis thaliana]

```
148119
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  121
                  2.0e-55
E value
Match length
                  118
                  95
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  148120
Seq. No.
                  LIB3168-100-P1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159710
BLAST score
                  453
                  0.0e + 00
E value
                  453
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSD23, complete sequence
Seq. No.
                  148121
Seq. ID
                  LIB3168-100-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1628583
BLAST score
                  625
E value
                  2.0e-65
Match length
                  120
                  100
% identity
NCBI Description
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
                  148122
Seq. No.
Seq. ID
                  LIB3168-100-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2924509
BLAST score
                  208
E value
                  2.0e-16
Match length
                  84
% identity
                  48
NCBI Description
                  (AL022023) subtilisin proteinase-like [Arabidopsis
                  thaliana]
Seq. No.
                  148123
Seq. ID
                  LIB3175-001-Q1-K1-A1
Method
                  BLASTN
NCBI GI
                  q4263694
BLAST score
                  227
                  1.0e-124
E value
Match length
                  351
% identity
                  100
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
NCBI Description
```

18712

A 107

```
sequence, complete sequence [Arabidopsis thaliana]
                  148124
Seq. No.
                  LIB3175-001-Q1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2497753
BLAST score
                  263
E value
                  6.0e-23
Match length
                  95
% identity
                  49
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
                  >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                  [Prunus dulcis]
                  148125
Seq. No.
                  LIB3175-001-Q1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462746
BLAST score
                  212
                  4.0e-17
E value
Match length
                  52
% identity
                  87
                   (AC002292) Similar to ATP-citrate-lyase [Arabidopsis
NCBI Description
                  thaliana]
                  148126
Seq. No.
Seq. ID
                  LIB3175-001-Q1-K1-A2
                  BLASTX
Method
NCBI GI
                  g166765
                  621
BLAST score
E value
                  6.0e-65
Match length
                  118
                  100
% identity
                  (M23106) heat shock protein HSP70-1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148127
                  LIB3175-001-Q1-K1-A3
Seq. ID
Method
                  BLASTX
                  q132074
NCBI GI
BLAST score
                  550
                  1.0e-56
E value
Match length
                  104
                  99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                  148128
Seq. No.
                  LIB3175-001-Q1-K1-A4
Method
                  BLASTX
                  g3885943
                  605
```

Seq. ID

NCBI GI BLAST score E value 5.0e-63 Match length 119 % identity 100

NCBI Description (AF095455) PII protein [Arabidopsis thaliana]

>gi\_4558559\_gb\_AAD22652.1\_AC007138\_16 (AC007138) P II
nitrogen sensing protein GLB I [Arabidopsis thaliana]

148129 Seq. No. LIB3175-001-Q1-K1-A6 Seq. ID Method BLASTN NCBI GI g3702730 BLAST score 42 2.0e-14 E value 205 Match length 90 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MAB16, complete sequence [Arabidopsis thaliana] 148130 Seq. No. LIB3175-001-Q1-K1-A7 Seq. ID Method BLASTX g16245 NCBI GI 649 BLAST score 3.0e-68 E value 130 Match length % identity NCBI Description (X51514) precursor acetolactate synthase (670 AA) [Arabidopsis thaliana] Seq. No. 148131 Seq. ID LIB3175-001-Q1-K1-A9 Method BLASTX NCBI GI g3860277 BLAST score 71 2.0e-34 E value Match length 80 % identity 98 (AC005824) putative ribosomal protein L10 [Arabidopsis NCBI Description thaliana] >gi 4314394 gb AAD15604 (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana] Seq. No. 148132 Seq. ID LIB3175-001-Q1-K1-B1 BLASTX Method NCBI GI g2129538 BLAST score 320 E value 1.0e-29 Match length 62 100 % identity AT103 protein - Arabidopsis thaliana >gi\_1033195 (U38232) NCBI Description

 Seq. No.
 148133

 Seq. ID
 LIB3175-001-Q1-K1-B10

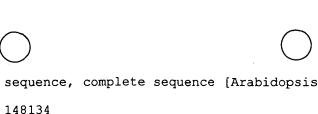
 Method
 BLASTN

 NCBI GI
 g3650026

NCBI GI g3650026 BLAST score 202 E value 1.0e-110 Match length 222 % identity 98

NCBI Description Arabidopsis thaliana chromosome II BAC T26I20 genomic

AT103 [Arabidopsis thaliana]



```
sequence, complete sequence [Arabidopsis thaliana]
                   148134
Seq. No.
                  LIB3175-001-Q1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2342734
BLAST score
                   614
                   7.0e-67
E value
Match length
                   121
% identity
                   95
                   (AC002341) DNA-binding protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                   148135
Seq. No.
                  LIB3175-001-Q1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4544412
BLAST score
                   237
E value
                   7.0e-20
Match length
                  84
                   45
% identity
                  (AC006955) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148136
Seq. ID
                  LIB3175-001-Q1-K1-B3
Method
                  BLASTN
NCBI GI
                  g2961335
BLAST score
                   396
E value
                   0.0e + 00
Match length
                   396
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20
NCBI Description
                   (ESSAII project)
Seq. No.
                   148137
Seq. ID
                   LIB3175-001-Q1-K1-B4
Method
                   BLASTN
NCBI GI
                   g4263694
BLAST score
                   207
E value
                   1.0e-113
Match length
                   375
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148138
                  LIB3175-001-Q1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2827636
BLAST score
                  514
                  2.0e-52
E value
Match length
                  106
% identity
                  98
                  (AL021636) aspartate aminotransferase [Arabidopsis
NCBI Description
                  thaliana]
```

Seq. No. 148139

```
Seq. ID
                  LIB3175-001-Q1-K1-B6
                  BLASTN
Method
NCBI GI
                  q3080352
BLAST score
                  19
E value
                  1.3e+00
Match length
                  389
                  95
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18
NCBI Description
                   (ESSAII project)
Seq. No.
                  148140
                  LIB3175-001-Q1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3869064
BLAST score
                  51
E value:
                  1.0e-19
Match length
                  148
                  90
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K1013, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148141
                  LIB3175-001-Q1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2262167
                  670
BLAST score
E value
                  1.0e-70
                  128
Match length
                  100
% identity
                   (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148142
                  LIB3175-001-Q1-K1-B9
Seq. ID
Method
                  BLASTX
                  g2660677
NCBI GI
BLAST score
                  702
                  2.0e-74
E value
                  132
Match length
                  100
% identity
                  (AC002342) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148143
                  LIB3175-001-Q1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2497542
BLAST score
                  598
                  3.0e-62
E value
                  132
Match length
% identity
NCBI Description
                  PYRUVATE KINASE, CHLOROPLAST ISOZYME G PRECURSOR
                  >gi 629696 pir S44287 pyruvate kinase, plastid - common
                  tobacco >gi 482938 emb CAA82223 (Z28374) Pyruvate kinase;
                  plastid isozyme [Nicotiana tabacum]
Seq. No.
                  148144
Seq. ID
                  LIB3175-001-Q1-K1-C10
```

Seq. No.

Seq. ID

148149

LIB3175-001-Q1-K1-C6

```
Method
                  BLASTX
                  g3879145
NCBI GI
                  195
BLAST score
                  6.0e-15
E value
                  73
Match length
% identity
                  51
                   (Z93386) predicted using Genefinder; Similarity to Human
NCBI Description
                  placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5
                  comes from this gene [Caenorhabditis elegans]
Seq. No.
                  148145
Seq. ID
                  LIB3175-001-Q1-K1-C11
Method
                  BLASTN
NCBI GI
                  q556473
BLAST score
                  298
E value
                  1.0e-167
Match length
                  337
% identity
                  100
NCBI Description
                  Arabidopsis thaliana mRNA for ERD14 protein, complete cds
Seq. No.
                  148146
Seq. ID
                  LIB3175-001-Q1-K1-C12
Method
                  BLASTX
NCBI GI
                  g3860277
BLAST score
                  410
E value
                  3.0e-40
Match length
                  81
                  100
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  148147
Seq. ID
                  LIB3175-001-Q1-K1-C4
Method
                  BLASTX
NCBI GI
                  q4107099
BLAST score
                  302
E value
                  9.0e - 34
Match length
                  90
% identity
NCBI Description
                   (AB015141) AHP1 [Arabidopsis thaliana]
                  >gi_4156245_dbj_BAA37112_ (AB012570) ATHP3 [Arabidopsis
                  thaliana]
                  148148
Seq. No.
Seq. ID
                  LIB3175-001-01-K1-C5
Method
                  BLASTN
NCBI GI
                  g3046852
BLAST score
                  302
E value
                  1.0e-169
Match length
                  404
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQJ16, complete sequence [Arabidopsis thaliana]
```

BLAST score

E value

292

1.0e-163

```
Method
                  BLASTN
NCBI GI
                   q4757395
BLAST score
                   359
E value
                   0.0e + 00
Match length
                   390
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21L13, complete sequence
                  148150
Seq. No.
                  LIB3175-001-Q1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4559339
BLAST score
                  153
                  5.0e-10
E value
                  58
Match length
                  59
% identity
                   (AC007087) putative ATP-dependent RNA helicase [Arabidopsis
NCBI Description
                   thaliana]
                   148151
Seq. No.
                  LIB3175-001-Q1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2146734
BLAST score
                   212
                   6.0e-17
E value
Match length
                   37
% identity
                  GAST1 protein homolog (clone GASA4) - Arabidopsis thaliana
NCBI Description
                   148152
Seq. No.
Seq. ID
                  LIB3175-001-Q1-K1-D1
Method
                  BLASTX
NCBI GI
                   q3738261
BLAST score
                   288
                   7.0e-26
E value
Match length
                   98
% identity
                   (AB018412) chloroplast phosphoglycerate kinase [Populus
NCBI Description
                   nigra]
Seq. No.
                   148153
Seq. ID
                  LIB3175-001-Q1-K1-D10
Method
                  BLASTX
NCBI GI
                  g4115377
BLAST score
                   368
E value
                   3.0e-35
Match length
                  109
                   71
% identity
                  (AC005967) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148154
                  LIB3175-001-Q1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4309747
```

E value

```
401
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T13E11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  148155
Seq. No.
                  LIB3175-001-Q1-K1-D12
Seq. ID
                  BLASTX
Method
                  g2130051
NCBI GI
                  379
BLAST score
                  1.0e-36
E value
                  100
Match length
                  70
% identity
                  xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                  >gi 1296807 emb CAA64544 (X95256) xylose isomerase
                   [Hordeum vulgare] >gi_1588664_prf__2209268A xylose
                  isomerase [Hordeum vulgare]
                  148156
Seq. No.
Seq. ID
                  LIB3175-001-Q1-K1-D2
Method
                  BLASTX
                  g1169476
NCBI GI
                  570
BLAST score
                  6.0e-59
E value
                  120
Match length
                  93
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
Seq. No.
                  148157
Seq. ID
                  LIB3175-001-Q1-K1-D3
Method
                  BLASTN
NCBI GI
                  q4049332
BLAST score
                   284
                   1.0e-158
E value
                   396
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
NCBI Description
                   (ESSAII project)
Seq. No.
                  148158
                  LIB3175-001-Q1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4678935
BLAST score
                   525
                   1.0e-53
E value
Match length
                   104
                   98
% identity
NCBI Description
                   (AL049711) putative protein [Arabidopsis thaliana]
Seq. No.
                  148159
Seq. ID
                  LIB3175-001-Q1-K1-D6
Method
                  BLASTN
                  q3176695
NCBI GI
                  208
BLAST score
```

1.0e-113

```
Match length
                   401
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F14J9 genomic
                   sequence contains phyA marker, complete sequence
                   [Arabidopsis thaliana]
Seq. No.
                   148160
Seq. ID
                   LIB3175-001-Q1-K1-D8
Method
                  BLASTX
NCBI GI
                   g99752
BLAST score
                   438
E value
                   2.0e-43
Match length
                   113
% identity
                  protochlorophyllide reductase (EC 1.3.1.33) precursor -
NCBI Description
                  Arabidopsis thaliana
Seq. No.
                   148161
Seq. ID
                  LIB3175-001-Q1-K1-D9
Method
                  BLASTX
NCBI GI
                   q2738248
BLAST score
                   535
E value
                   7.0e-55
                  102
Match length
                  100
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   148162
Seq. No.
Seq. ID
                  LIB3175-001-Q1-K1-E1
Method
                  BLASTX
                  g1550740
NCBI GI
BLAST score
                   577
E value
                   9.0e-60
Match length
                  111
% identity
                  100
NCBI Description (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
Seq. No.
                  148163
Seq. ID
                  LIB3175-001-Q1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4006834
BLAST score
                   614
                   4.0e-64
E value
                  120
Match length
% identity
                   (AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148164
Seq. ID
                  LIB3175-001-Q1-K1-E11
Method
                  BLASTX
NCBI GI
                  g116527
BLAST score
                  556
                  3.0e-57
E value
Match length
                  120
% identity
                  87
```

```
PROBABLE CLPP-LIKE PROTEASE (ENDOPEPTIDASE CLP) (ORF 196)
NCBI Description
                  >gi 1143166 (U32397) ClpP protease [Nicotiana tabacum]
                  >gi 2924270 emb CAA77422 (Z00044) ATP-dependent protease
                  proteolytic subuni [Nicotiana tabacum]
                  148165
Seq. No.
                  LIB3175-001-Q1-K1-E3
Seq. ID
                  BLASTX
Method 4
                  g4589398
NCBI GI
BLAST score
                  373
                  7.0e-36
E value
Match length
                  81
% identity
                  81
                  (D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]
NCBI Description
                  148166
Seq. No.
                  LIB3175-001-Q1-K1-E4
Seq. ID
Method
                  BLASTX
                  g2499542
NCBI GI
BLAST score
                  515
E value
                  2.0e-52
Match length
                  123
% identity
                  IRON(III)-ZINC(II) PURPLE ACID PHOSPHATASE PRECURSOR (PAP)
NCBI Description
                  >qi 1218042 (U48448) secreted purple acid phosphatase
                  precursor [Arabidopsis thaliana]
Seq. No.
                  148167
                  LIB3175-001-Q1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g231587
BLAST score
                  64
E value
                  2.0e-40
Match length
                  115
% identity
                  76
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >qi 283001 pir S25304 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain precursor, mitochondrial - rice
                  >gi 218147 dbj BAA01372 (D10491) mitochondrial F1-ATPase
                  [Oryza sativa]
Seq. No.
                  148168
Seq. ID
                  LIB3175-001-Q1-K1-E6
                  BLASTX
Method
NCBI GI
                  g3201632
                  285
BLAST score
                  1.0e-25
E value
                  104
Match length
                  54
% identity
                  (AC004669) putative 2A6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148169
Seq. ID
                  LIB3175-001-Q1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3123271
                  499
BLAST score
E value
                  1.0e-50
```

```
114
Match length
                    85
% identity
                    40S RIBOSOMAL PROTEIN S6 >gi_2224751_emb_CAA74381_ (Y14052)
NCBI Description
                    ribosomal protein S6 [Arabidopsis thaliana]
                    148170
Seq. No.
                    LIB3175-001-Q1-K1-E8
Seq. ID
Method
                    BLASTX
NCBI GI
                    q399013
BLAST score
                    478
E value
                    4.0e-48
Match length
                    93
                    100
% identity
                    ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                    (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                    >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)
                    adenylate translocator [Arabidopsis thaliana]
                    >gi 445607 prf 1909354A adenylate translocator
                    [Arabidopsis thaliana]
Seq. No.
Seq. ID
                    LIB3175-001-Q1-K1-E9
Method
                    BLASTX
NCBI GI
                    q2245030
BLAST score
                    410
                    3.0e-40
E value
                    113
Match length
                    74
% identity
                    (Z97341) apetala2 domain TINY homolog [Arabidopsis
NCBI Description
                    thaliana]
                    148172
Seq. No.
                    LIB3175-001-Q1-K1-F1
Seq. ID
                    BLASTX
Method
NCBI GI
                    q3763919
BLAST score
                    517
E value
                    9.0e-53
                    125
Match length
% identity
NCBI Description
                    (AC004450) putative isopropylmalate dehydratase
                    [Arabidopsis thaliana] >gi 4531436 gb AAD22121.1 AC006224 3
                    (AC006224) putative isopropylmalate dehydratase
                    [Arabidopsis thaliana]
Seq. No.
                    148173
                    LIB3175-001-Q1-K1-F10
Seq. ID
                    BLASTX
Method
                    g1237102
NCBI GI
BLAST score
                    207
E value
                    2.0e-16
Match length
                    87
'% identity
                    53
                    (L40358) calmodulin-binding protein [Arabidopsis thaliana]
NCBI Description
```

[Arabidopsis thaliana]

>gi 1589171 prf 2210340A calmodulin-binding protein

```
Seq. No.
                  148174
Seq. ID
                  LIB3175-001-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g2252840
BLAST score
                  470
E value
                  3.0e-47
Match length
                  125
% identity
                  67
NCBI Description
                  (AF013293) contains regions of similarity to Haemophilus
                  influenzae permease (SP:P38767) [Arabidopsis thaliana]
Seq. No.
                  148175
                  LIB3175-001-Q1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1550740
BLAST score
                  568
E value
                  1.0e-58
Match length
                  110
                  99
% identity
                  (Y07961) GDP-associated inhibitor [Arabidopsis thaliana]
NCBI Description
                  148176
Seq. No.
Seq. ID
                  LIB3175-001-Q1-K1-F2
Method
                  BLASTN
NCBI GI
                  g3869073
BLAST score
                  120
E value
                  6.0e-61
Match length
                  337
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKN22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148177
                  LIB3175-001-Q1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2117612
                  717
BLAST score
                  3.0e-76
E value
                  131
Match length
% identity
                  catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
NCBI Description
Seq. No.
                  148178
Seq. ID
                  LIB3175-001-Q1-K1-F4
Method
                  BLASTX
NCBI GI
                  q1669387
BLAST score
                  439
E value
                  1.0e-43
Match length
                  82
% identity
                  100
NCBI Description
                  (U41998) actin 2 [Arabidopsis thaliana]
Seq. No.
                  148179
                  LIB3175-001-Q1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115778
BLAST score
                  85
```

```
E value
                  9.0e-16
Match length
                  79
% identity
                  65
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-1) (LHCP) >gi 282896 pir S22511 chlorophyll
                  a/b-binding protein (cab-1) - white mustard
                  >gi 21138 emb CAA34459 (X16436) chlorophyll a/b-binding
                  protein (AA 1-266) [Sinapis alba] >qi 21140 emb CAA33903
                   (X15894) chlorophyll a/b-binding polypeptide [Sinapis alba]
Seq. No.
                  148180
Seq. ID
                  LIB3175-001-Q1-K1-F6
Method
                  BLASTX
NCBI GI
                  g1246019
BLAST score
                  576
                  1.0e-59
E value
Match length
                  115
% identity
                  96
NCBI Description
                  (S80554) chalcone synthase, CHS [Arabidopsis, Landsberg
                  erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]
Seq. No.
                  148181
Seq. ID
                  LIB3175-001-Q1-K1-F7
Method
                  BLASTN
NCBI GI
                  q4220510
BLAST score
                  220
                  1.0e-120
E value
Match length
                  378
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                  (ESSAII project)
Seq. No.
                  148182
Seq. ID
                  LIB3175-001-Q1-K1-F8
Method
                  BLASTX
NCBI GI
                  q4538943
BLAST score
                  493
                  6.0e-50
E value
Match length
                  126
% identity
                   (ALO49483) putative beta-galactosidase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148183
Seq. ID
                  LIB3175-001-Q1-K1-F9
Method
                  BLASTX
                  g1718097
NCBI GI
                  322
BLAST score
                  7.0e-30
E value
                  95
Match length
% identity
                  60
                  VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT)
NCBI Description
                  (41 KD ACCESSORY PROTEIN) (DVA41) >gi 626048 pir A55016
                  lysosomal membrane protein DVA41 - slime mold
                  (Dictyostelium discoideum) >qi 532733 (U13150) vacuolar
```

ATPase subunit DVA41 [Dictyostelium discoideum]

```
148184
Seq. No.
Seq. ID
                  LIB3175-001-Q1-K1-G1
Method
                  BLASTX
NCBI GI
                  g4262180
                   699
BLAST score
                   4.0e-74
E value
Match length
                  131
                  99
% identity
                   (AC005508) 29621 [Arabidopsis thaliana]
NCBI Description
                   148185
Seq. No.
                  LIB3175-001-Q1-K1-G11
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1698582
                  253
BLAST score
                  9.0e-22
E value
                  75
Match length
                   72
% identity
                  (U60767) integral membrane protein OsNramp3 [Oryza sativa]
NCBI Description
                   148186
Seq. No.
Seq. ID
                  LIB3175-001-Q1-K1-G12
                  BLASTN
Method
NCBI GI
                  q2924653
                   228
BLAST score
                   1.0e-125
E value
                   398
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDA7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148187
                   LIB3175-001-Q1-K1-G3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1350680
BLAST score
                   662
                   1.0e-69
E value
Match length
                   126
                   99
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L1
Seq. No.
                   148188
                   LIB3175-001-Q1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1695719
BLAST score
                   569
                   8.0e-59
E value
                   135
Match length
% identity
                   86
                   (D89342) luminal binding protein [Arabidopsis thaliana]
NCBI Description
                   148189
Seq. No.
                   LIB3175-001-Q1-K1-G5
Seq. ID
                   BLASTX
Method
                   g417381
NCBI GI
                   629
BLAST score
                   7.0e-66
E value
```

```
Match length
                  125
% identity
                  98
NCBI Description
                  NITRILASE 1 >gi_99738 pir S22398 nitrilase (EC 3.5.5.1) -
                  Arabidopsis thaliana \overline{>}gi_{16}400_{emb_{CAA4}5041_{10}} (X63445)
                  nitrilase I [Arabidopsis *thaliana]
                  148190
Seq. No.
                  LIB3175-001-Q1-K1-G6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586265
BLAST score
                  531
E value
                  2.0e-54
Match length
                  120
% identity
                   (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  148191
Seq. No.
                  LIB3175-001-Q1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129759
                   453
BLAST score
E value
                   3.0e-45
Match length
                  90
                  100
% identity
                  UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana
NCBI Description
                  >gi 1143392 emb CAA90941 (Z54214) uridine diphosphate
                  glucose epimerase [Arabidopsis thaliana]
Seq. No.
                  148192
Seq. ID
                  LIB3175-001-Q1-K1-G8
Method
                  BLASTN
NCBI GI
                  g3367567
                  311
BLAST score
                  1.0e-175
E value
                  371
Match length
                  100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20
NCBI Description
                   (ESSAII project)
                  148193
Seq. No.
Seq. ID
                  LIB3175-001-Q1-K1-G9
Method
                  BLASTX
NCBI GI
                  g112741
BLAST score
                  661
E value
                  1.0e-69
Match length
                  123
% identity
                  99
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68855 pir NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  _3 precursor [Arabidopsis thaliana] >gi 395201 emb CAA80868
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >qi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
Seq. No.
                  148194
                  LIB3175-001-Q1-K1-H10
Seq. ID
```

```
Method
                  BLASTX
NCBI GI
                  q4567249
BLAST score
                  518
                  7.0e-53
E value
Match length
                  113
% identity
                  87
                 (AC007070) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148195
                  LIB3175-001-Q1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q120667
                  518
BLAST score
                  6.0e-53
E value
Match length
                  116
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi 81622 pir JQ1287 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                  thaliana >qi 166706 (M64116) cystolic
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                  dehydrogenase [Arabidopsis thaliana]
                  148196
Seq. No.
                  LIB3175-001-Q1-K1-H12
Seq. ID
                                                                . . .
Method
                  BLASTN
NCBI GI
                  g2252823
BLAST score
                  247
E value
                  1.0e-136
Match length
                  296
% identity
NCBI Description Arabidopsis thaliana BAC IG005I10
Seq. No.
                  148197
                  LIB3175-001-Q1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3850568
BLAST score
                  475
E value
                  8.0e-48
Match length
                  106
% identity
NCBI Description
                  (AC005278) Similar to hypothetical protein SPAC2F7.14c
                  gi 1052797 from Schizosaccharomyces pombe cosmid gb Z50142.
                  [Arabidopsis thaliana]
Seq. No.
                  148198
                  LIB3175-001-Q1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4262186
                  521
BLAST score
                  2.0e-53
E value
Match length
                  105
% identity
                  (AC005508) Highly similar to cullin 3 [Arabidopsis
NCBI Description
```

thaliana]

```
Seq. No.
                  148199
                  LIB3175-001-Q1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4538963
BLAST score
                  460
E value
                  5.0e-46
Match length
                  117
                  77
% identity
                   (ALO49488) chlorophyll a/b-binding protein-like
NCBI Description
                   [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                  148200
Seq. No.
                  LIB3175-001-Q1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4581084
BLAST score
                  283
E value
                  1.0e-158
Match length
                  379
                  100
% identity
                  Arabidopsis thaliana chromosome I BAC T30F21 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  148201
Seq. ID
                  LIB3175-001-Q1-K1-H6
                  BLASTX
Method
                  g2347192
NCBI GI
BLAST score
                  289
                  1.0e-54
E value
                  113
Match length
                  95
% identity
                   (ACO02338) spliceosomal protein U2B isolog [Arabidopsis
NCBI Description
                  thaliana]
                  148202
Seq. No.
Seq. ID
                  LIB3175-001-Q1-K1-H7
Method
                  BLASTX
NCBI GI
                  g4218123
BLAST score
                  336
                  2.0e-31
E value
Match length
                  125
% identity
                   (AL035353) photosystem I subunit PSI-E-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  148203
                  LIB3175-002-Q1-K1-A10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1669389
BLAST score
                   252
E value
                  7.0e-22
Match length
                   47
                   100
% identity
                  (U42007) actin 8 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148204
                  LIB3175-002-Q1-K1-A11
Seq. ID
```

```
Method
                  BLASTN
NCBI GI
                  g1069997
BLAST score
                  132
E value
                  4.0e-68
Match length
                  264
% identity
                  95
                  B.napus chloroplast accD gene
NCBI Description
Seq. No.
                  148205
                  LIB3175-002-Q1-K1-A2
Seq. ID
Method
                  BLASTX
                  g2911055
NCBI GI
BLAST score
                  317
E value
                  1.0e-29
Match length
                  87
                  72
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
                  148206
Seq. No.
                  LIB3175-002-Q1-K1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2288979
BLAST score
                  293
E value
                  1.0e-164
Match length
                  297
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T01024 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148207
Seq. ID
                  LIB3175-002-Q1-K1-A6
Method
                  BLASTN
NCBI GI
                  q4519191
BLAST score
                  180
                  8.0e-97
E value
Match length
                  234
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K9P8, complete sequence
Seq. No.
                  148208
Seq. ID
                  LIB3175-002-Q1-K1-A8
Method
                  BLASTX
NCBI GI
                  g2129578
                  274
BLAST score
                  2.0e-24
E value
Match length
                  55
% identity
                  dTDP-glucose 4-6-dehydratases homolog - Arabidopsis
NCBI Description
                  thaliana >gi_928932_emb_CAA89205_ (Z49239) homolog of
                  dTDP-glucose 4-6-dehydratases [Arabidopsis thaliana]
                  >gi_1585435_prf__2124427B diamide resistance gene
```

Seq. No. 148209

Seq. ID LIB3175-002-Q1-K1-A9

[Arabidopsis thaliana]

Method BLASTX

E value

9.0e-66

```
NCBI GI
                   g2781394
BLAST score
                   362
E value
                   8.0e-35
Match length
                   75
                   100
% identity
                   (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148210
                   LIB3175-002-Q1-K1-B10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3582341
BLAST score
                   294
E value
                   8.0e-27
                   96
Match length
% identity
                   64
NCBI Description
                   (AC005496) putative flavonol 3-o-glucosyltransferase
                   [Arabidopsis thaliana]
                   148211
Seq. No.
                   LIB3175-002-Q1-K1-B11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4589411
BLAST score
                   272
                   1.0e-151
E value
Match length
                   296
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F5H8, complete sequence
Seq. No.
                   148212
Seq. ID
                   LIB3175-002-Q1-K1-B12
Method
                   BLASTX
NCBI GI
                   g3176874
BLAST score
                   398
                   5.0e-39
E value
                   79
Match length
                   97
% identity
NCBI Description
                   (AF065639) cucumisin-like serine protease [Arabidopsis
                   thaliana]
                   148213
Seq. No.
Seq. ID
                  LIB3175-002-Q1-K1-B2
Method
                   BLASTX
NCBI GI
                   g3914740
BLAST score
                   387
                   9.0e-38
E value
Match length
                   84
% identity
                   60S RIBOSOMAL PROTEIN L26 >gi 2160300 dbj BAA18941
NCBI Description
                   (D78495) ribosomal protein [Brassica rapa]
Seq. No.
                   148214
                   LIB3175-002-Q1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4757403
BLAST score
                   128
```

NCBI GI

```
266
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJL12, complete sequence
                  148215
Seq. No.
                  LIB3175-002-Q1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2088652
                  423
BLAST score
                  6.0e-42
E value
                  94
Match length
                  86
% identity
                  (AF002109) 26S proteasome regulatory subunit S12 isolog
NCBI Description
                  [Arabidopsis thaliana] >gi_2351376 (U54561) translation
                  initiation factor eIF2 p47 subunit homolog [Arabidopsis
                  thaliana]
                  148216
Seq. No.
                  LIB3175-002-Q1-K1-B6
Seq. ID
                  BLASTX
Method
                  g4432860
NCBI GI
                  483
BLAST score
                  6.0e-49
E value
                  99
Match length
% identity
                  (AC006300) putative glucose-induced repressor protein
NCBI Description
                  [Arabidopsis thaliana]
                  148217
Seq. No.
                  LIB3175-002-Q1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115783
                  324
BLAST score
                  2.0e-30
E value
                  62
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543
                                                             (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  148218
Seq. No.
                  LIB3175-002-Q1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4544399
                  169
BLAST score
                  4.0e-12
E value
                  74
Match length
% identity
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
                  148219
Seq. No.
                  LIB3175-002-Q1-K1-C1
Seq. ID
                  BLASTX
Method
```

18731

q4263704

E value

6.0e-73

```
204
BLAST score
E value
                   3.0e-16
Match length
                   72
% identity
NCBI Description
                   (AC006223) putative sugar starvation-induced protein
                   [Arabidopsis thaliana]
Seq. No.
                   148220
                   LIB3175-002-Q1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2623962
BLAST score
                   273
E value
                   2.0e-24
Match length
                   55
                   95
% identity
                   (Y12540) isocitrate dehydrogenase (NADP+) [Apium
NCBI Description
                  graveolens]
Seq. No.
                   148221
Seq. ID
                   LIB3175-002-Q1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1172977
BLAST score
                   439
E value
                  8.0e-44
Match length
                   90
                   99
% identity
                   60S RIBOSOMAL PROTEIN L18 >gi 606970 (U15741) cytoplasmic
NCBI Description
                   ribosomal protein L18 [Arabidopsis thaliana]
Seq. No.
                   148222
                  LIB3175-002-Q1-K1-C2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3080430
                   294
BLAST score
                   1.0e-165
E value
                   298
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
                   (ESSAII project)
                   148223
Seq. No.
                  LIB3175-002-Q1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3421123
BLAST score
                   472
                  1.0e-47
E value
Match length
                  95
% identity
NCBI Description
                   (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
                   thaliana]
Seq. No.
                  148224
Seq. ID
                  LIB3175-002-Q1-K1-C4
Method
                  BLASTN
NCBI GI
                  q4757403
BLAST score
                   140
```

Method

BLASTN

```
300
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJL12, complete sequence
Seq. No.
                  148225
                  LIB3175-002-Q1-K1-C6
Seq. ID
Method
                  BLASTX
                  q113026
NCBI GI
                  271
BLAST score
                  4.0e-24
E value
                  99
Match length
% identity
                  59
                  ISOCITRATE LYASE (ISOCITRASE) (ISOCITRATASE) (ICL)
NCBI Description
                  >gi 68211 pir WZRPI isocitrate lyase (EC 4.1.3.1) - rape
                  >gi 255220 bbs 112862 isocitrate lyase, threo-D
                  S-isocitrate glyoxylate-lyase, IL {EC 4.1.3.1} [Brassica
                  napus, seedlings, Peptide, 576 aa] >gi 167144 (L08482)
                  isocitrate lyase [Brassica napus] >gi 447142 prf 1913424A
                  isocitrate lyase [Brassica napus]
                  148226
Seq. No.
Seq. ID
                  LIB3175-002-Q1-K1-C7
Method
                  BLASTN
NCBI GI
                  g4519187
BLAST score
                  137
E value
                  2.0e-71
Match length
                  137
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K1G2, complete sequence
Seq. No.
                  148227
Seq. ID
                  LIB3175-002-Q1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4191778
                  392
BLAST score
                  3.0e-38
E value
Match length
                  98
% identity
                  (AC005917) putative nucleosome assembly protein I
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  148228
                  LIB3175-002-Q1-K1-C9
Seq. ID
                  BLASTX
Method
                  q3806098
NCBI GI
BLAST score
                  461
E value
                  2.0e-46
Match length
                  84
% identity
                  100
                  (AF079100) arginine-tRNA-protein transferase 1; Atelp
NCBI Description
                  [Arabidopsis thaliana]
                  148229
Seq. No.
Seq. ID
                  LIB3175-002-Q1-K1-D1
```

```
NCBI GI
                  g2264317
                  111
BLAST score
                  1.0e-55
E value
                  118
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUG13, complete sequence [Arabidopsis thaliana]
                  148230
Seq. No.
                  LIB3175-002-Q1-K1-D10
Seq. ID
Method
                  BLASTX
                  q1362007
NCBI GI
                   457
BLAST score
                   6.0e-46
E value
                   87
Match length
                   99
% identity
                   thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana
NCBI Description
                   >gi 871992_emb_CAA55787_ (X79195) thioglucosidase
                   [Arabidopsis thaliana]
Seq. No.
                   148231
                   LIB3175-002-Q1-K1-D12
Seq. ID
                   BLASTN
Method
                   g4490734
NCBI GI
                   204
BLAST score
                   1.0e-111
E value
                   298
Match length
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone (ESSA
NCBI Description
                   project)
                   148232
Seq. No.
Seq. ID
                   LIB3175-002-Q1-K1-D3
                   BLASTX
Method
NCBI GI
                   g3122387
BLAST score
                   381
                   5.0e-37
E value
Match length
                   82
                   88
% identity
                   WD-40 REPEAT PROTEIN MSI1 >gi_2394229 (AF016846) WD-40
NCBI Description
                   repeat protein [Arabidopsis thaliana]
                   148233
Seq. No.
                   LIB3175-002-Q1-K1-D4
Seq. ID
Method
                   BLASTN
                   g3046852
NCBI GI
                   213
BLAST score
                   1.0e-116
E value
                   300
Match length
                   95
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQJ16, complete sequence [Arabidopsis thaliana]
                   148234
Seq. No.
                   LIB3175-002-Q1-K1-D5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129583
```

```
BLAST score
                   388
                   8.0e-38
E value
Match length
                   92
% identity
                   86
                   ferritin - Arabidopsis thaliana >gi_1246401 emb CAA63932
NCBI Description
                   (X94248) ferritin [Arabidopsis thaliana]
                   148235
Seq. No.
                   LIB3175-002-Q1-K1-D6
Seq. ID
Method
                   BLASTX
                   q4585882
NCBI GI
BLAST score
                   284
E value
                   1.0e-25
                   56
Match length
                   100
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   148236
                   LIB3175-002-Q1-K1-D8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q450879
BLAST score
                   78
E value
                   2.0e-36
Match length
                   90
                   97
% identity
NCBI Description
                   A.thaliana hsc70-1 gene
Seq. No.
                   148237
                   LIB3175-002-Q1-K1-D9
Seq. ID
Method
                   BLASTN
                   g3702728
NCBI GI
                   38
BLAST score
E value
                   4.0e-12
                   94
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19M13, complete sequence [Arabidopsis thaliana]
                   148238
Seq. No.
                   LIB3175-002-Q1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2702268
BLAST score
                   414
E value
                   7.0e-41
                   79
Match length
                   100
% identity
NCBI Description
                   (AC003033) putative cellulase [Arabidopsis thaliana]
                   148239
Seq. No.
Seq. ID
                   LIB3175-002-Q1-K1-E12
Method
                   BLASTN
NCBI GI
                   q3702731
BLAST score
                   296
                   1.0e-166
E value
Match length
                   296
                   100
% identity
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFC19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148240
Seq. ID
                  LIB3175-002-Q1-K1-E2
Method
                  BLASTX
NCBI GI
                  q4263525
BLAST score
                  403
                  1.0e-39
E value
                  99
Match length
                  80
% identity
                  (AC004044) putative photosystem I reaction center subunit
NCBI Description
                  II precursor [Arabidopsis thaliana]
                  148241
Seq. No.
                  LIB3175-002-Q1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2088654
BLAST score
                  340
                  3.0e-32
E value
Match length
                  78
% identity
NCBI Description
                   (AF002109) 60S acidic ribosomal protein PO isolog
                   [Arabidopsis thaliana]
Seq. No.
                  148242
Seq. ID
                  LIB3175-002-Q1-K1-E4
Method
                  BLASTX
NCBI GI
                  g462181
BLAST score
                  150
                  6.0e-10
E value
Match length
                  83
                  36
% identity
                  GLUTAMINE SYNTHETASE (GLUTAMATE--AMMONIA LIGASE) (GS)
NCBI Description
                  >gi_294445 (L12410) unnamed protein product [Pyrococcus
                  furiosus]
Seq. No.
                  148243
Seq. ID
                  LIB3175-002-Q1-K1-E5
Method
                  BLASTN
NCBI GI
                  g4585952
BLAST score
                  294
E value
                  1.0e-165
Match length
                  298
                  100
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F26F24,
NCBI Description
                  complete sequence
                  148244
Seq. No.
Seq. ID
                  LIB3175-002-Q1-K1-E6
Method
                  BLASTX
NCBI GI
                  q3875246
BLAST score
                  241
E value
                  1.0e-20
Match length
                  86
% identity
                  52
                  (Z81490) similar to WD domain, G-beta repeats (2 domains);
NCBI Description
```

NCBI Description

```
cDNA EST EMBL: T00482 comes from this gene; cDNA EST
                  EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes
                   from this gene; cDNA EST yk449d4.5 comes from this gene;
Seq. No.
                  148245
                  LIB3175-002-Q1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4220640
                  210
BLAST score
                  1.0e-114
E value
                  294
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MPE11, complete sequence [Arabidopsis thaliana]
                  148246
Seq. No.
Seq. ID
                  LIB3175-002-Q1-K1-E8
                  BLASTX
Method
NCBI GI
                  q4741940
BLAST score
                   540
                   1.0e-55
E value
                   97
Match length
% identity
                   65
                   (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
                   148247
Seq. No.
                  LIB3175-002-Q1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3892050
BLAST score
                   220
                   4.0e-18
E value
Match length
                   62
                   69
% identity
                   (AC002330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   148248
Seq. No.
                  LIB3175-002-Q1-K1-F1
Seq. ID
                  BLASTN
Method
                   g3241916
NCBI GI
                   70
BLAST score
                   2.0e-31
E value
                  123
Match length
                   88
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15N18, complete sequence [Arabidopsis thaliana]
                   148249
Seq. No.
Seq. ID
                  LIB3175-002-Q1-K1-F10
Method
                  BLASTN
                  g3063690
NCBI GI
                   278
BLAST score
                   1.0e-155
E value
Match length
                   278
% identity
                   100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
```

18737

(ESSAII project)

91.00

```
Seq. No.
                  148250
Seq. ID
                  LIB3175-002-Q1-K1-F11
Method
                  BLASTX
NCBI GI
                  g3176685
BLAST score
                  519
                  3.0e-53
E value
                  98
Match length
% identity
                  100
NCBI Description
                  (AC003671) Strong similarity to spermidine synthase 1,
                  gb Y08252 and possibly closer similarity to spermidine
                  synthase 2 gb Y08253 from Datura stramonium. ESTs
                  gb N38155, gb T41738, gb AA597626, gb AA712967 and
                  qb AA712346 come from this ge
Seq. No.
                  148251
Seq. ID
                  LIB3175-002-Q1-K1-F12
Method
                  BLASTN
                  g1765898
NCBI GI
                  227
BLAST score
                  1.0e-125
E value
Match length
                  227
% identity
                  100
                  A.thaliana mRNA for Spot 3 protein
NCBI Description
Seq. No.
                  148252
Seq. ID
                  LIB3175-002-Q1-K1-F2
Method
                  BLASTX
                  g2586127
NCBI GI
                  243
BLAST score
                  8.0e-21
E value
Match length
                  94
% identity
                  (U89510) b-keto acyl reductase [Hordeum vulgare]
NCBI Description
                  148253
Seq. No.
                  LIB3175-002-Q1-K1-F6
Seq. ID
Method
                  BLASTX
                  g1703220
NCBI GI
BLAST score
                  453
E value
                  2.0e-45
                  97
Match length
% identity
                  AIG2 PROTEIN >gi 1127806 (U40857) AIG2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148254
Seq. ID
                  LIB3175-002-Q1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2130051
BLAST score
                  214
                  2.0e-17
E value
                  70
Match length
% identity
                  59
                  xylose isomerase (EC 5.3.1.5) - barley
NCBI Description
                  >gi 1296807 emb CAA64544 (X95256) xylose isomerase
                  [Hordeum vulgare] >gi 1588664 prf 2209268A xylose
                  isomerase [Hordeum vulgare]
```

```
Seq. No.
                  148255
                  LIB3175-002-Q1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129579
BLAST score
                  474
                  6.0e-48
E value
                  90
Match length
                  100
% identity
                  Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400)
NCBI Description
                  Dwarf1 [Arabidopsis thaliana]
                  148256
Seq. No.
                  LIB3175-002-Q1-K1-F9
Seq. ID
                  BLASTX
Method
                  g1109699
NCBI GI
                  506
BLAST score
                  1.0e-51
E value
                  96
Match length
                  100
% identity
                   (X83381) gibberellin 20-oxidase [Arabidopsis thaliana]
NCBI Description
                  148257
Seq. No.
                  LIB3175-002-Q1-K1-G1
Seq. ID
Method
                  BLASTN
                  g3241917
NCBI GI
BLAST score
                  69
                  1.0e-30
E value
Match length
                  157
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19B1, complete sequence [Arabidopsis thaliana]
                  148258
Seq. No.
Seq. ID
                  LIB3175-002-Q1-K1-G11
                  BLASTX
Method
NCBI GI
                  g115783
BLAST score
                   396
                   9.0e-39
E value
Match length
                  74
                   100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  148259
Seq. No.
                  LIB3175-002-Q1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629669
BLAST score
                  169
                  2.0e-12
E value
                  61
Match length
                  51
% identity
NCBI Description
                  hypothetical protein - tomato
                  148260
Seq. No.
```

```
LIB3175-002-Q1-K1-G2
Seq. ID
                  BLASTX
Method
                  g4538963
NCBI GI
BLAST score
                  278
                  5.0e-25
E value
Match length
                  84
% identity
                  68
                  (AL049488) chlorophyll a/b-binding protein-like
NCBI Description
                  [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129 1
                  (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                  148261
Seq. No.
                  LIB3175-002-Q1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267073
BLAST score
                  382
                  4.0e-37
E value
                  70
Match length
% identity
                  100
                  TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi 166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
                  148262
Seq. No.
                  LIB3175-002-Q1-K1-G6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2245000
BLAST score
                  430
E value
                  1.0e-42
Match length
                  85
% identity
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148263
                  LIB3175-002-Q1-K1-G7
Seq. ID
Method
                  BLASTX
                  q2459421
NCBI GI
BLAST score
                  438
                  1.0e-43
E value
                  97
Match length
% identity
                   (AC002332) putative calcium-binding EF-hand protein
NCBI Description
                  [Arabidopsis thaliana]
                  148264
Seq. No.
                  LIB3175-002-Q1-K1-G8
Seq. ID
Method
                  BLASTN
                  g4262276
NCBI GI
BLAST score
                  79
E value
                  3.0e - 37
                  79
Match length
                  100
% identity
                  Arabidopsis thaliana gamma-glutamylcysteine synthetase
NCBI Description
                  gene, complete cds
                  148265
Seq. No.
```

BLAST score

```
Seq. ID
                   LIB3175-002-Q1-K1-H1
Method
                   BLASTN
                   g4589950
NCBI GI
BLAST score
                   185
E value
                   1.0e-100
                   300
Match length
                   94
% identity
                  Arabidopsis thaliana chromosome II BAC T28P16 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   148266
Seq. ID
                   LIB3175-002-Q1-K1-H10
Method
                   BLASTX
NCBI GI
                   q4544456
BLAST score
                   434
                   3.0e-43
E value
                   97
Match length
                   89
% identity
                   (AC006592) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                   148267
Seq. No.
Seq. ID
                   LIB3175-002-Q1-K1-H11
Method
                   BLASTX
NCBI GI
                   q1619602
BLAST score
                   217
E value
                   9.0e-18
Match length
                   54
% identity
NCBI Description
                   (Y08726) MtN3 [Medicago truncatula]
                   148268
Seq. No.
Seq. ID
                   LIB3175-002-Q1-K1-H12
Method
                   BLASTN
NCBI GI
                   q4455321
BLAST score
                   75
E value
                   1.0e-34
Match length
                   114
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
                   (ESSAII project)
                   148269
Seq. No.
                  LIB3175-002-Q1-K1-H2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4220632
BLAST score
                   136
                   2.0e-70
E value
                   232
Match length
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K6M13, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148270
                  LIB3175-002-Q1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024702
```



Seq. No. 148275

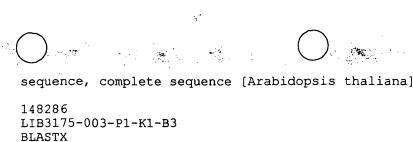
Seq. ID LIB3175-003-P1-K1-A2

Method BLASTX NCBI GI g4587615 BLAST score 406

BLAST score

```
1.0e-39
E value
                   123
Match length
% identity
                   67
                   (AC006951) putative acyl-CoA synthetase [Arabidopsis
NCBI Description
                   thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213)
                   putative acyl-CoA synthetase [Arabidopsis thaliana]
                   148276
Seq. No.
                   LIB3175-003-P1-K1-A3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q421826
BLAST score
                   667
E value
                   3.0e-70
                   144
Match length
                   88
% identity
                   chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                   >gi 298036_emb_CAA50712_ (X71878) CP29 [Arabidopsis
                   thaliana]
                   148277
Seq. No.
                   LIB3175-003-P1-K1-A4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4733953
BLAST score
                   229
                   1.0e-126
E value
Match length
                   288
                   95
% identity
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F13011 genomic
                   sequence, complete sequence
                   148278
Seq. No.
                   LIB3175-003-P1-K1-A5
Seq. ID
Method
                   BLASTX
                   g3790548
NCBI GI
                   781
BLAST score
                   1.0e-83
E value
                   150
Match length
% identity
NCBI Description
                   (AF064064) flavanone 3-hydroxylase [Arabidopsis thaliana]
                   148279
Seq. No.
                   LIB3175-003-P1-K1-A6
Seq. ID
Method
                   BLASTX
                   g3123188
NCBI GI
BLAST score
                   729
E value
                   2.0e-77
Match length
                   142
% identity
NCBI Description
                   CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis
                   thaliana] >gi_{\overline{2}511726} (AF021937) catalase 3 [Arabidopsis
                   thaliana]
Seq. No.
                   148280
                   LIB3175-003-P1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4063749
```

```
E value
                   5.0e-12
Match length
                   68
% identity
                  26
NCBI Description
                   (AC005851) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   148281
Seq. ID
                  LIB3175-003-P1-K1-B1
Method
                  BLASTN
NCBI GI
                  g4539331
BLAST score
                  67
                  2.0e-29
E value
                  203
Match length
                  83
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22I13
NCBI Description
                   (ESSA project)
                  148282
Seq. No.
                  LIB3175-003-P1-K1-B10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2351066
BLAST score
                  151
E value
                  3.0e-79
                  466
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOP9, complete sequence [Arabidopsis thaliana]
                  148283
Seq. No.
Seq. ID
                  LIB3175-003-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q1773330
BLAST score
                   634
                   2.0e-66
E value
Match length
                  141
% identity
                  87
NCBI Description
                   (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
Seq. No.
                   148284
Seq. ID
                  LIB3175-003-P1-K1-B12
Method
                  BLASTX
                  g3540199
NCBI GI
BLAST score
                   475
                  1.0e-47
E value
Match length
                  139
% identity
                  73
                   (AC004260) Putative monosaccharide transport protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  148285
Seq. ID
                  LIB3175-003-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q2281081
BLAST score
                  41
E value
                  1.0e-13
                  199
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC F18019 genomic
NCBI Description
```



NCBI GI g2633727
BLAST score 191
E value 2.0e-14
Match length 106
% identity 42
NCBI Description (Z99111) ykrT [Bacillus subtilis]

 Seq. No.
 148287

 Seq. ID
 LIB3175-003-P1-K1-B4

 Method
 BLASTN

 NCBI GI
 g4263753

 BLAST score
 269

 E value
 1.0e-149

E value 1.0eMatch length 440
% identity 98

Seq. No.

Seq. ID

Method

NCBI Description Arabidopsis thaliana chromosome V map near 60.5 cM, complete sequence [Arabidopsis thaliana]

 Seq. No.
 148288

 Seq. ID
 LIB3175-003-P1-K1-B5

 Method
 BLASTX

 NCBI GI
 g3687252

 BLAST score
 673

 E value
 6.0e-71

 Match length
 137

E value 6.0e
Match length 137
% identity 37
NCBI Description (ACO

NCBI Description (AC005169) hypothetical protein, 3' partial [Arabidopsis thaliana]

Seq. No. 148289

Seq. ID LIB3175-003-P1-K1-B6

Method BLASTN
NCBI GI g3688169
BLAST score 210
E value 1.0e-115
Match length 228
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21

(ESSAII project)

Seq. No. 148290

Seq. ID LIB3175-003-P1-K1-B7

Method BLASTX
NCBI GI g2459443
BLAST score 673
E value 5.0e-71
Match length 133
% identity 97

NCBI Description (AC002332) putative NAD(P)-dependent cholesterol

dehydrogenase [Arabidopsis thaliana]

Seq. No. 148291

```
Seq. ID
                   LIB3175-003-P1-K1-B8
Method
                   BLASTN
NCBI GI
                   q2947056
BLAST score
                   277
E value
                   1.0e-154
Match length
                   466
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20F6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148292
                   LIB3175-003-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                   q2827538
                   396
BLAST score
E value
                   0.0e+00
                   417
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17
NCBI Description
                   (ESSAII project)
Seq. No.
                   148293
Seq. ID
                  LIB3175-003-P1-K1-C1
                   BLASTX
Method
NCBI GI
                   g2244896
BLAST score
                   575
                   1.0e-59
E value
                   127
Match length
                   88
% identity
NCBI Description
                   (Z97338) similar to HSR201 protein N.tabacum [Arabidopsis
                   thaliana]
                   148294
Seq. No.
                   LIB3175-003-P1-K1-C10
Seq. ID
Method
                   BLASTX
                   g3157937
NCBI GI
BLAST score
                   657
                   1.0e-68
E value
Match length
                   150
% identity
NCBI Description
                   (AC002131) Identical to aspartic proteinase cDNA gb U51036
                   from A. thaliana. ESTs gb N96313, gb T21893, gb R30158,
                   gb T21482, gb T43650, gb R64749, gb R65157, gb T88269,
                   gb T44552, gb T22542, gb T76533, gb T44350, gb Z34591,
                   gb AA728734, gb
                   148295
Seq. No.
                  LIB3175-003-P1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3402751
BLAST score
                   43
                  8.0e-72
E value
Match length
                  146
% identity
                   (ALO31187) putative protein [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

```
LIB3175-003-P1-K1-C2
Seq. ID
                    BLASTX
Method
                    g2633727
NCBI GI
BLAST score
                    192
                    1.0e-14
E value
                    103
Match length
                    42
% identity
                    (Z99111) ykrT [Bacillus subtilis]
NCBI Description
                    148297
Seq. No.
                    LIB3175-003-P1-K1-C3
Seq. ID
                    BLASTN
Method
                    g4063735
NCBI GI
                    125
BLAST score
                    8.0e-64
E value
                    377
Match length
                    99
% identity
                    Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5
NCBI Description
                    cM, complete sequence [Arabidopsis thaliana]
                    148298
Seq. No.
                    LIB3175-003-P1-K1-C4
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2244904
BLAST score
                    570
                    7.0e-59
E value
                    136
Match length
% identity
NCBI Description
                    (Z97339) similar to hypothetical protein C02F5.7 - Caenorha
                    [Arabidopsis thaliana]
                    148299
Seq. No.
                    LIB3175-003-P1-K1-C5
Seq. ID
                    BLASTX
Method
NCBI GI
                    g2058282
BLAST score
                    518
                    9.0e-53
E value
Match length
                    125
                    82
% identity
NCBI Description
                    (X97377) atranbpla [Arabidopsis thaliana]
Seq. No.
                    148300
                    LIB3175-003-P1-K1-C6
Seq. ID
                    BLASTX
Method
                    q1076708
NCBI GI
BLAST score
                    698
                    7.0e-74
E value
                    140
Match length
                    25
% identity
                    seed tetraubiquitin - common sunflower
NCBI Description
                    >gi 303901 dbj_BAA03764 (D16248) ubiquitin [Glycine max]
                    >gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max] >gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin [Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
                    Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
                    putative polyubiquitin [Arabidopsis thaliana]
                    >gi_1096513_prf__2111434A tetraubiquitin [Helianthus
```

```
annuus]
                  148301
Seq. No.
                  LIB3175-003-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3168840
BLAST score
                  383
E value
                  6.0e-37
Match length
                  121
% identity
NCBI Description
                  (U88711) copper homeostasis factor [Arabidopsis thaliana]
Seq. No.
                  148302
                  LIB3175-003-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2618721
BLAST score
                  392
E value
                  5.0e-38
Match length
                  94
% identity
NCBI Description
                  (U49072) IAA16 [Arabidopsis thaliana]
Seq. No.
                  148303
                  LIB3175-003-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  q1175013
NCBI GI
                  521
BLAST score
                  3.0e-53
E value
Match length
                  109
                  94
% identity
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi 472877 emb CAA53477 (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
Seq. No.
                  148304
Seq. ID
                  LIB3175-003-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g2244896
BLAST score
                  302
                  5.0e-59
E value
Match length
                  127
                  83
% identity
NCBI Description
                  (Z97338) similar to HSR201 protein N.tabacum [Arabidopsis
                  thaliana
Seq. No.
                  148305
Seq. ID
                  LIB3175-003-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q1173345
BLAST score
                  513
                  3.0e-52
E value
                  139
Match length
% identity
NCBI Description
                  SEDOHEPTULOSE-1,7-BISPHOSPHATASE CHLOROPLAST PRECURSOR
                  (SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE)
                  >gi_1076403 pir S51838 sedoheptulose-1,7-biphosphatase -
```

BLAST score

```
Arabidopsis thaliana >gi 786466_bbs_159034 (S74719)
                  sedoheptulose-1,7-bisphosphatase, SBPase {EC 3.1.3.37}
                   [Arabidopsis thaliana, C24, Peptide Chloroplast, 393 aa]
                   [Arabidopsis thaliana]
Seq. No.
                  148306
Seq. ID
                  LIB3175-003-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g542157
BLAST score
                  596
E value
                  6.0e-62
Match length
                  138
                  81
% identity
                  ribosomal 5S RNA-binding protein - Rice
NCBI Description
Seq. No.
                  148307
Seq. ID
                  LIB3175-003-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  770
E value
                  2.0e-82
                  146
Match length
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  148308
Seq. ID
                  LIB3175-003-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g4586265
BLAST score
                  532
                  2.0e-54
E value
                  130
Match length
% identity
                  78
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  148309
Seq. No.
Seq. ID
                  LIB3175-003-P1-K1-D3
Method
                  BLASTX
                  g4371297
NCBI GI
BLAST score
                  303
E value
                  1.0e-27
Match length
                  59
                  100
% identity
NCBI Description
                  (AC006260) phenylalanine ammonia-lyase 1, 3' partial
                  [Arabidopsis thaliana]
Seq. No.
                  148310
Seq. ID
                  LIB3175-003-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g3157944
```

Seq. No.

148315

5.0e-77 E value 140 Match length 99 % identity (AC002131) Very strong similarity to aminomethyltransferase NCBI Description precursor gb U79769 from Mesembryanthemum crystallinum. ESTs gb  $T431\overline{6}7$ , gb T21076, gb H36999, gb T22773, gb\_N38038, gb\_T13742, gb\_Z26545, gb\_T20753 and gb\_W43123 come from this ge 148311 Seq. No. LIB3175-003-P1-K1-D5 Seq. ID BLASTX Method NCBI GI g2645971 BLAST score 531 E value 8.0e-74 141 Match length 96 % identity (AF034255) reversibly glycosylated polypeptide-3 NCBI Description [Arabidopsis thaliana] 148312 Seq. No. Seq. ID LIB3175-003-P1-K1-D7 Method BLASTX NCBI GI g132074 BLAST score 782 E value 1.0e-83 Match length 148 -% identity NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain Al precursor - Arabidopsis thaliana Seq. No. 148313 Seq. ID LIB3175-003-P1-K1-D8 Method BLASTX NCBI GI g3915032 BLAST score 481 E value 2.0e-48 Match length 122 % identity 75 ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR NCBI Description (STEAROYL-ACP DESATURASE) >gi 508603 (L34346) stearoyl-acyl carrier protein desaturase [Glycine max] Seq. No. 148314 LIB3175-003-P1-K1-D9 Seq. ID Method BLASTN g4006815 NCBI GI BLAST score 206 E value 1.0e-112 443 Match length 95 % identity NCBI Description Arabidopsis thaliana chromosome II BAC T6P5 genomic

18750

sequence, complete sequence [Arabidopsis thaliana]

```
Seq. ID
                  LIB3175-003-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q2911050
BLAST score
                  449
E value
                  1.0e-44
Match length
                  135
                  49
% identity
                  (AL021961) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                  LIB3175-003-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g166867
BLAST score
                  667
E value
                  3.0e-70
Match length
                  147
% identity
                  88
                  (J05216) ribosomal protein S11 (probable start codon at bp
NCBI Description
                   67) [Arabidopsis thaliana]
Seq. No.
                   148317
                  LIB3175-003-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2914703
                  374
BLAST score
                  7.0e-36
E value
                  127
Match length
% identity
                  (AC003974) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148318
Seq. ID
                  LIB3175-003-P1-K1-E3
Method
                  BLASTX
                  g4006890
NCBI GI
BLAST score
                   642
                   3.0e-67
E value
                   136
Match length
% identity
                   (Z99708) ubiquitin--protein ligase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   148319
Seq. ID
                   LIB3175-003-P1-K1-E4
Method
                  BLASTX
NCBI GI
                   g115783
BLAST score
                   675
                   4.0e-71
E value
Match length
                  133
% identity
                   95
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
```

148320

BLASTX

LIB3175-003-P1-K1-E5

Seq. No.

Seq. ID Method

```
NCBI GI
                   q3157937
BLAST score
                   47
E value
                   4.0e-61
Match length
                   134
% identity
                   91
NCBI Description
                   (AC002131) Identical to aspartic proteinase cDNA gb U51036
                   from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,
                   gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269, gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
                   gb_AA728734, gb
Seq. No.
                   148321
Seq. ID
                   LIB3175-003-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   g3395421
BLAST score
                   440
                   0.0e+00
E value
                   454
Match length
                   99
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T19C21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   148322
Seq. No.
Seq. ID
                   LIB3175-003-P1-K1-E7
Method
                   BLASTX
                   g602076
NCBI GI
                   376
BLAST score
                   3.0e-36
E value
Match length
                   84
% identity
                   (X77456) pentameric polyubiquitin [Nicotiana tabacum]
NCBI Description
Seq. No.
                   148323
Seq. ID
                   LIB3175-003-P1-K1-E8
Method
                   BLASTX
NCBI GI
                   q135444
BLAST score
                   582
                   2.0e-60
E value
Match length
                   120
% identity
NCBI Description
                   TUBULIN BETA-1 CHAIN >gi 16122 emb CAA38630 (X54852)
                   beta-tubulin [Avena sativa]
Seq. No.
                   148324
                   LIB3175-003-P1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1084415
BLAST score
                   335
E value
                   2.0e-31
Match length
                   111
                   60
% identity
NCBI Description
                   RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_
                   (D26182) RNA-binding glycine rich protein (RGP-2)
                   [Nicotiana sylvestris]
                   148325
Seq. No.
Seq. ID
                   LIB3175-003-P1-K1-F1
```

```
BLASTX
Method
NCBI GI
                  g2781354
BLAST score
                  169
E value
                  2.0e-31
Match length
                  125
% identity
NCBI Description
                  (AC003113) F2401.10 [Arabidopsis thaliana]
                  148326
Seq. No.
Seq. ID
                  LIB3175-003-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g119143
BLAST score
                  639
                  6.0e-67
E value
                  123
Match length
                  99
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_81606_pir__S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453
                  (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                  >qi 1369927 emb CAA34454 (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                  >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                  148327
Seq. ID
                  LIB3175-003-P1-K1-F12
Method
                  BLASTN
NCBI GI
                  q1305454
BLAST score
                  72
                  5.0e-32
E value
                  147
Match length
                  93
% identity
                  Arabidopsis thaliana cytosolic cyclophilin (ROC3) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  148328
                  LIB3175-003-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006827
BLAST score
                  360
E value
                  3.0e-34
Match length
                  150
% identity
                  46
NCBI Description
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
                  148329
Seq. No.
                  LIB3175-003-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462834
BLAST score
                  199
                  2.0e-15
E value
Match length
                  107
% identity
                  41
                  (AF000657) hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

```
148330
Seq. No.
Seq. ID
                  LIB3175-003-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g132102
BLAST score
                  246
E value
                  5.0e-21
                  79
Match length
% identity
                  68
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir
                                                              RKMUB2
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B2 precursor - Arabidopsis thaliana >gi 16194 emb CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  148331
Seq. No.
Seq. ID
                  LIB3175-003-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g2642158
                  429
BLAST score
                  3.0e-42
E value
                  117
Match length
% identity
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  148332
Seq. No.
                  LIB3175-003-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q543565
BLAST score
                  218
                  1.0e-17
E value
Match length
                  87
% identity
NCBI Description
                  hypothetical 10.0K protein - Zinnia elegans
                  >gi 493721 dbj BAA06462 (D30802) TED4 [Zinnia elegans]
                  >gi 641903 (U19266) putative nonspecific lipid transfer;
                  auxin induced gene [Zinnia elegans]
Seq. No.
                  148333
Seq. ID
                  LIB3175-003-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g2244759
BLAST score
                  606
E value
                  4.0e-63
                  144
Match length
                  75
% identity
NCBI Description
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
                  148334
Seq. No.
Seq. ID
                  LIB3175-003-P1-K1-G1
Method
                  BLASTX
                  g3402713
NCBI GI
BLAST score
                  731
E value
                  1.0e-77
Match length
                  147
% identity
                  97
```

```
NCBI Description
                   (AC004261) hypothetical protein [Arabidopsis thaliana]
 Seq. No.
                   148335
                   LIB3175-003-P1-K1-G12
 Seq. ID
 Method
                   BLASTX
 NCBI GI
                   g3915826
 BLAST score
                   589
 E value
                   4.0e-61
                   137
 Match length
 % identity
                   60S RIBOSOMAL PROTEIN L5
 NCBI Description
 Seq. No.
                   148336
                   LIB3175-003-P1-K1-G2
 Seq. ID
 Method
                   BLASTN
 NCBI GI
                   q4467094
 BLAST score
                   411
                   0.0e + 00
 E value
Match length
                   433
                   99
 % identity
 NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
                    (ESSA project)
 Seq. No.
                   148337
 Seq. ID
                   LIB3175-003-P1-K1-G5
Method
                   BLASTX
 NCBI GI
                   g3157927
 BLAST score
                   288
 E value
                   8.0e-26
                   90
Match length
                   63
 % identity
                    (AC002131) Contains similarity to GDP-dissociation
 NCBI Description
                   inhibitor gb L07918 from Mus musculus. [Arabidopsis
                   thaliana]
                   148338
 Seq. No.
 Seq. ID
                   LIB3175-003-P1-K1-G6
Method
                   BLASTX
 NCBI GI
                   q2129978
 BLAST score
                   571
                   6.0e-59
 E value
Match length
                   122
 % identity
                   60
 NCBI Description
                   calmodulin (clone PCM5) - potato >gi 677903 (U20295)
                   calmodulin [Solanum tuberosum] >gi_687704 (U20294)
                   calmodulin [Solanum tuberosum] >gi_687706 (U20296)
                   calmodulin [Solanum tuberosum] >gi_687708 (U20297)
                   calmodulin [Solanum tuberosum]
 Seq. No.
                   148339
                   LIB3175-003-P1-K1-G7
 Seq. ID
Method
                   BLASTN
 NCBI GI
                   q2737903
 BLAST score
                   387
 E value
                   0.0e+00
Match length
                   419
 % identity
                   98
```

## NCBI Description Arabidopsis thaliana retrotransposon TSCL genomic sequence 148340 Seq. No. Seq. ID LIB3175-003-P1-K1-G8 Method BLASTX NCBI GI g267070 BLAST score 622 E value 5.0e-65 Match length 118 % identity 97 NCBI Description TUBULIN ALPHA-6 CHAIN >gi\_282852\_pir\_\_JQ1597 tubulin alpha-6 chain - Arabidopsis thaliana >gi 166920 (M84699) TUA6 [Arabidopsis thaliana] >gi\_2244853\_emb\_CAB10275\_ (Z97337) tubulin alpha-6 chain (TUA6) [Arabidopsis thalianal 148341 Seq. No. LIB3175-003-P1-K1-G9 Seq. ID BLASTX Method NCBI GI g4337175 BLAST score 613 6.0e-64 E value 140 Match length % identity NCBI Description (ACO06416) ESTs gb\_T20589, gb\_T04648, gb\_AA597906, gb\_T04111, gb\_R84180, gb\_R65428, gb\_T44439, gb\_T76570, gb\_R90004, gb\_T45020, gb\_T42457, gb\_T20921, gb\_AA042762 and gb\_AA720210 come from this gene. [Arabidopsis thaliana] Seq. No. 148342 Seq. ID LIB3175-003-P1-K1-H1 Method BLASTX g2245141 NCBI GI BLAST score 509 E value 1.0e-51 Match length 98 % identity 99 NCBI Description (Z97344) acetylornithine deacetylase [Arabidopsis thaliana] Seq. No. 148343 Seq. ID LIB3175-003-P1-K1-H10 Method BLASTX NCBI GI g3024666 BLAST score 585 E value 1.0e-60 Match length 137 84 % identity NCBI Description STRICTOSIDINE SYNTHASE 1/2 PRECURSOR >gi 1754983 (U43713) strictosidine synthase [Arabidopsis thaliana] >gi 1754985 (U43945) strictosidine synthase [Arabidopsis thaliana] Seq. No. 148344 Seq. ID LIB3175-003-P1-K1-H11 Method BLASTX g2497753 NCBI GI BLAST score 263

7.0e-23

E value

```
95
Match length
                  49
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi 1321915 emb_CAA65477_ (X96716) lipid transfer protein
                  [Prunus dulcis]
                  148345
Seq. No.
                  LIB3175-003-P1-K1-H12
Seq. ID
Method
                  BLASTN
                  q4519187
NCBI GI
BLAST score
                  368
E value
                  0.0e + 00
                  416
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                  K1G2, complete sequence
Seq. No.
                  148346
                  LIB3175-003-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351239
BLAST score
                  355
                  1.0e-33
E value
                  99
Match length
                  65
% identity
                  THIOREDOXIN M-TYPE PRECURSOR (TRX-M) >gi 481594 pir S38909
NCBI Description
                  thioredoxin m precursor - garden pea
                  >gi_431957_emb_CAA53900_ (X76269) thioredoxin m [Pisum
                  sativum]
Seq. No.
                  148347
Seq. ID
                  LIB3175-003-P1-K1-H3
Method
                  BLASTX
                  g2981475
NCBI GI
BLAST score
                  563
                  5.0e-58
E value
                  140
Match length
% identity
                   (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
NCBI Description
                  domestica]
Seq. No.
                  148348
                  LIB3175-003-P1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2911797
BLAST score
                  217
                  1.0e-17
E value
Match length
                  85
                   47
% identity
                  (AF008183) 4-coumarate:CoA ligase 2 [Populus balsamifera
NCBI Description
                  subsp. trichocarpa X Populus deltoides]
Seq. No.
                  148349
                  LIB3175-003-P1-K1-H8
Seq. ID
Method
                  BLASTN
                  g3335356
NCBI GI
```

299

BLAST score

```
1.0e-167
E value
Match length
                  441
                  98
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  148350
Seq. No.
Seq. ID
                  LIB3175-003-P1-K1-H9
Method
                  BLASTX
                  g132110
NCBI GI
BLAST score
                  49
                  2.0e-67
E value
Match length
                  136
                  95
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 3B) >qi 68060 pir RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  148351
Seq. No.
Seq. ID
                  LIB3175-004-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  g2351072
BLAST score
                  47
                  1.0e-17
E value
Match length
                  125
% identity
                  90
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYC6, complete sequence [Arabidopsis thaliana]
                  148352
Seq. No.
                  LIB3175-004-P1-K1-A10
Seq. ID
Method
                  BLASTX
                  q3859606
NCBI GI
                  596
BLAST score
                  5.0e-62
E value
Match length
                  132
% identity
                   (AF104919) contains similarity to cysteine proteases (Pfam:
NCBI Description
                  PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]
                  148353
Seq. No.
                  LIB3175-004-P1-K1-A11
Seq. ID
                  BLASTN
Method
                  g3176701
NCBI GI
                  117
BLAST score
                  3.0e-59
E value
                  247
Match length
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC T20K24 genomic
NCBI Description
```

Seq. No. 148354

Seq. ID LIB3175-004-P1-K1-A12

Method BLASTN

sequence, complete sequence [Arabidopsis thaliana]

```
q4220631
NCBI GI
BLAST score
                   121
                   2.0e-61
E value
Match length
                   402
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K5J14, complete sequence [Arabidopsis thaliana]
                   148355
Seq. No.
Seq. ID
                   LIB3175-004-P1-K1-A3
Method
                  BLASTX
NCBI GI
                   q2911057
BLAST score
                   199
                   5.0e-16
E value
                   51
Match length
% identity
                   (AL021961) caffeoyl-CoA O-methyltransferase - like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   148356
Seq. ID
                   LIB3175-004-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q3668175
BLAST score
                   582
E value
                   3.0e-60
                   119
Match length
                   94
% identity
                   (AB006778) vegetative storage protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   148357
Seq. ID
                   LIB3175-004-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q4567232
BLAST score
                   64
                   1.0e-34
E value
Match length
                  87
% identity
NCBI Description
                   (AC007119) putative 40S ribosomal protein S25 [Arabidopsis
                   thaliana]
                   148358
Seq. No.
                   LIB3175-004-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2760833
BLAST score
                   357
                   5.0e-34
E value
Match length
                  74
% identity
                   99
                   (AC003105) unknown protein [Arabidopsis thaliana]
NCBI Description
                   148359
Seq. No.
Seq. ID
                  LIB3175-004-P1-K1-B10
Method
                  BLASTX
                  g2146728
NCBI GI
BLAST score
                  144
E value
                   6.0e-09
```

```
98
Match length
                   46
% identity
                  cyclin cyclb - Arabidopsis thaliana >gi_1360646 (L27223)
NCBI Description
                   cyclin [Arabidopsis thaliana]
                   148360
Seq. No.
                   LIB3175-004-P1-K1-B12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4159709
BLAST score
                   364
E value
                   0.0e + 00
                   368
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLN21, complete sequence
                   148361
Seq. No.
Seq. ID
                   LIB3175-004-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   q4567235
                   550
BLAST score
E value
                   2.0e-56
                   119
Match length
% identity
                   (AC007119) putative phosphatidylinositol/phophatidylcholine
NCBI Description
                   transfer protein [Arabidopsis thaliana]
                   148362
Seq. No.
Seq. ID
                   LIB3175-004-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q3785978
BLAST score
                   682
E value
                   5.0e-72
Match length
                   140
% identity
                   93
                   (AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148363
Seq. ID
                   LIB3175-004-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g4033467
BLAST score
                   416
                   5.0e-41
E value
Match length
                   86
                   51
% identity
                  ARGININE/SERINE-RICH SPLICING FACTOR RSP31
NCBI Description
                   >gi 1707366 emb CAA67798 (X99435) splicing factor
                   [Arabidopsis thaliana]
                   148364
Seq. No.
                   LIB3175-004-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4678943
BLAST score
                   266
E value
                   2.0e-23
Match length
                   102
% identity
                   30
```

```
NCBI Description
                   (AL049711) putative protein [Arabidopsis thaliana]
                   148365
Seq. No.
Seq. ID
                   LIB3175-004-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   q1246019
BLAST score
                   670
E value
                   1.0e-70
Match length
                   131
% identity
                   97
NCBI Description
                   (S80554) chalcone synthase, CHS [Arabidopsis, Landsberg
                   erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]
Seq. No.
                   148366
Seq. ID
                   LIB3175-004-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   g2244788
BLAST score
                   323
                   0.0e + 00
E value
                   408
Match length
% identity
                   93
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   148367
Seq. No.
Seq. ID
                   LIB3175-004-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g67842
BLAST score
                   360
E value
                   3.0e-34
Match length
                   84
% identity
NCBI Description
                  H+-transporting ATP synthase (EC 3.6.1.34) beta chain -
                   spinach chloroplast >gi 343355 (J01441) ATPase beta subunit
                   [Spinacia oleracea] >gi 223530 prf 0811259A ATPase beta
                   [Spinacia oleracea]
Seq. No.
                   148368
Seq. ID
                   LIB3175-004-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g3661595
BLAST score
                   370
E value
                   2.0e-35
Match length
                   68
% identity
                   100
NCBI Description
                   (AF091844) aminoalcoholphosphotransferase [Arabidopsis
                   thaliana]
Seq. No.
                  148369
Seq. ID
                  LIB3175-004-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2944446
BLAST score
                  320
E value
                  1.0e-29
                  77
Match length
% identity
                   78
                   (AF050756) cysteine endopeptidase precursor [Ricinus
NCBI Description
```

```
communis]
                  148370
Seq. No.
Seq. ID
                  LIB3175-004-P1-K1-C2
                  BLASTN
Method
                  g1707006
NCBI GI
BLAST score
                  245
                  1.0e-135
E value
                  390
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T1B8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148371
                  LIB3175-004-P1-K1-C3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3702731
                  302
BLAST score
                  1.0e-169
E value
                  357
Match length
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFC19, complete sequence [Arabidopsis thaliana]
                  148372
Seq. No.
                  LIB3175-004-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2351062
                  48
BLAST score
                  9.0e-18
E value
                  147
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAH20, complete sequence [Arabidopsis thaliana]
                  148373
Seq. No.
Seq. ID
                  LIB3175-004-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3122673
BLAST score
                   609
E value
                  2.0e-63
Match length
                  140
                  84
% identity
                  60S RIBOSOMAL PROTEIN L15 >gi 2245027 emb CAB10447
NCBI Description
                   (Z97341) ribosomal protein [Arabidopsis thaliana]
                  148374
Seq. No.
```

Seq. ID LIB3175-004-P1-K1-C6

Method BLASTX
NCBI GI g3914370
BLAST score 631
E value 5.0e-66
Match length 149
% identity 84

NCBI Description GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT)

>gi\_419754\_pir\_\_S31083 glycerol-3-phosphate

O-acyltransferase (EC 2.3.1.15) precursor - Arabidopsis

```
thaliana >gi_217845_dbj_BAA00575_ (D00672)
                  glycerol-3-phosphate acyltransferase [Arabidopsis thaliana]
                  >gi_217847_dbj_BAA00576_ (D00673) glycerol-3-phosphate
                  acyltransferase precursor [Arabidopsis thaliana]
Seq. No.
                  148375
                  LIB3175-004-P1-K1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3128135
BLAST score
                  318
E value
                  1.0e-179
Match length
                  366
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19E1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148376
Seq. ID
                  LIB3175-004-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  g4587525
BLAST score
                  142
E value
                  8.0e-09
                  95
Match length
                  34
% identity
                   (AC007060) Contains the PF 00650 CRAL/TRIO
NCBI Description
                  phosphatidyl-inositol-transfer protein domain.
                  gb T76582, gb N06574 and gb Z25700 come from this gene.
                   [Arabidopsis thaliana]
                  148377
Seq. No.
Seq. ID
                  LIB3175-004-P1-K1-D1
Method
                  BLASTX
                  q481031
NCBI GI
BLAST score
                  478
E value
                  4.0e-48
                  127
Match length
% identity
                  transcription factor SF3 - common sunflower
NCBI Description
Seq. No.
                  148378
Seq. ID
                  LIB3175-004-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                  178
E value
                  2.0e-13
Match length
                  36
% identity
                  94
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
Seq. No.
                  148379
                  LIB3175-004-P1-K1-D11
Seq. ID
Method
                  BLASTN
                  g4469002
NCBI GI
BLAST score
                  254
E value
                  1.0e-141
Match length
                  399
```

```
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
NCBI Description
                  (ESSA project)
                  148380
Seq. No.
                  LIB3175-004-P1-K1-D2
Seq. ID
Method
                  BLASTX
                  g3184100
NCBI GI
BLAST score
                  181
E value
                  2.0e-13
Match length
                  51
% identity
                  61
                  (AL023777) rna binding protein [Schizosaccharomyces pombe]
NCBI Description
                  148381
Seq. No.
Seq. ID
                  LIB3175-004-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q4314363
BLAST score
                  564
E value
                  3.0e-58
Match length
                  121
% identity
                  (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148382
                  LIB3175-004-P1-K1-D5
Seq. ID
Method
                  BLASTN
                  g16452
NCBI GI
BLAST score
                  52
                  6.0e-21
E value
                  81
Match length
% identity
                  91
                  Arabidopsis thaliana atslA gene for ribulose 1.5-biphoshate
NCBI Description
                  carboxylase small subunit (EC 4.1.1.39)
Seq. No.
                  148383
Seq. ID
                  LIB3175-004-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g3687239
BLAST score
                  612
E value
                  8.0e-64
Match length
                  123
% identity
                  (AC005169) putative clathrin coat assembly protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  148384
                  LIB3175-004-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4589366
                  275
BLAST score
                  2.0e-24
E value
Match length
                  117
% identity
                  (AF140505) DEAD box RNA helicase [Candida albicans]
NCBI Description
Seq. No.
                  148385
```

```
LIB3175-004-P1-K1-E1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2497486
BLAST score
                   628
E value
                   1.0e-65
Match length
                   123
% identity
                   99
                   URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP
NCBI Description
                   KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis
                   thaliana]
Seq. No.
                   148386
Seq. ID
                   LIB3175-004-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   q166834
BLAST score
                   84
E value
                   3.0e-68
Match length
                   137 ...
% identity
                   97
NCBI Description
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
                   activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                   Rubisco activase [Arabidopsis thaliana]
Seq. No.
                   148387
                  LIB3175-004-P1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2182287
                   327
BLAST score
                   0.0e+00
E value
Match length
                   355
% identity
                   98
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T7N9,
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   148388
                  LIB3175-004-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4490331
BLAST score
                   583
E value
                   2.0e-60
Match length
                   131
% identity
NCBI Description
                   (AL035656) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   148389
                  LIB3175-004-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024697
BLAST score
                   379
                  1.0e-36
E value
Match length
                  79
% identity
                  T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)
NCBI Description
                   (CCT-EPSILON) >gi 2213618 (AC000103) F21J9.12 [Arabidopsis
                  thaliana]
Seq. No.
                  148390
```

Seq. ID

```
LIB3175-004-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4102839
BLAST score
                   251
E value
                   2.0e-21
Match length
                  136
% identity
                   40
NCBI Description
                   (AF016713) LeOPT1 [Lycopersicon esculentum]
                  148391
Seq. No.
Seq. ID
                  LIB3175-004-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q3702735
BLAST score
                   41
                   7.0e-14
E value
                   61
Match length
% identity
                   92
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148392
Seq. ID
                  LIB3175-004-P1-K1-E7
Method
                  BLASTX
NCBI GI
                   q4455215
                   146
BLAST score
                  2.0e-09
E value
                   87
Match length
% identity
                   41
                   (AL035440) putative homeodomain protein [Arabidopsis
NCBI Description
                   thaliana]
                   148393
Seq. No.
                  LIB3175-004-P1-K1-E8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2829899
BLAST score
                   224
                   1.0e-18
E value
Match length
                   71
                   61
% identity
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   148394
Seq. ID
                   LIB3175-004-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2493646
BLAST score
                   267
E value
                   1.0e-23
Match length
                   70
                   74
% identity
                  MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR >gi 309559
NCBI Description
                   (L21008) chaperonin 60 [Zea mays] >gi_309561 (\overline{L}21006)
                  mitochondrial chaperonin 60 [Zea mays]
Seq. No.
                   148395
                  LIB3175-004-P1-K1-F11
```

```
Method
                   BLASTX
NCBI GI
                   g4006848
                   309
BLAST score
                   3.0e-28
E value
Match length
                   107
                   53
% identity
NCBI Description
                   (AJ131433) selenocysteine methyltransferase [Astragalus
                   bisulcatus]
                   148396
Seq. No.
                   LIB3175-004-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129639
BLAST score
                   184
                   9.0e-14
E value
Match length
                   72
% identity
                   57
                   luminal binding protein (BiP) - Arabidopsis thaliana
NCBI Description
                   >gi 1303695 dbj_BAA12348 (D84414) luminal binding protein
                   (BiP) [Arabidopsis thaliana]
Seq. No.
                   148397
Seq. ID
                   LIB3175-004-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q2760843
BLAST score
                   345
E value
                   2.0e-32
Match length
                   142
% identity
                   56
                   (AC003105) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148398
Seq. ID
                   LIB3175-004-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g4741960
BLAST score
                   597
E value
                   5.0e-62
                   132
Match length
                   86
% identity
NCBI Description
                   (AF134130) Lhcb6 protein [Arabidopsis thaliana]
Seq. No.
                   148399
                   LIB3175-004-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1174162
BLAST score
                   461
                   4.0e-46
E value
Match length
                   82
                   99
% identity
NCBI Description
                   (U44976) ubiquitin-conjugating enzyme [Arabidopsis
                   thaliana] >gi 3746915 (AF091106) E2
                   ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                   148400
Seq. No.
                   LIB3175-004-P1-K1-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4096078
```

E value

```
BLAST score
                  48
E value
                  7.0e-18
Match length
                  175
                  93
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T5A14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  148401
Seq. No.
                  LIB3175-004-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4417271
BLAST score
                   755
                  1.0e-80
E value
                  143
Match length
                  98
% identity
                   (AC007019) putative cellulose synthase catalytic subunit
NCBI Description
                   [Arabidopsis thaliana]
                   148402
Seq. No.
Seq. ID
                  LIB3175-004-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g1175012
BLAST score
                  626
E value
                  2.0e-65
                  136
Match length
                  91
% identity
                  PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
NCBI Description
                  B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane
                  protein TMP-B [Arabidopsis thaliana]
Seq. No.
                  148403
Seq. ID
                  LIB3175-004-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g1408473
BLAST score
                  343
E value
                  2.0e-32
                  79
Match length
% identity
                   (U48939) actin depolymerizing factor 2 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148404
Seq. ID
                  LIB3175-004-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g4138137
BLAST score
                  363
                  1.0e - 34
E value
                  128
Match length
                  55
% identity
NCBI Description
                  (AJ012796) ss-galactosidase [Lycopersicon esculentum]
Seq. No.
                  148405
                  LIB3175-004-P1-K1-G4
Seq. ID
Method
                  BLASTX
                  g3157937
NCBI GI
BLAST score
                  640
```

18768

.....

4.0e-67

```
132
Match length
                   97
% identity
NCBI Description
                   (AC002131) Identical to aspartic proteinase cDNA gb U51036
                   from A. thaliana. ESTs gb N96313, gb_T21893, gb R3\overline{0}158,
                   gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269,
                   gb T44552, gb T22542, gb T76533, gb T44350, gb Z34591,
                   gb_AA728734, gb
Seq. No.
                   148406
Seq. ID
                   LIB3175-004-P1-K1-G5
Method
                   BLASTN
NCBI GI
                   q3650026
BLAST score
                   397
                   0.0e + 00
E value
Match length
                   445
                   97
% identity
                   Arabidopsis thaliana chromosome II BAC T26I20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   148407
Seq. No.
                   LIB3175-004-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3747111
BLAST score
                   573
E value
                   3.0e-59
Match length
                   127
% identity
                   (AF095641) MTN3 homolog [Arabidopsis thaliana]
NCBI Description
                   148408
Seq. No.
Seq. ID
                   LIB3175-004-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   q3367500
BLAST score
                   288
E value
                   1.0e-161
Match length
                   428
% identity
                   98
                   REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
NCBI Description
                   TO: 93489, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148409
Seq. ID
                   LIB3175-004-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   q3668080
BLAST score
                   383
E value
                   4.0e-37
Match length
                   96
% identity
                   (AC004667) unknown protein [Arabidopsis thaliana]
NCBI Description
                   148410
Seq. No.
Seq. ID
                   LIB3175-004-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g3107903
BLAST score
                   254
E value
                   5.0e-22
Match length
                   66
```

```
% identity
                  (D83719) polycomb-like protein [Daucus carota]
NCBI Description
Seq. No.
                  148411
                  LIB3175-004-P1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4263774
BLAST score
                   426
E value
                  0.0e + 00
Match length
                  442
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T20F21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148412
Seq. ID
                  LIB3175-004-P1-K1-H10
Method
                  BLASTN
NCBI GI
                  g2342717
                  97
BLAST score
                  4.0e-47
E value
Match length
                  282
% identity
                  Arabidopsis thaliana chromosome II BAC T14G11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  148413
Seq. No.
                  LIB3175-004-P1-K1-H11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3355463
BLAST score
                  37
E value
                  2.0e-11
                  357
Match length
                  85
% identity
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  148414
Seq. No.
                  LIB3175-004-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q535780
BLAST score
                  706
E value
                  8.0e-75
Match length
                  134
                  100
% identity
NCBI Description
                  (D26609) transmembrane protein [Arabidopsis thaliana]
Seq. No.
                  148415
                  LIB3175-004-P1-K1-H3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g81952
BLAST score
                  662
E value
                  1.0e-69
Match length
                  147
                  87
% identity
                  tubulin beta-2 chain - garden pea (fragment)
NCBI Description
                  148416
Seq. No.
```

```
LIB3175-004-P1-K1-H4
Seq. ID
Method
                   BLASTX
                   g2493045
NCBI GI
BLAST score
                   566
                   2.0e-58
E value
Match length
                   131
% identity
                   84
NCBI Description
                   ATP SYNTHASE DELTA' CHAIN, MITOCHONDRIAL PRECURSOR
                   >gi_1655484_dbj_BAA13601_ (D88376) delta-prime subunit of
                   mitochondrial FI-ATPase [Arabidopsis thaliana]
Seq. No.
                   148417
                   LIB3175-004-P1-K1-H6
Seq. ID
Method
                   BLASTX
                   q4586265
NCBI GI
                   375
BLAST score
E value
                   4.0e-42
                   129
Match length
                   71
% identity
                   (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148418
Seq. ID
                   LIB3175-004-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g1172872
BLAST score
                   468
E value
                   5.0e-47
                   119
Match length
                   79
% identity
                   CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718
NCBI Description
                   drought-inducible cysteine proteinase (\overline{\text{EC}} 3.4.\overline{22}.-) RD19A
                   precursor - Arabidopsis thaliana >gi 435618 dbj BAA02373
                   (D13042) thiol protease [Arabidopsis thaliana]
                   >gi 4539328 emb CAB38829.1 (AL035679) drought-inducible
                   cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                   148419
                   LIB3175-004-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4741962
BLAST score
                   409
E value
                   5.0e-40
Match length
                   118
% identity
NCBI Description
                   (AF134131) PsbS protein [Arabidopsis thaliana]
Seq. No.
                   148420
                   LIB3175-004-P1-K1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3046847
BLAST score
                   143
E value
                   1.0e-74
Match length
                   355
                   96
% identity
                   Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
NCBI Description
                   K11J9, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                  148421
                  LIB3175-005-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2160716
BLAST score
                  349
E value
                  0.0e + 00
Match length
                  386
                  97
% identity
NCBI Description
                  Arabidopsis thaliana GUT15 mRNA, complete cds
                  148422
Seq. No.
Seq. ID
                  LIB3175-005-P1-K1-A2
Method
                  BLASTX
                  q4741940
NCBI GI
                  609
BLAST score
                  2.0e-63
E value
Match length
                  135
% identity
                  62
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
                  148423
Seq. No.
Seq. ID
                  LIB3175-005-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3860258
BLAST score
                  84
                  5.0e-14
E value
                  79
Match length
                  56
% identity
                  (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148424
                  LIB3175-005-P1-K1-A4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4539303
BLAST score
                  604
E value
                  7.0e-63
Match length
                  139
% identity
NCBI Description
                  (AL049480) putative protein [Arabidopsis thaliana]
                  148425
Seq. No.
Seq. ID
                  LIB3175-005-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q119143
BLAST score
                  50
E value
                  6.0e-65
Match length
                  129
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
                  >gi_81606_pir__S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                  (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi_1369927_emb_CAA34454 (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi 1369928 emb CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
```

```
>gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
```

148426 Seq. No. Seq. ID LIB3175-005-P1-K1-A6 Method BLASTX NCBI GI g4091810 BLAST score 254 7.0e-22 E value 79 Match length

NCBI Description (AF053345) fatty acid elongase 3-ketoacyl-CoA synthase 1

[Arabidopsis thaliana]

148427 Seq. No.

% identity

LIB3175-005-P1-K1-A7 Seq. ID

70

Method BLASTX NCBI GI g4185505 BLAST score 370 E value 2.0e-35 Match length 101 % identity 73

NCBI Description (AF101038) nonspecific lipid-transfer protein precursor

[Brassica napus]

148428 Seq. No.

LIB3175-005-P1-K1-A8 Seq. ID

Method BLASTN g3176695 NCBI GI 32 BLAST score E value 1.0e-08 Match length 68

% identity

Arabidopsis thaliana chromosome I BAC F14J9 genomic NCBI Description

sequence contains phyA marker, complete sequence

[Arabidopsis thaliana]

148429 Seq. No.

LIB3175-005-P1-K1-A9 Seq. ID

Method BLASTX NCBI GI q4140326 BLAST score 252 E value 1.0e-21 Match length 98 % identity

NCBI Description (AL031282) dJ283E3.6.1 (PUTATIVE novel protein similar to

many (archae) bacterial, worm and yeast hypothetical

proteins) [Homo sapiens]

148430 Seq. No.

Seq. ID LIB3175-005-P1-K1-B10

BLASTX Method NCBI GI g3360289 464 BLAST score 6.0e-47 E value Match length 131 % identity

NCBI Description (AF023164) leucine-rich repeat transmembrane protein kinase





```
148431
Seq. No.
Seq. ID
                   LIB3175-005-P1-K1-B11
Method
                   BLASTN
NCBI GI
                   g3241917
BLAST score
                   331
E value
                   0.0e + 00
Match length
                   343
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K19B1, complete sequence [Arabidopsis thaliana]
                   148432
Seq. No.
                   LIB3175-005-P1-K1-B2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1332579
                                                                  y...(1)
BLAST score
                   535
                   8.0e-55
E value
                   109
Match length
                   10
% identity
NCBI Description
                   (X98063) polyubiquitin [Pinus sylvestris]
                   148433
Seq. No.
Seq. ID
                   LIB3175-005-P1-K1-B3
Method
                   BLASTN
NCBI GI
                   g2191126
BLAST score
                   325
                   0.0e+00
E value
Match length
                   381
                   95
% identity
                  Arabidopsis thaliana BAC IG002N01
NCBI Description
Seq. No.
                   148434
Seq. ID
                   LIB3175-005-P1-K1-B4
Method
                   BLASTX
NCBI GI
                   q4678276
BLAST score
                   589
                   3.0e-61
E value
Match length
                   117
% identity
                   97
NCBI Description
                  (AL049660) putative protein [Arabidopsis thaliana]
Seq. No.
                   148435
                   LIB3175-005-P1-K1-B5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   643
                   2.0e-67
E value
Match length
                   126
% identity
                   97
```

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll

a/b-binding protein ab165 - Arabidopsis thaliana

>gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding

protein (LHCP AB 65) [Arabidopsis thaliana]

>gi\_16372\_emb\_CAA27541\_ (X03908) chlorophyll a/b binding

NCBI Description

Seq. No.

148441

.

```
protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   148436
Seq. ID
                   LIB3175-005-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g4741940
BLAST score
                   536
E value
                   4.0e-55
Match length
                   105
% identity
                   96
                   (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148437
                   LIB3175-005-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829899
BLAST score
                   370
E value
                   2.0e-35
Match length
                   102
% identity
                   67
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp_AJ001449_2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
Seq. No.
                   148438
                   LIB3175-005-P1-K1-B8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4589427
BLAST score
                   166
E value
                   3.0e-88
Match length
                   301
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFG13, complete sequence
                   148439
Seq. No.
Seq. ID
                   LIB3175-005-P1-K1-B9
Method
                   BLASTN
NCBI GI
                   g3080430
BLAST score
                   219
E value
                   1.0e-120
                   283
Match length
                   94
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19
                   (ESSAII project)
Seq. No.
                   148440
                   LIB3175-005-P1-K1-C1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2435510
BLAST score
                   196
E value
                   1.0e-106
Match length
                   457
% identity
                   98
```

18775

Arabidopsis thaliana BAC TM017A05

Method

BLASTX

LIB3175-005-P1-K1-C2 Seq. ID Method BLASTX NCBI GI g1350680 BLAST score 628 E value 1.0e-65 123 Match length % identity 96 NCBI Description 60S RIBOSOMAL PROTEIN L1 148442 Seq. No. LIB3175-005-P1-K1-C3 Seq. ID Method BLASTX NCBI GI g2213622 BLAST score 380 1.0e-36 E value 79 Match length 99 % identity NCBI Description (AC000103) F21J9.25 [Arabidopsis thaliana] 148443 Seq. No. LIB3175-005-P1-K1-C5 Seq. ID Method BLASTX NCBI GI q1531762 BLAST score 191 2.0e-14 E value Match length 36 100 % identity NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis thaliana] 148444 Seq. No. Seq. ID LIB3175-005-P1-K1-C6 Method BLASTN NCBI GI g2264319 102 BLAST score 4.0e-50 E value Match length 298 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MXA21, complete sequence [Arabidopsis thaliana] 148445 Seq. No. Seq. ID LIB3175-005-P1-K1-D1 Method BLASTX g115783 NCBI GI BLAST score 623 4.0e-65 E value 126 Match length % identity 94 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana] Seq. No. 148446 Seq. ID LIB3175-005-P1-K1-D10

NCBI GI

q417103

```
g4263703
NCBI GI
BLAST score
                  202
E value
                  1.0e-15
Match length
                  89
% identity
                  54
                   (AC006223) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  148447
Seq. No.
                  LIB3175-005-P1-K1-D3
Seq. ID
Method
                  BLASTN
                  g2696018
NCBI GI
BLAST score
                  44
E value
                  7.0e-16
                  76
Match length
                  89
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC9, complete sequence [Arabidopsis thaliana]
                  148448
Seq. No.
                  LIB3175-005-P1-K1-D4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120675
BLAST score
                   472
                  2.0e-47
E value
Match length
                  116
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                  >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                  >gi 21143 emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                  alba]
Seq. No.
                  148449
Seq. ID
                  LIB3175-005-P1-K1-D6
Method
                  BLASTX
                  q2244977
NCBI GI
                   462
BLAST score
                  3.0e-46
E value
                  106
Match length
% identity
                   (Z97340) cysteine proteinase [Arabidopsis thaliana]
NCBI Description
                  148450
Seq. No.
Seq. ID
                  LIB3175-005-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g2760172
BLAST score
                  126
                  9.0e-65
E value
                  170
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148451
Seq. ID
                  LIB3175-005-P1-K1-D8
Method
                  BLASTX
```

BLAST score E value 1.0e-31 Match length 68 % identity 99 HISTONE H3.2, MINOR >gi\_282871\_pir\_\_ S24346 histone NCBI Description H3.3-like protein - Arabidopsis thaliana >gi 16324 emb CAA42957 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 404825 emb CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi 488563 (U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa]  $>gi_488577$  (U09465) histone H3.2 [Medicago sativa] >gi 510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum]  $>gi_1\overline{435157}$  emb CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >qi 2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi 3273350 dbj BAA31218 (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_ (AL035708) Histon H3 [Arabidopsis thaliana] Seq. No. 148452 Seq. ID LIB3175-005-P1-K1-D9 Method BLASTN q710625 NCBI GI BLAST score 36 7.0e-11 E value 140 Match length % identity NCBI Description Arabidopsis thaliana mRNA for ERD15 protein, complete cds Seq. No. 148453 Seq. ID LIB3175-005-P1-K1-E1 Method BLASTX NCBI GI q4455253 476 BLAST score 5.0e-48 E value 98 Match length % identity (AL035523) superoxide dismutase (EC 1.15.1.1) NCBI Description (Fe) (fragment) [Arabidopsis thaliana] Seq. No. 148454 Seq. ID LIB3175-005-P1-K1-E10 Method BLASTX NCBI GI g3738092 BLAST score 90 E value 2.0e-51

NCBI Description

Match length % identity

(AC005617) similar to glyoxysomal malate dehydrogenase [Arabidopsis thaliana]

Seq. No. 148455

LIB3175-005-P1-K1-E11 BLASTX

Seq. ID Method q1076366 NCBI GI 696 BLAST score 1.0e-73 E value 131 Match length 98 % identity

peptidylprolyl isomerase (EC 5.2.1.8) - Arabidopsis NCBI Description thaliana >gi 460968 (U07276) peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana] >gi\_992643 (U32186)

cyclophilin [Arabidopsis thaliana]

>gi 1091580 prf\_\_2021266A peptidyl-Pro cis-trans isomerase

[Arabidopsis thaliana]

148456 Seq. No. LIB3175-005-P1-K1-E2 Seq. ID Method BLASTN NCBI GI g3510343 BLAST score 303

E value 1.0e-170 Match length 368 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MJC20, complete sequence [Arabidopsis thaliana]

148457 Seq. No.

Seq. ID LIB3175-005-P1-K1-E3

Method BLASTX NCBI GI g1352663 BLAST score 481 2.0e-48 E value Match length 91 100 % identity

SERINE/THREONINE PROTEIN PHOSPHATASE PP2A-3 CATALYTIC NCBI Description

SUBUNIT >gi\_1076388\_pir\_\_S52659 phosphoprotein phosphatase (EC 3.1.3.16) 2A isoform 3 - Arabidopsis thaliana

>qi 466441 (M96841) Ser/Thr protein phosphatase

[Arabidopsis thaliana]

>qi 4559341 qb AAD23003.1 AC007087 22 (AC007087) serine/threonine protein phosphatase PP2A-3 catalytic

subunit [Arabidopsis thaliana]

>gi 4567320 gb\_AAD23731.1\_AC005956 20 (AC005956)

serine/threonine protein phosphatase [Arabidopsis thaliana]

Seq. No. 148458

Seq. ID LIB3175-005-P1-K1-E4

Method BLASTX NCBI GI g3193293 BLAST score 670 1.0e-70 E value Match length 143 % identity

NCBI Description (AF069298) contains a short region of similarity to another

Arabidopsis hypothetical protein F19K23.8 (GB:AC000375)

[Arabidopsis thaliana]

148459 Seq. No.

NCBI GI

BLAST score

```
LIB3175-005-P1-K1-E5
Seq. ID
Method
                   BLASTX
                   g3152596
NCBI GI
BLAST score
                   262
E value
                   1.0e-26
Match length
                   92
% identity
                   74
NCBI Description
                   (AC002986) YUP8H12R.36 [Arabidopsis thaliana]
Seq. No.
                   148460
Seq. ID
                   LIB3175-005-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q3785983
BLAST score
                   546
E value
                   4.0e-56
Match length
                   105
% identity
                   99
NCBI Description
                   (AC005560) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   148461
Seq. ID
                   LIB3175-005-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   g543565
BLAST score
                   145
E value
                   2.0e-09
Match length
                   43
% identity
                   51
                  hypothetical 10.0K protein - Zinnia elegans
NCBI Description
                   >gi 493721 dbj BAA06462 (D30802) TED4 [Zinnia elegans]
                   >gi 641903 (U19266) putative nonspecific lipid transfer;
                   auxin induced gene [Zinnia elegans]
                   148462
Seq. No.
Seq. ID
                   LIB3175-005-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g3056594
BLAST score
                   528
E value
                   5.0e-54
Match length
                   110
% identity
NCBI Description
                   (AC004255) T1F9.15 [Arabidopsis thaliana]
                   148463
Seq. No.
Seq. ID
                   LIB3175-005-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q2781354
BLAST score
                   609
E value
                   5.0e-64
Match length
                   123
% identity
NCBI Description
                   (AC003113) F2401.10 [Arabidopsis thaliana]
Seq. No.
                  148464
Seq. ID
                  LIB3175-005-P1-K1-F10
Method
                  BLASTX
```

18780

q4582468

```
4.0e-54
E value
Match length
                   108
                   99
% identity
NCBI Description
                   (AC007071) putative 40S ribosomal protein; contains
                   C-terminal domain [Arabidopsis thaliana]
Seq. No.
                   148465
                   LIB3175-005-P1-K1-F11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3702732
BLAST score
                   37
E value
                   1.0e-11
Match length
                   156
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MGF10, complete sequence [Arabidopsis thaliana]
                   148466
Seq. No.
Seq. ID
                   LIB3175-005-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g2317725
BLAST score
                   304
                   8.0e-28
E value
                   109
Match length
% identity
                   52
                   (AF015811) putative lysophosphatidic acid acyltransferase
NCBI Description
                   [Mus musculus]
                   148467
Seq. No.
Seq. ID
                   LIB3175-005-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   g2245093
BLAST score
                   461
E value
                   4.0e-46
Match length
                   132
% identity
                  (Z97343) membrane channel protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148468
Seq. ID
                   LIB3175-005-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   q4105772
BLAST score
                   408
                   5.0e-40
E value
Match length
                   86
% identity
                   (AF049917) PGP9B [Petunia x hybrida]
NCBI Description
Seq. No.
                   148469
                   LIB3175-005-P1-K1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3341716
BLAST score
                   43
E value
                   4.0e-15
Match length
                   190
                   80
% identity
NCBI Description
                  Arabidopsis thaliana ACC oxidase (ACO2) mRNA, complete cds
```

NCBI GI

BLAST score

Seq. No. 148470 Seq. ID LIB3175-005-P1-K1-G10 Method BLASTN NCBI GI g3402745 BLAST score 59 1.0e-24 E value 197 Match length % identity 85 Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 NCBI Description (ESSAII project) Seq. No. 148471 Seq. ID LIB3175-005-P1-K1-G2 BLASTX Method g3850573 NCBI GI 632 BLAST score 8.0e-69 E value 137 Match length 98 % identity (ACO05278) Similar to gi 1652733 glycogen operon protein NCBI Description GlgX from Synechocystis sp. genome gb\_D90908. ESTs gb H36690, gb AA712462, gb AA651230 and gb N95932 come from this gene. [Arabidopsis thaliana] Seq. No. 148472 Seq. ID LIB3175-005-P1-K1-G3 Method BLASTX NCBI GI g3157947 BLAST score 629 E value 8.0e-66 Match length 120 % identity 52 (AC002131) Similar to protein gb Z74962 from Brassica NCBI Description oleracea which is similar to bacterial YRN1 and HEAHIO proteins. ESTs gb T21954, gb T04283, gb Z37609, gb N37366, gb R90704, gb F15500 and gb F14353 come from this gene. [Arabidopsis tha Seq. No. 148473 Seq. ID LIB3175-005-P1-K1-G6 Method BLASTX NCBI GI q4587525 BLAST score 221 E value 5.0e-18 Match length 104 % identity (AC007060) Contains the PF 00650 CRAL/TRIO NCBI Description phosphatidyl-inositol-transfer protein domain. ESTs gb T76582, gb N06574 and gb Z25700 come from this gene. [Arabidopsis thaliana] Seq. No. 148474 LIB3175-005-P1-K1-G7 Seq. ID Method BLASTX

g2766448

E value 3.0e-28
Match length 103
% identity 54
NCBI Description (AF029856) cytochrome P450 CYP98A1 [Sorghum bicolor]

Seq. No. 148475

Seq. ID LIB3175-005-P1-K1-G8

Method BLASTX
NCBI GI g120667
BLAST score 480
E value 2.0e-48
Match length 120
% identity 77

NCBI Description GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC

>gi\_81622\_pir\_\_JQ1287 glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis

thaliana >gi\_166706 (M64116) cystolic

glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
thaliana] >gi\_166710 (M64119) glyceraldehyde-3-phosphate

dehydrogenase [Arabidopsis thaliana]

Seq. No. 148476

Seq. ID LIB3175-005-P1-K1-G9

Method BLASTX
NCBI GI g2827139
BLAST score 355
E value 7.0e-34
Match length 66
% identity 100

NCBI Description (AF027172) cellulose synthase catalytic subunit

[Arabidopsis thaliana] >gi\_4049343\_emb\_CAA22568\_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis

thaliana]

Seq. No. 148477

Seq. ID LIB3175-005-P1-K1-H1

Method BLASTX
NCBI GI g3157944
BLAST score 638
E value 7.0e-67
Match length 122
% identity 100

NCBI Description (AC002131) Very strong similarity to aminomethyltransferase

precursor gb\_U79769 from Mesembryanthemum crystallinum.

ESTs gb\_T43167, gb\_T21076, gb\_H36999, gb\_T22773,

gb\_N38038, gb\_T13742, gb\_Z26545, gb\_T20753 and gb W43123

come from this ge

Seq. No. 148478

Seq. ID LIB3175-005-P1-K1-H2

Method BLASTX
NCBI GI g3953466
BLAST score 585
E value 8.0e-61
Match length 118
% identity 97

NCBI Description (AC002328) F20N2.11 [Arabidopsis thaliana]

```
Seq. No.
                  148479
Seq. ID
                  LIB3175-005-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2651307
BLAST score
                   265
                   4.0e-23
E value
                   72
Match length
                   64
% identity
                  _(AC002336) putative uroporphyinogen decarboxylase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   148480
                  LIB3175-005-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2832625
BLAST score
                   510
E value
                  8.0e-52
Match length
                   112
% identity
                   86
                   (AL021711) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148481
                  LIB3175-005-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2662343
BLAST score
                   517
                                      .
                   9.0e-53
E value
Match length
                  107
% identity
                   93
                   (D63581) EF-1 alpha [Oryza sativa]
NCBI Description
Seq. No.
                   148482
Seq. ID
                  LIB3175-005-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g4218120
BLAST score
                   227
                  6.0e-19
E value
                   62
Match length
% identity
NCBI Description
                   (AL035353) Proline-rich APG-like protein [Arabidopsis
                  thaliana]
                   148483
Seq. No.
                  LIB3175-005-P1-K1-H8
Seq. ID
Method
                  BLASTX
                  q3080376
NCBI GI
BLAST score
                  264
E value
                   3.0e-23
Match length
                  93
                  58
% identity
                  (AL022580) putative protein [Arabidopsis thaliana]
NCBI Description
                  148484
Seq. No.
                  LIB3175-005-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4756963
```

```
BLAST score
                  120
E value
                   6.0e-61
Match length
                  326
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23
NCBI Description
                   (ESSA project)
                  148485
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  q4691223
BLAST score
                  187
E value
                  1.0e-101
Match length
                  282
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
                   (ESSA project)
Seq. No.
                  148486
                  LIB3175-006-P1-K1-A10
Seq. ID
Method
                  BLASTN
                  g4539309
NCBI GI
                  80
BLAST score
E value
                  2.0e-37
                  144
Match length
                  90
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F19H22
NCBI Description
                   (ESSA project)
                  148487
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1817544
                  508
BLAST score
E value
                  1.0e-51
                  102
Match length
                  97
% identity
                  (D83025) proline oxidase precursor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148488
Seq. ID
                  LIB3175-006-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  q4159709
BLAST score
                  241
E value
                  1.0e-133
Match length
                  293
% identity
                  95
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MLN21, complete sequence
Seq. No.
                  148489
                  LIB3175-006-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  410
                  2.0e-40
E value
Match length
                  81
```





% identity 96 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR NCBI Description (CAB-165/180) (LHCP) >gi\_81603\_pir\_\_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana >gi\_16368 emb CAA27540 (X03907) chlorophyll a/b binding protein (LHCP AB 65) [Arabidopsis thaliana] >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding protein (LHCP AB 180) [Arabidopsis thaliana] Seq. No. 148490 Seq. ID LIB3175-006-P1-K1-A3 Method BLASTX NCBI GI q3249100 BLAST score 530 3.0e-54E value Match length 105 % identity 94 NCBI Description (ACO03114) Match to calreticulin (AtCRTL) mRNA gb U27698 and DNA gb U66344. ESTs gb T45719, gb T22451, gb H36323 and gb AA042519 come from this gene. [Arabidopsis thaliana] Seq. No. 148491 Seq. ID LIB3175-006-P1-K1-A5 Method BLASTX NCBI GI q2501101 491 BLAST score 1.0e-49 E value 127 Match length 83 % identity SYNTAXIN HOMOLOG (PEP12 HOMOLOG) >gi 899122 (L41651) NCBI Description syntaxin [Arabidopsis thaliana] Seq. No. 148492 LIB3175-006-P1-K1-A6 Seq. ID Method BLASTX NCBI GI q1705677 BLAST score 342 3.0e-32 E value Match length 81 % identity NCBI Description CELL DIVISION CYCLE PROTEIN 48 HOMOLOG >qi 2118115 pir S60112 cell division control protein CDC48 homolog - Arabidopsis thaliana >qi 1019904 (U37587) cell

division cycle protein [Arabidopsis thaliana]

Seq. No. 148493

LIB3175-006-P1-K1-A8 Seq. ID

Method BLASTN NCBI GI g1877523 BLAST score 72 E value 3.0e-32 Match length 169 56 % identity

NCBI Description Arabidopsis thaliana BAC T7I23, complete sequence

[Arabidopsis thaliana]

Seq. No. 148494

```
LIB3175-006-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1518540
BLAST score
                  393
                  3.0e-38
E value
                  83
Match length
                  92
% identity
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
                  148495
Seq. No.
                  LIB3175-006-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4505369
                   235
BLAST score
                   1.0e-19
E value
Match length
                  132
                   39
% identity
                  NADH dehydrogenase (ubiquinone) Fe-S protein 4 (18kD)
NCBI Description
                   (NADH-coenzyme Q reductase)
                   >gi_3287881_sp_043181_NUYM_HUMAN NADH-UBIQUINONE
                   OXIDOREDUCTASE 18 KD SUBUNIT PRECURSOR (COMPLEX I-18 KD)
                   (CI-18 KD) (COMPLEX I-AQDQ) (CI-AQDQ) >gi_2655053
                   (AF020351) NADH: ubiquinone oxidoreductase 18 kDa IP subunit
                   [Homo sapiens]
                   148496
Seq. No.
                   LIB3175-006-P1-K1-B4
Seq. ID
Method
                   BLASTX
                   q2829891
NCBI GI
                   530
BLAST score
                   3.0e-54
E value
                   118
Match length
                   88
% identity
                   (AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
                   148497
Seq. No.
                   LIB3175-006-P1-K1-B5
Seq. ID
                   BLASTX
Method
                   g2827712
NCBI GI
                   351
BLAST score
                   1.0e-33
E value
                   70
Match length
                   99
% identity
                   (AL021684) endoxyloglucan tranferase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   148498
Seq. ID
                   LIB3175-006-P1-K1-B6
                   BLASTX
Method
NCBI GI
                   g2244750
BLAST score
                   551
E value
                   4.0e-65
                   136
Match length
% identity
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                   >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
```

```
148499
Seq. No.
                  LIB3175-006-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3449334
BLAST score
                  155
                  8.0e-82
E value
Match length
                  277
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
                  148500
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-B9
Method
                  BLASTX
                  g1706749
NCBI GI
                  557
BLAST score
                  2.0e-57
E value
                  117
Match length
                  96
% identity
                  3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE I PRECURSOR
NCBI Description
                  (BETA-KETOACYL-ACP SYNTHASE I) (KAS I) >gi_780814 (U24177)
                  3-ketoacyl-acyl carrier protein synthase I [Arabidopsis
                  thaliana]
                  148501
Seq. No.
                  LIB3175-006-P1-K1-C1
Seq. ID
Method
                  BLASTX
                  g1175013
NCBI GI
                  395
BLAST score
                  1.0e-38
E value
                  91
Match length
% identity
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir__S44084
NCBI Description
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi_472877_emb_CAA53477 (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
                  148502
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-C10
                  BLASTX
Method
NCBI GI
                  g940288
BLAST score
                  263
                  5.0e-23
E value
                  78
Match length
% identity
                  (L43510) protein localized in the nucleoli of pea nuclei;
NCBI Description
                  ORF; putative [Pisum sativum]
                  148503
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-C11
                  BLASTX
Method
NCBI GI
                  g267073
BLAST score
                  613
E value
                  6.0e-64
Match length
                  113
% identity
                  99
```

```
NCBI Description
                  TUBULIN BETA-2/BETA-3 CHAIN >gi 320184_pir__JQ1587 tubulin
                  beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  148504
                  LIB3175-006-P1-K1-C12
Seq. ID
                  BLASTN
Method
                  g3659491
NCBI GI
BLAST score
                  152
                  5.0e-80
E value
                  196
Match length
                  94
% identity
                  Sequence of BAC T22H22 from Arabidopsis thaliana chromosome
NCBI Description
                  1, complete sequence [Arabidopsis thaliana]
                  148505
Seq. No.
                  LIB3175-006-P1-K1-C3
Seq. ID
                  BLASTX
Method
                  g3786324
NCBI GI
BLAST score
                  375
                  5.0e-36
E value
Match length
                  136
% identity
                  (AB015139) chlorophyll a oxygenase [Chlamydomonas
NCBI Description
                  reinhardtii]
Seq. No.
                  148506
                  LIB3175-006-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129559
BLAST score
                  171
E value
                  7.0e-38
Match length
                  96
% identity
                  cellulase homolog OR16pep - Arabidopsis thaliana
NCBI Description
                  >gi 1022807 (U37702) cellulase [Arabidopsis thaliana]
                  >gi 3493633 (AF074092) cellulase [Arabidopsis thaliana]
                      3598956 (AF074375) cellulase [Arabidopsis thaliana]
                  >gi 3978258 (AF073875) endo-1,4-beta-D-glucanase KORRIGAN
                  [Arabidopsis thaliana]
                  148507
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-C6
Method
                  BLASTX
```

g3128228 NCBI GI BLAST score 57 3.0e-58 E value 131 Match length % identity

(AC004077) putative ribosomal protein L18A [Arabidopsis NCBI Description thaliana] >gi 3337376 (AC004481) putative ribosomal protein

L18A [Arabidopsis thaliana]

Seq. No. 148508

Seq. ID LIB3175-006-P1-K1-C9

Method BLASTX

```
NCBI GI
                   g3135254
BLAST score
                   142
                   9.0e-09
E value
                  129
Match length
                   35
% identity
NCBI Description
                  (AC003058) hypothetical protein [Arabidopsis thaliana]
                  148509
Seq. No.
                  LIB3175-006-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242719
BLAST score
                  218
                   4.0e-48
E value
                  103
Match length
% identity
                   96
NCBI Description
                   (AC003040) putative acetone-cyanohydrin lyase [Arabidopsis
                  thaliana]
Seq. No.
                  148510
Seq. ID
                  LIB3175-006-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g1136402
BLAST score
                  143
                   7.0e-09
E value
Match length
                   90
                   30
% identity
                   (D79993) similar to hypothetical protein L8167.6 of
NCBL Description
                  Saccharomyces cerevisiae. [Homo sapiens]
Seq. No.
                  148511
Seq. ID
                  LIB3175-006-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g4455202
BLAST score
                   449
E value
                   1.0e-44
Match length
                   98
                   89
% identity
                   (AL035440) putative APG protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148512
                  LIB3175-006-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2224931
BLAST score
                   510
E value
                  7.0e-52
Match length
                  105
% identity
                   97
NCBI Description
                   (AF004215) ethylene-insensitive3-like3 [Arabidopsis
                  thaliana]
                  148513
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g4490329
BLAST score
                  333
                   4.0e-31
E value
Match length
                  118
```

```
% identity
                  (AL035656) extensin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  453
E value
                  3.0e-45
                  120
Match length
% identity
                  74
                   (AF091455) translationally controlled tumor protein [Hevea
NCBI Description
                  brasiliensis]
                  148515
Seq. No.
                  LIB3175-006-P1-K1-D5
Seq. ID
                  BLASTN
Method
                  g166611
NCBI GI
                  69
BLAST score
                  2.0e-30
E value
Match length
                  223
% identity
                  A.thaliana at 2S3 gene encoding albumin 2S subunit 3,
NCBI Description
                  complete cds
                  148516
Seq. No.
                  LIB3175-006-P1-K1-D9
Seq. ID
                  BLASTN
Method
                  g4314354
NCBI GI
BLAST score
                  81
E value
                  1.0e-37
                  363
Match length
                   97
% identity
                  Arabidopsis thaliana chromosome II BAC T9I22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  148517
Seq. No.
                  LIB3175-006-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q267082
BLAST score
                   609
E value
                   2.0e-63
Match length
                   114
% identity
                  TUBULIN BETA-8 CHAIN >gi_320189_pir__JQ1592 tubulin beta-8
NCBI Description
                   chain - Arabidopsis thaliana >gi 166908 (M84705) beta-8
                  tubulin [Arabidopsis thaliana]
                  148518
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-E10
                  BLASTN
Method
                  q1669386
NCBI GI
BLAST score
                  32
                  1.0e-08
E value
Match length
                  72
                   92
% identity
                  Arabidopsis thaliana actin 2 (ACT2) gene, complete cds
NCBI Description
```

```
Seq. No.
                   148519
                  LIB3175-006-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4678298
BLAST score
                   43
E value
                   4.0e-55
Match length
                   125
                   92
% identity
NCBI Description
                  (AL049655) putative protein [Arabidopsis thaliana]
Seq. No.
                   148520
                  LIB3175-006-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4454037
BLAST score
                   366
E value
                   3.0e - 35
                   79
Match length
                   84
% identity
NCBI Description
                   (AL035394) putative major latex protein [Arabidopsis
                   thaliana]
                   148521
Seq. No.
                  LIB3175-006-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2447107
BLAST score
                  380
E value
                  1.0e-36
Match length
                  135
% identity
                   53
NCBI Description (U42580) A638R [Paramecium bursaria Chlorella virus 1]
                  148522
Seq. No.
                  LIB3175-006-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g127041
BLAST score
                  172
E value
                   2.0e-12
Match length
                  36
                  89
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi 81647 pir JN0131 methionine adenosyltransferase (EC
                  2.5.1.6) - Arabidopsis thaliana >gi 166872 (M55077)
                  S-adenosylmethionine synthetase [Arabidopsis thaliana]
Seq. No.
                  148523
Seq. ID
                  LIB3175-006-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2244850
BLAST score
                  447
E value
                  2.0e-44
                  106
Match length
% identity
                  91
NCBI Description (297337) hypothetical protein [Arabidopsis thaliana]
                  148524
Seq. No.
```

.

```
Seq. ID
                   LIB3175-006-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   g4115930
BLAST score
                   37
E value
                   2.0e-11
Match length
                   61
% identity
                   89
NCBI Description
                  Arabidopsis thaliana BAC T4B21
Seq. No.
                   148525
Seq. ID
                  LIB3175-006-P1-K1-F1
Method
                  BLASTN
NCBI GI
                   g3928074
BLAST score
                   151
E value
                   1.0e-79
Match length
                   198
% identity
                   93
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T7F6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                 148526
                   LIB3175-006-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829893
BLAST score
                   616
E value
                   3.0e-64
Match length
                   140
% identity
NCBI Description
                  (AC002311) phosphoglucomutase [Arabidopsis thaliana]
Seq. No.
                   148527
                  LIB3175-006-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2160133
BLAST score
                   429
                   2.0e-42
E value
Match length
                   118
% identity
NCBI Description
                   (AC000375) Strong similarity to Arabidopsis
                   gb X91953, F19K23.3, F19K23.15. ESTs
                   gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this
                   gene. [Arabidopsis thaliana]
                  148528
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g2244909
BLAST score
                  457
E value
                  1.0e-45
Match length
                  118
                  81
% identity
NCBİ Description
                  (Z97339) pyruvate, orthophosphate dikinase [Arabidopsis
                  thaliana]
Seq. No.
                  148529
                  LIB3175-006-P1-K1-F7
Seq. ID
Method
                  BLASTN
```

```
NCBI GI
                  g3985957
                  382
BLAST score
                  0.0e + 00
E value
                  401
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYN8, complete sequence [Arabidopsis thaliana]
                  148530
Seq. No.
                  LIB3175-006-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2129628
                  547
BLAST score
                  3.0e-58
E value
Match length
                  128
                  87
% identity
                  ketoconazole resistent protein - Arabidopsis thaliana
NCBI Description
                  >qi 928938 emb CAA61433 (X89036) ketoconazole resistent
                  protein [Arabidopsis thaliana]
Seq. No.
                  148531
                  LIB3175-006-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131398
BLAST score
                  455
E value
                  2.0e-45
                  105
Match length
                  86
% identity
                  PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
NCBI Description
                  >gi 72714 pir__F2MU10 photosystem II 10K protein precursor
                  - Arabidopsis thaliana >gi 16447 emb CAA39441 (X55970)
                  photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
                  >gi_3152571 (AC002986) Match to photosystem II 10kDa
                  polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616,
                  gb T41858, gb T88021, gb_R37531, gb_T04679, gb_N37520,
                  gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400
                  come from this gene. [Arabidopsis
Seq. No.
                  148532
                  LIB3175-006-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3063450
                  533
BLAST score
                  1.0e-54
E value
Match length
                  127
% identity
                  (AC003981) F22013.12 [Arabidopsis thaliana]
NCBI Description
                  148533
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-G11
Method
                  BLASTN
                  g4559344
NCBI GI
BLAST score
                  222
                  1.0e-121
E value
                  335
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC F27C12 genomic
NCBI Description
```

```
sequence, complete sequence
Seq. No.
                   148534
                   LIB3175-006-P1-K1-G3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4220633
BLAST score
                   324
                   0.0e+00
E value
Match length
                   365
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K7J8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148535
Seq. ID
                   LIB3175-006-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g3273751
BLAST score
                   579
E value
                   5.0e-60
Match length
                   133
% identity
                   86
                   (AF061518) manganese superoxide dismutase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   148536
                   LIB3175-006-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4454473
BLAST score
                   302
                   1.0e-27
E value
Match length
                   99
% identity
NCBI Description
                   (AC006234) putative beta-expansin protein [Arabidopsis
                   thaliana]
                   148537
Seq. No.
Seq. ID
                   LIB3175-006-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   g4220636
BLAST score
                   34
E value
                   4.0e-10
Match length
                   51
% identity
                   90
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFB16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148538
                   LIB3175-006-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3913379
BLAST score
                   44
E value
                   4.0e-77
Match length
                   142
% identity
                   99
                  CRYPTOCHROME 2 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR)
NCBI Description
```

thaliana]

>qi 1857038 (U43397) cryptochrome 2 apoprotein [Arabidopsis

BLAST score

```
Seq. No.
                  148539
Seq. ID
                  LIB3175-006-P1-K1-G9
Method
                  BLASTN
                  q4584351
NCBI GI
                  377
BLAST score
E value
                  0.0e+00
                  412
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T12H3 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  148540
                  LIB3175-006-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3063449
BLAST score
                  435
E value
                  4.0e-43
Match length
                  103
% identity
NCBI Description
                  (AC003981) F22013.11 [Arabidopsis thaliana]
Seq. No.
                  148541
                  LIB3175-006-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729470
BLAST score
                  424
                  7.0e-42
E value
Match length
                  123
% identity
                  MITOCHONDRIAL FORMATE DEHYDROGENASE PRECURSOR
NCBI Description
                  (NAD-DEPENDENT FORMATE DEHYDROGENASE) (FDH)
                  >gi 542089 pir JQ2272 formate dehydrogenase (EC 1.2.1.2)
                  precursor, mitochondrial - potato >gi 297798 emb CAA79702
                  (Z21493) mitochondrial formate dehydrogenase precursor
                  [Solanum tuberosum]
                  148542
Seq. No.
Seq. ID
                  LIB3175-006-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g3157924
                  196
BLAST score
                  3.0e-15
E value
                  37
Match length
% identity
                  100
                  (AC002131) Contains homology to extensin-like protein
NCBI Description
                  gb D83227 from Populus nigra. ESTs gb H76425, gb_T13883,
                  gb T45348, gb H37743, gb AA042634, gb Z26960 and gb Z25951
                  come from this gene. There is a similar ORF on the
                  opposite strand. [... >gi 4063707 (AF104327) extensin-like
                  protein [Arabidopsis thaliana]
Seq. No.
                  148543
                  LIB3175-006-P1-K1-H12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3608126
```

```
E value
                   1.0e-129
Match length
                   289
                   94
% identity
                  Arabidopsis thaliana chromosome II BAC T32F12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   148544
Seq. No.
                   LIB3175-006-P1-K1-H3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g16228
                   55
BLAST score
                   3.0e-22
E value
                   193
Match length
                   89
% identity
                  A.thaliana cor47 mRNA
NCBI Description
                   148545
Seq. No.
                   LIB3175-006-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4490732
                   502
BLAST score
                   7.0e-51
E value
                   99
Match length
% identity
                   (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
NCBI Description
                   protein [Arabidopsis thaliana]
Seq. No.
                   148546
Seq. ID
                   LIB3175-006-P1-K1-H5
Method
                   BLASTN
                   g3985958
NCBI GI
                   91
BLAST score
                   1.0e-43
E value
Match length
                   168
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MZN1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148547
                   LIB3175-006-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q114335
                   564
BLAST score
                   3.0e-58
E value
                   123
Match length
% identity
                   PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                   >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                   type 2, plasma membrane - Arabidopsis thaliana >gi_166629
                   (J05570) H+-ATPase [Arabidopsis thaliana]
                   148548
Seq. No.
                   LIB3175-006-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1402904
BLAST score
                   626
                   2.0e-65
E value
```

```
Match length
                  125
% identity
NCBI Description
                  (X98313) peroxidase [Arabidopsis thaliana]
                  148549
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  q3482964
BLAST score
                  136
E value
                   2.0e-70
Match length
                  386
                   97
% identity
                  Arabidopsis thaliana DNA chromosome 2, BAC clone F13D4
NCBI Description
                   (ESSAII project)
                  148550
Seq. No.
                  LIB3175-007-P1-K1-A10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4757662
BLAST score
                  147
                   6.0e-77
E value
Match length
                   361
                  96
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F10B6 from
NCBI Description
                  chromosome I, complete sequence
Seq. No.
                  148551
Seq. ID
                  LIB3175-007-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g4106339
                   345
BLAST score
                  0.0e + 00
E value
                  369
Match length
% identity
                  Arabidopsis thaliana protein phosphatase 2A regulatory
NCBI Description
                  subunit isoform B' delta mRNA, complete cds
Seq. No.
                  148552
Seq. ID
                  LIB3175-007-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g2511588
BLAST score
                   677
                  2.0e-71
E value
Match length
                  133
                  100
% identity
                  (Y13691) multicatalytic endopeptidase complex, proteasome
NCBI Description
                  component, alpha subunit [Arabidopsis thaliana]
Seq. No.
                  148553
                  LIB3175-007-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406780
BLAST score
                  485
                  5.0e-49
E value
                  98
Match length
% identity
                  (AC006532) putative multispanning membrane protein
NCBI Description
```



## [Arabidopsis thaliana]

```
Seq. No.
                   148554
                   LIB3175-007-P1-K1-A3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3702736
BLAST score
                   43
                   7.0e-15
E value
                   203
Match length
                   80
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MRI1, complete sequence [Arabidopsis thaliana]
                   148555
Seq. No.
Seq. ID
                   LIB3175-007-P1-K1-A5
Method
                   BLASTX
NCBI GI
                   q2829903
BLAST score
                   68
E value
                   6.0e-62
                   136
Match length
                   91
% identity
NCBI Description
                   (AC002311) unknown protein [Arabidopsis thaliana]
                   148556
Seq. No.
                   LIB3175-007-P1-K1-A7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4159710
BLAST score
                   297
E value
                   1.0e-166
Match length
                   417
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MSD23, complete sequence
                   148557
Seq. No.
                   LIB3175-007-P1-K1-A9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2264307
BLAST score
                   291
                   1.0e-163
E value
                   382
Match length
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MED24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148558
Seq. ID
                   LIB3175-007-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   g4538963
BLAST score
                   626
E value
                   2.0e-65
Match length
                   146
                   65
% identity
NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
```

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

[Arabidopsis thaliana] >gi\_4741958\_gb\_AAD28776.1\_AF134129\_1

```
148559
Seq. No.
                  LIB3175-007-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4185153
BLAST score
                  251
                  2.0e-21
E value
                  101
Match length
                  54
% identity
                  (AC005724) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  148560
Seq. No.
                  LIB3175-007-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4454478
                  641
BLAST score
                  3.0e-67
E value
                  144
Match length
                  87
% identity
                  (AC006234) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  148561
Seq. No.
                  LIB3175-007-P1-K1-B12
Seq. ID
Method
                  BLASTX
                  g2501056
NCBI GI
                  541
BLAST score
                  1.0e-55
E value
Match length
                  112
                  97
% identity
                  SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
NCBI Description
                  >gi_2129737_pir__S71293 seryl-tRNA synthetase - Arabidopsis
                  thaliana >gi_1359497 emb_CAA94388_ (Z70313) seryl-tRNA
                  Synthetase [Arabidopsis thaliana]
Seq. No.
                  148562
                  LIB3175-007-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4589396
BLAST score
                  249
E value
                  3.0e-21
                  100
Match length
                  47
% identity
                  (D89971) asparaginyl endopeptidase (VmPE-1) [Vigna mungo]
NCBI Description
Seq. No.
                  148563
                  LIB3175-007-P1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3928150
BLAST score
                  391
E value
                  7.0e-38
                  135
Match length
% identity
                  58
                  (AJ131049) hypothetical protein [Cicer arietinum]
NCBI Description
                  148564
Seq. No.
                  LIB3175-007-P1-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924728
```

```
BLAST score
                   168
E value
                   2.0e-89
                   450
Match length
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXH1, complete sequence [Arabidopsis thaliana]
                   148565
Seq. No.
                   LIB3175-007-P1-K1-B6
Seq. ID
                   BLASTX
Method
NCBI GI
                   g728904
                   236
BLAST score
                   1.0e-19
E value
                   111
Match length
                   48
% identity
                   CALCIUM-TRANSPORTING ATPASE 2 (VACUOLAR CA2+-ATPASE)
NCBI Description
                   >gi 1077041 pir S48877 Ca2+-transporting ATPase (EC
                   3.6.1.38) - yeast (Saccharomyces cerevisiae) >gi_454003
                   (U03060) calcium ATPase [Saccharomyces cerevisiae]
                   >gi 1322457 emb CAA96706 (Z72528) ORF YGL006w
                   [Saccharomyces cerevisiae]
Seq. No.
                   148566
                   LIB3175-007-P1-K1-B7
Seq. ID
Method
                   BLASTX
                   q2879811
NCBI GI
                   522
BLAST score
E value
                   3.0e-53
Match length
                   112
% identity
                   (AJ223316) ribosomal protein L30 [Lupinus luteus]
NCBI Description
                   148567
Seq. No.
                   LIB3175-007-P1-K1-B8
Seq. ID
Method
                   BLASTN
                   g2351061
NCBI GI
                   228
BLAST score
                   1.0e-125
E value
Match length
                   375
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAF19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148568
                   LIB3175-007-P1-K1-B9
Seq. ID
                   BLASTX
Method
                   g1352347
NCBI GI
                   511
BLAST score
E value
                   5.0e-52
                   122
Match length
                   84
% identity
                   ELONGATION FACTOR 1-BETA A1 (EF-1-BETA)
NCBI Description
                   >gi_480620_pir__S37103 translation elongation factor eEF-1 beta-A1 chain - Arabidopsis thaliana (cv. Colombia)
                   >gi_398608_emb_CAA52751_ (X74733) elongation factor-1 beta
                   Al [Arabidopsis thaliana]
```

```
148569
Seq. No.
                  LIB3175-007-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2738248
BLAST score
                  485
E value
                  5.0e-49
Match length
                  119
                  82
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                  148570
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q4127456
BLAST score
                  124
                  2.0e-27
E value
                  89
Match length
                  60
% identity
                  (AJ010818) Cpn21 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148571
                  LIB3175-007-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1518540
BLAST score
                  545
                  6.0e-56
E value
Match length
                  117
                  91
% identity
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                  148572
Seq. No.
                  LIB3175-007-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1705677
BLAST score
                  729
E value
                  2.0e-77
Match length
                  144
                  59
% identity
                  CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
NCBI Description
                  >gi_2118115_pir__S60112 cell division control protein CDC48
                  homolog - Arabidopsis thaliana >gi 1019904 (U37587) cell
                  division cycle protein [Arabidopsis thaliana]
                  148573
Seq. No.
                  LIB3175-007-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3461838
                  456
BLAST score
E value
                  2.0e-45
                  142
Match length
% identity
                   (AC005315) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  148574
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-C6
```

```
Method
                   BLASTX
NCBI GI
                   q1402916
BLAST score
                   384
E value
                   4.0e-37
Match length
                  121
% identity
NCBI Description
                   (X98319) peroxidase [Arabidopsis thaliana]
                   >gi_1429217_emb_CAA67311_ (X98775) peroxidase ATP12a
                   [Arabidopsis thaliana]
Seq. No.
                   148575
                  LIB3175-007-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2160133
BLAST score
                   380
                   1.0e-36
E value
                  89
Match length
% identity
                   (AC000375) Strong similarity to Arabidopsis
NCBI Description
                   gb_X91953,F19K23.3,F19K23.15. ESTs
                  gb T21984, gb ATTS0219, gb ATTS0207, gb T21984 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   148576
                  LIB3175-007-P1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                q4544461
                   333
BLAST score
                   0.0e + 00
E value
                   364
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC F23E6 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   148577
Seq. ID
                   LIB3175-007-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g4427003
BLAST score
                   406
E value
                   1.0e-39
Match length
                   123
% identity
                   (AF127664) NBD-like protein [Arabidopsis thaliana]
NCBI Description
                   148578
Seq. No.
                   LIB3175-007-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539292
BLAST score
                   494
                   6.0e-50
E value
Match length
                  96
% identity
NCBI Description
                   (AL049480) putative ribosomal protein S10 [Arabidopsis
                   thaliana]
Seq. No.
                   148579
Seq. ID
                   LIB3175-007-P1-K1-D10
```

```
Method
                  BLASTX
NCBI GI
                  q113782
BLAST score
                  535
E value
                  7.0e-55
Match length
                  104
                  99
% identity
                  BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE)
NCBI Description
                  >gi 486824_pir__S36094 beta-amylase (EC 3.2.1.2) -
                  Arabidopsis thaliana >gi_166602 (M73467) beta-amylase
                  [Arabidopsis thaliana] >gi_228699_prf__1808329A beta
                  amylase [Arabidopsis thaliana]
Seq. No.
                  148580
                  LIB3175-007-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924505
BLAST score
                  333
E value
                  0.0e + 00
Match length
                  439
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13
                  (ESSAII project)
                  148581
Seq. No.
                  LIB3175-007-P1-K1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4455339
BLAST score
                  58
E value
                  5.0e-24
Match length
                  141
                  86
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T12J5
                  (ESSAII project)
Seq. No.
                  148582
Seq. ID
                  LIB3175-007-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q166834
BLAST score
                  408
                  6.0e-40
E value
Match length
                  81
% identity
NCBI Description
                  (M86720) ribulose bisphosphate carboxylase/oxygenase
                  activase [Arabidopsis thaliana] >gi_2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
Seq. No.
                  148583
Seq. ID
                  LIB3175-007-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q4584548
BLAST score
                  601
                  2.0e-62
E value
Match length
                  115
% identity
                  (ALO49608) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148584
```

```
Seq. ID
                  LIB3175-007-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  q3449326
BLAST score
                  250
                  1.0e-138
E value
                  385
Match length
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19M22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148585
Seq. ID
                  LIB3175-007-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g584892
BLAST score
                  390
E value
                  7.0e-38
Match length
                  97
% identity
NCBI Description
                  SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
                  >gi 629805 pir S43516 serine carboxypeptidase I - rice
                  >gi_409580_dbj_BAA04510 (D17586) serine carboxypeptidase I
                   [Oryza sativa]
Seq. No.
                  148586
Seq. ID
                  LIB3175-007-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q1246019
BLAST score
                  670
E value
                  1.0e-70
Match length
                  128
                  100
% identity
NCBI Description
                  (S80554) chalcone synthase, CHS [Arabidopsis, Landsberg
                  erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]
Seq. No.
                  148587
Seq. ID
                  LIB3175-007-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4586265
BLAST score
                  469
E value
                  4.0e-47
Match length
                  111
% identity
NCBI Description
                  (AL049640) putative protein [Arabidopsis thaliana]
Seq. No.
                  148588
Seq. ID
                  LIB3175-007-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2459417
BLAST score
                  383
E value
                  4.0e-37
Match length
                  84
% identity
NCBI Description
                  (AC002332) putative pre-mRNA splicing factor PRP19
                  [Arabidopsis thaliana]
Seq. No.
                  148589
                  LIB3175-007-P1-K1-E1
Seq. ID
```

```
Method
                  BLASTX
                  g4262228
NCBI GI
BLAST score
                  386
E value
                  2.0e-37
Match length
                  76
% identity
                  97
                  (AC006200) putative receptor protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  148590
Seq. No.
                  LIB3175-007-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  594
                  9.0e-62
E value
                  125
Match length
                  92
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  148591
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  q2494106
BLAST score
                  250
                  1.0e-138
E value
                  430
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  148592
                  LIB3175-007-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3318611
                  289
BLAST score
                  6.0e-26
E value
Match length
                  68
                  82
% identity
                  (AB016063) mitochondrial phosphate transporter [Glycine
NCBI Description
                  max]
                  148593
Seq. No.
                  LIB3175-007-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2119846
BLAST score
                  630
E value
                  5.0e-66
Match length
                  119
                  100
% identity
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
```

[Arabidopsis thaliana] >gi\_3128230 (AC004077) photosystem

BLAST score

Match length

E value

376

78

2.0e-36

II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi\_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

```
Seq. No.
                  148594
                  LIB3175-007-P1-K1-E3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3004543
BLAST score
                  66
E value
                  1.0e-28
Match length
                  214
% identity
                  87
                  Arabidopsis thaliana chromosome II BAC F19F24 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  148595
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-E5
Method
                  BLASTN
NCBI GI
                  q4531433
BLAST score
                  432
E value
                  0.0e+00
Match length
                  447
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II P1 MFL8 genomic
                  sequence, complete sequence
Seq. No.
                  148596
Seq. ID
                  LIB3175-007-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  q4049332
BLAST score
                  303
E value
                  1.0e-170
Match length
                  391
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
                   (ESSAII project)
                  148597
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q1346263
BLAST score
                  440
E value
                  1.0e-43
Match length
                  100
                  98
% identity
NCBI Description
                  GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR)
                  >gi_2146736_pir__S65773 glutamyl-tRNA reductase 2 precursor
                  - Arabidopsis thaliana >gi 1049057 (U27118) glutamyl-tRNA
                  reductase [Arabidopsis thaliana]
                  148598
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q2623962
```

```
% identity
NCBI Description
                  (Y12540) isocitrate dehydrogenase (NADP+) [Apium
                  graveolens]
Seq. No.
                  148599
Seq. ID
                  LIB3175-007-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  g4538947
BLAST score
                   463
E value
                   2.0e-46
                  95
Match length
                   49
% identity
NCBI Description
                   (AL049483) putative mitochondrial carrier protein
                   [Arabidopsis thaliana]
                  148600
Seq. No.
                  LIB3175-007-P1-K1-F12
Seq. ID
Method
                  BLASTN
                  g2160155
NCBI GI
BLAST score
                  231
                  1.0e-127
E value
Match length
                   422
                   99
% identity
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148601
Seq. ID
                  LIB3175-007-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1174851
BLAST score
                   61
E value
                   6.0e-48
                  124
Match length
                   77
% identity
                  UBIQUITIN-CONJUGATING ENZYME E2-21 KD 3 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 6) (UBIQUITIN CARRIER PROTEIN 6)
Seq. No.
                  148602
                  LIB3175-007-P1-K1-F3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3641837
BLAST score
                   475
E value
                   9.0e-48
Match length
                   95
% identity
                   98
                   (AL023094) Nonclathrin coat protein gamma - like protein
NCBI Description
                   [Arabidopsis thaliana]
                  148603
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-F4
Method
                  BLASTX
                  g1170191
NCBI GI
BLAST score
                   621
E value
                  7.0e-65
Match length
                  132
                   94
% identity
                  HOMEOBOX PROTEIN HD1 >gi 1076449 pir S47535
NCBI Description
```

Seq. No.

Seq. ID

Method

NCBI GI BLAST score

E value

Match length

% identity

Seq. No.

BLAST score

Match length

% identity

Seq. ID

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

Method NCBI GI

```
homeodomain-containing protein - rape
                   >gi_453949_emb_CAA82314 (Z29073) homeodomain-containing
protein [Brassica napus] >gi_1090522_prf__2019252A homeobox
                   protein [Brassica napus]
                   148604
                   LIB3175-007-P1-K1-F6
                   BLASTN
                   g3608126
                   172
                   8.0e-92
                   394
                   79
                   Arabidopsis thaliana chromosome II BAC T32F12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   148605
                   LIB3175-007-P1-K1-F7
                   BLASTX
                   q2369714
                   481
                   1.0e-48
                   102
                   91
                   (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   148606
                   LIB3175-007-P1-K1-F8
                   BLASTX
                   g112681
                   489
                   2.0e-49
                   118
                   81
                   12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                   >gi_166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                   148607
                   LIB3175-007-P1-K1-F9
                   BLASTX
                   g3128168
                   573
                   3.0e-59
                   124
                   (AC004521) putative carboxyl-terminal peptidase
                   [Arabidopsis thaliana]
```

Seq. No. Seq. ID

Method NCBI GI BLAST score E value

Match length % identity

NCBI Description

Seq. No. 148608

LIB3175-007-P1-K1-G1 Seq. ID

Method BLASTX NCBI GI g629541 BLAST score 627 1.0e-65 E value

```
Match length
                   134
                   93
% identity
NCBI Description
                  plasma membrane intrinsic protein 1c - Arabidopsis thaliana
                   >gi_472875 emb CAA53476 (X75882) plasma membrane intrinsic
                  protein 1c [Arabidopsis thaliana]
Seq. No.
                   148609
                  LIB3175-007-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3169182
BLAST score
                   394
E value
                   3.0e-38
Match length
                  75
                   100
% identity
NCBI Description
                  (AC004401) unknown protein [Arabidopsis thaliana]
Seq. No.
                   148610
                  LIB3175-007-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q166927
BLAST score
                   296
                   1.0e-166
E value
Match length
                   300
% identity
                  Arabidopsis thaliana unidentified mRNA sequence, complete
NCBI Description
                   cds
Seq. No.
                   148611
Seq. ID
                  LIB3175-007-P1-K1-G2
Method
                  BLASTX
NCBI GI
                   q1174779
BLAST score
                   649
E value
                   4.0e-68
Match length
                   142
% identity
                   89
NCBI Description
                  TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi 166894
                   (M81620) tryptophan synthase beta-subunit [Arabidopsis
                   thaliana] >gi 4490703 emb CAB38837.1 (AL035680) tryptophan
                   synthase beta-subunit (TSB2) [Arabidopsis thaliana]
Seq. No.
                   148612
                  LIB3175-007-P1-K1-G3
Seq. ID.
Method
                  BLASTX
NCBI GI
                  g3021506
BLAST score
                   396
                   2.0e-38
E value
Match length
                  122
% identity
NCBI Description
                   (X96727) isocitrate dehydrogenase (NAD+) [Nicotiana
                   tabacum]
Seq. No.
                  148613
Seq. ID
                  LIB3175-007-P1-K1-G4
Method
                  BLASTN
NCBI GI
                  g2618602
BLAST score
                  59
E value
                  2.0e-24
```

```
Match length
                   192
% identity
                   88
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148614
Seq. ID
                  LIB3175-007-P1-K1-G5
Method
                  BLASTN
NCBI GI
                   g2244950
BLAST score
                   340
                   0.0e+00
E value
Match length
                   359
                   99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                   148615
Seq. ID
                   LIB3175-007-P1-K1-G6
Method
                  BLASTX
NCBI GI
                   q3152600
BLAST score
                   473
E value
                   1.0e-48
Match length
                   106
% identity
                   94
NCBI Description
                   (AC002986) Contains similarity to S. cerevisiae
                  hypothetical protein YOR197w, gb Z75105. ESTs gb H37409,
                   gb AA395290, and gb T43907 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   148616
Seq. ID
                  LIB3175-007-P1-K1-G7
Method
                  BLASTX
NCBI GI
                   g3386611
BLAST score
                   747
E value
                   1.0e-79
Match length
                   144
                   99
% identity
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148617
Seq. ID
                  LIB3175-007-P1-K1-G8
Method
                  BLASTX
NCBI GI
                   g4432867
BLAST score
                   192
E value
                   1.0e-14
Match length
                   59
% identity
                   61
                   (AC006300) putative dnaJ-like protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                  148618
Seq. ID
                  LIB3175-007-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1769968
BLAST score
                  317
                  3.0e - 29
E value
Match length
                  134
```

```
% identity
NCBI Description (Y10156) myrosinase-associated protein [Brassica napus]
                  148619
Seq. No.
                  LIB3175-007-P1-K1-H1
Seq. ID
Method
                  BLASTX
                  g548847
NCBI GI
                   337
BLAST score
                  8.0e-32
E value
                  75
Match length
                  100
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S12
NCBI Description
                  >gi_1086182_pir__S39501 ribosomal protein S12 -
                  curled-leaved tobacco >gi_225248_prf__1211235CG ribosomal
                  protein S12 [Nicotiana tabacum]
                  148620
Seq. No.
                  LIB3175-007-P1-K1-H11
Seq. ID
Method
                  BLASTX
                  q3549670
NCBI GI
                  423
BLAST score
                  1.0e-41
E value
                  83
Match length
                  100
% identity
                  (AL031394) putative protein [Arabidopsis thaliana]
NCBI Description
                  148621
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-H12
Method
                  BLASTN
                  q1469225
NCBI GI
                  88
BLAST score
                  9.0e-42
E value
Match length
                  168
% identity
                  89
NCBI Description B.oleracea mRNA for putative major latex protein
                  148622
Seq. No.
                  LIB3175-007-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  g2979555
NCBI GI
                   750
BLAST score
                  5.0e-80
E value
                  142
Match length
% identity
                  (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
                  148623
Seq. No.
                  LIB3175-007-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3785983
BLAST score
                  317
E value
                  3.0e-29
                  99
Match length
% identity
                  (AC005560) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  148624
Seq. No.
```

Method

BLASTX

```
Seq. ID
                  LIB3175-007-P1-K1-H5
Method
                  BLASTN
NCBI GI
                  q3860243
BLAST score
                  266
                  1.0e-148
E value
                   323
Match length
% identity
                  94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  148625
Seq. No.
                  LIB3175-007-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  g3128176
NCBI GI
BLAST score
                  306
E value
                  7.0e-28
Match length
                  108
                  48
% identity
                  (AC004521) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148626
                  LIB3175-007-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1864017
BLAST score
                  548
                  2.0e-56
E value
Match length
                  104
                  100
% identity
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
                  148627
Seq. No.
Seq. ID
                  LIB3175-007-P1-K1-H8
                  BLASTN
Method
NCBI GI
                  g2656031
BLAST score
                  90
E value
                  4.0e-43
Match length
                  303
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC20
Seq. No.
                  148628
Seq. ID
                  LIB3175-007-P1-K1-H9
Method
                  BLASTX
                  g2661422
NCBI GI
BLAST score
                  293
E value
                  9.0e-27
Match length
                  68
                  85
% identity
NCBI Description
                  (AJ001342) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana] >gi_3096936_emb_CAA18846.1
                   (AL023094) Putative S-phase-specific ribosomal protein
                   [Arabidopsis thaliana]
                  148629
Seq. No.
                  LIB3175-009-P1-K1-A12
Seq. ID
```

```
g1408471
NCBI GI
BLAST score
                   159
                   3.0e-11
E value
Match length
                   36
                   92
% identity
NCBI Description
                   (U48938) actin depolymerizing factor 1 [Arabidopsis
                   thaliana] >gi 3851707 (AF102173) actin depolymerizing
                   factor 1 [Arabidopsis thaliana]
Seq. No.
                  148630
Seq. ID
                  LIB3175-009-P1-K1-A8
                  BLASTN
Method
                  g396217
NCBI GI
                  39
BLAST score
E value
                  1.0e-12
Match length
                  110
                  86
% identity
NCBI Description A.thaliana mRNA for transmembrane protein TMP-B
                  148631
Seq. No.
Seq. ID
                  LIB3175-009-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  g4741953
BLAST score
                  54
E value
                  1.0e-21
Match length
                  122
% identity
                  82
NCBI Description
                  Arabidopsis thaliana Lhcb4.2 protein (Lhcb4.2) mRNA,
                  complete cds
Seq. No.
                  148632
                  LIB3175-009-P1-K1-B3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2264304
BLAST score
                  40
E value
                   3.0e-13
Match length
                  153
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBG8, complete sequence [Arabidopsis thaliana]
                  148633
Seq. No.
                  LIB3175-009-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4580392
BLAST score
                  433
E value
                   5.0e-43
Match length
                  99
% identity
                  87
NCBI Description
                  (AC007171) hypothetical protein [Arabidopsis thaliana]
                  148634
Seq. No.
Seq. ID
                  LIB3175-009-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g3688161
BLAST score
                  34
E value
                  6.0e-10
```

```
Match length
                   56
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for centrin
                   148635
Seq. No.
                  LIB3175-009-P1-K1-D3
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4510360
BLAST score
                   111
E value
                   1.0e-55
Match length
                  234
                   84
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
                   sequence, complete sequence
                   148636
Seq. No.
                  LIB3175-009-P1-K1-D7
Seq. ID
                  BLASTN
Method
                  g1592684
NCBI GI
BLAST score
                  50
                  1.0e-19
E value
                  86
Match length
                   90
% identity
                  A.thaliana mRNA for oleosin type3 protein
NCBI Description
Seq. No.
                  148637
Seq. ID
                  LIB3175-009-P1-K1-E11
Method
                  BLASTN
                  g2656028
NCBI GI
BLAST score
                   42
                   1.0e-14
E value
Match length
                   125
                   80
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNF13
Seq. No.
                   148638
Seq. ID
                  LIB3175-009-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q4263525
                   407
BLAST score
                   7.0e-40
E value
Match length
                  119
% identity
                   (AC004044) putative photosystem I reaction center subunit
NCBI Description
                   II precursor [Arabidopsis thaliana]
                  148639
Seq. No.
Seq. ID
                  LIB3175-009-P1-K1-E5
                  BLASTX
Method
                  g3176668
NCBI GI
BLAST score
                  295
                   5.0e-27
E value
Match length
                  80
% identity
                   76
                  (AC004393) Similar to ribosomal protein L17 gb X62724 from
NCBI Description
```

Hordeum vulgare. ESTs gb\_Z34728, gb\_F19974, gb\_T75677 and

No.

```
gb_Z33937 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  148640
                  LIB3175-009-P1-K1-F10
Seq. ID
                  BLASTN
Method
NCBI GI
                   g4371278
BLAST score
                   62
                   1.0e-26
E value
                  137
Match length
                   83
% identity
                  Arabidopsis thaliana chromosome II BAC T2N18 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148641
Seq. ID
                  LIB3175-009-P1-K1-F2
Method
                  BLASTN
NCBI GI
                   g3241926
BLAST score
                   55
E value
                   2.0e-22
Match length
                  111
% identity
                   84
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSG15, complete sequence [Arabidopsis thaliana]
                   148642
Seq. No.
                  LIB3175-009-P1-K1-F5
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4309719
BLAST score
                   74
                   1.0e-33
E value
Match length
                   179
% identity
                   82
                   Arabidopsis thaliana chromosome II BAC T30D6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   148643
Seq. No.
                   LIB3175-009-P1-K1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g16185
BLAST score
                   39
                   5.0e-13
E value
                   74
Match length
                   86
% identity
                  A.thaliana atpgpl gene for P-glycoprotein, homologous to
NCBI Description
                  mammalian mdr genes
                   148644
Seq. No.
                  LIB3175-009-P1-K1-G3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1402909
BLAST score
                   47
                  1.0e-17
E value
Match length
                  163
                   79
% identity
                  A.thaliana mRNA for peroxidase, prxr4
NCBI Description
                  148645
Seq. No.
```

```
Seq. ID
                  LIB3175-009-P1-K1-G4
                  BLASTX
Method
NCBI GI
                  q1076414
BLAST score
                  476
E value
                  4.0e-48
                  101
Match length
                  92
% identity
                  subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis
NCBI Description
                  thaliana (fragment) >gi 757534 emb CAA59963 (X85974)
                  subtilisin-like protease [Arabidopsis thaliana]
Seq. No.
                  148646
                  LIB3175-009-P1-K1-G7
Seq. ID
Method
                  BLASTN
                  g1359496
NCBI GI
BLAST score
                  33
                  4.0e-09
E value
                  268
Match length
                  45
% identity
                  A.thaliana mRNA for seryl-tRNA synthetase
NCBI Description
                  148647
Seq. No.
                  LIB3175-009-P1-K1-H8
Seq. ID
Method
                  BLASTN
                  q2244991
NCBI GI
                  20
BLAST score
                  9.1e-02
E value
Match length
                  99
                  89
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
Seq. No.
                  148648
Seq. ID
                  LIB3175-009-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g1168748
                  584
BLAST score
                  2.0e-60
E value
Match length
                  121
% identity
                  58
                  CALMODULIN-4 >gi 479693 pir S35185 calmodulin 4 -
NCBI Description
                  Arabidopsis thaliana >gi 16223 emb CAA78057 (Z12022)
                  calmodulin [Arabidopsis thaliana]
                  148649
Seq. No.
                  LIB3175-015-P1-K1-A10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220643
BLAST score
                  240
                  1.0e-132
E value
Match length
                  405
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148650
                  LIB3175-015-P1-K1-A11
Seq. ID
```

```
BLASTX
Method
NCBI GI
                   g2655420
                   556
BLAST score
                   3.0e-57
E value
                   114
Match length
% identity
                   92
                   (AF035414) heat shock cognate protein HSC70 [Brassica
NCBI Description
                   napus]
                   148651
Seq. No.
                   LIB3175-015-P1-K1-A12
Seq. ID
Method
                   BLASTX
                   g2226202
NCBI GI
BLAST score
                   175
                   1.0e-12
E value
                   102
Match length
                   42
% identity
                   (Y14082) hypothetical protein [Bacillus subtilis]
NCBI Description
                   >qi 2633281 emb CAB12785 (Z99109) similar to amino acid
                   transporter [Bacillus subtilis]
                   148652
Seq. No.
                   LIB3175-015-P1-K1-A3
Seq. ID
                   BLASTN
Method
                   g2264315
NCBI GI
                   85
BLAST score
                   3.0e-40
E value
Match length
                   168
% identity
                   88
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MRN17, complete sequence [Arabidopsis thaliana]
                   148653
Seq. No.
                   LIB3175-015-P1-K1-A5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g535780
BLAST score
                   683
                   3.0e-72
E value
Match length
                   133
% identity
                   98
                   (D26609) transmembrane protein [Arabidopsis thaliana]
NCBI Description
                   148654
Seq. No.
                   LIB3175-015-P1-K1-A6
Seq. ID
Method
                   BLASTN
                   g3449327
NCBI GI
                   275
BLAST score
                   1.0e-153
E value
Match length
                   391
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCA23, complete sequence [Arabidopsis thaliana]
                   148655
Seq. No.
                   LIB3175-015-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4128133
```

```
BLAST score
                   184
E value
                   1.0e-13
Match length
                   60
% identity
                   55
                  (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
NCBI Description
                  148656
Seq. No.
                  LIB3175-015-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3738320
BLAST score
                   358
                   4.0e-34
E value
                   108
Match length
% identity
                   (AC005170) putative cinnamoyl CoA reductase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                  148657
                  LIB3175-015-P1-K1-A9
Seq. ID
Method
                  BLASTN
                   g3046854
NCBI GI
BLAST score
                   37
E value
                   2.0e-11
                   53
Match length
                   92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRG7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148658
                  LIB3175-015-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4826972
                   159
BLAST score
E value
                   9.0e-11
                   66
Match length
% identity
                   53
                  RNA binding motif protein 8 >gi 4455129_gb_AAD21089.1_
NCBI Description
                   (AF127761) ribonucleoprotein RBM8 [Homo sapiens]
Seq. No.
                  148659
Seq. ID
                  LIB3175-015-P1-K1-B10
Method
                  BLASTX
                   q4185511
NCBI GI
BLAST score
                   527
                   7.0e-54
E value
                  102
Match length
                   99
% identity
                   (AF102822) actin depolymerizing factor 4 [Arabidopsis
NCBI Description
                  thaliana]
                  148660
Seq. No.
                  LIB3175-015-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170939
                   646
BLAST score
                  7.0e-68
E value
                  132
Match length
```

```
% identity
                  93
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi_429108_emb_CAA80867_ (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
                  148661
Seq. No.
Seq. ID
                  LIB3175-015-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g4741948
BLAST score
                  628
                  9.0e-66
E value
                  118
Match length
                  100
% identity
                  (AF134124) Lhcb2 protein [Arabidopsis thaliana]
NCBI Description
                  148662
Seq. No.
                  LIB3175-015-P1-K1-B2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4539376
                  171
BLAST score
                  4.0e-12
E value
                  81
Match length
                  56
% identity
NCBI Description
                  (AL049525) hypothetical protein [Arabidopsis thaliana]
                  148663
Seq. No.
                  LIB3175-015-P1-K1-B4
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4159706
BLAST score
                  405
                  0.0e+00
E value
                  405
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MGL6, complete sequence
Seq. No.
                  148664
                  LIB3175-015-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  g4063739
NCBI GI
BLAST score
                  509
                  9.0e-52
E value
                  133
Match length
                  75
% identity
                  (AC005851) putative copper/zinc superoxide dismutase
NCBI Description
                  [Arabidopsis thaliana]
```

Seq. No. 148665

Seq. ID LIB3175-015-P1-K1-B6

Method BLASTX
NCBI GI g114339
BLAST score 200
E value 1.0e-21
Match length 102

```
% identity
                  PLASMA MEMBRANE ATPASE 3 (PROTON PUMP)
NCBI Description
                   >gi_67974_pir__PXMUP3 H+-transporting ATPase (EC 3.6.1.35)
                   type 3, plasma membrane - Arabidopsis thaliana >gi_166625
                   (J04737) ATPase [Arabidopsis thaliana]
Seq. No.
                   148666
                   LIB3175-015-P1-K1-B7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4741952
BLAST score
                   207
E value
                   2.0e-43
                  92
Match length
                   98
% identity
                   (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148667
                   LIB3175-015-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2462935
BLAST score
                   530
                   3.0e-54
E value
Match length
                   131
% identity
                  (Y12321) open reading frame 1 [Brassica oleracea]
NCBI Description
                   148668
Seq. No.
Seq. ID
                   LIB3175-015-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   q3021336
BLAST score
                   646
                   7.0e-68
E value
Match length
                   126
% identity
                   (AJ224957) RGA-like [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148669
                   LIB3175-015-P1-K1-C1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2832639
BLAST score
                   380
E value
                   0.0e + 00
Match length
                   396
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F28J12
                   (ESSAII project)
                   148670
Seq. No.
Seq. ID
                   LIB3175-015-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   q2129577
BLAST score
                   426
                   5.0e-42
E value
Match length
                   81
% identity
                   100
                   DnaJ homolog protein - Arabidopsis thaliana >gi 727357
NCBI Description
                   (U22340) DnaJ homolog [Arabidopsis thaliana]
```

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Seq. No.
                  148671
Seq. ID
                  LIB3175-015-P1-K1-C11
Method
                  BLASTN
                  q4468801
NCBI GI
BLAST score
                  46
E value
                  7.0e-17
                  193
Match length
                  90
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F6G17
NCBI Description
                  (ESSA project)
Seq. No.
                  148672
                  LIB3175-015-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4406816
BLAST score
                  671
E value
                  9.0e-71
Match length
                  127
                  100
% identity
                  (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148673
Seq. ID
                  LIB3175-015-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  403
E value
                  2.0e-39
Match length
                  110
% identity
NCBI Description
                  (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
Seq. No.
                  148674
                  LIB3175-015-P1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4557061
BLAST score
                  386
E value
                  0.0e + 00
Match length
                  410
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC F23M2 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  148675
                  LIB3175-015-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2224931
BLAST score
                  425
E value
                  6.0e-42
Match length
                  88
% identity
NCBI Description
                  (AF004215) ethylene-insensitive3-like3 [Arabidopsis
                  thaliana]
Seq. No.
                  148676
                  LIB3175-015-P1-K1-C5
Seq. ID
```

```
Method
                   BLASTN
NCBI GI
                   a3341671
BLAST score
                   131
E value
                   2.0e-67
Match length
                   410
% identity
                   Arabidopsis thaliana chromosome II BAC F16B22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148677
Seq. ID
                   LIB3175-015-P1-K1-C6
Method
                   BLASTX
                   g2213592
NCBI GI
BLAST score
                   329
E value
                   1.0e-30
Match length
                   134
                   26
% identity
NCBI Description
                   (AC000348) T7N9.12 [Arabidopsis thaliana]
                   148678
Seq. No.
Seq. ID
                   LIB3175-015-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   g3241917
BLAST score
                   136
E value
                   2.0e-70
Match length
                   349
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19B1, complete sequence [Arabidopsis thaliana]
                   148679
Seq. No.
Seq. ID
                   LIB3175-015-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   g4581156
BLAST score
                   211
E value
                   7.0e-17
Match length
                   40
% identity
                   100
NCBI Description
                   (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
                   148680
Seq. No.
Seq. ID
                   LIB3175-015-P1-K1-D11
Method
                   BLASTX
                   g2160133
NCBI GI
BLAST score
                   386
E value
                   2.0e-37
Match length
                   91
% identity
NCBI Description
                   (AC000375) Strong similarity to Arabidopsis
                   gb X91953, F19K23.3, F19K23.15. ESTs
                   gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   148681
                   LIB3175-015-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g974294
```

```
BLAST score
                   164
                   2.0e-11
E value
Match length
                   70
% identity
                   53
NCBI Description
                   (U31309) LP6 [Pinus taeda]
Seq. No.
                   148682
                   LIB3175-015-P1-K1-D2
Seq. ID
Method
                   BLASTX
                   g4773885
NCBI GI
BLAST score
                   555
E value
                   3.0e-57
Match length
                   121
                   87
% identity
                   (AF076243) putative aspartic protease [Arabidopsis
NCBI Description
                   thaliana]
                   148683
Seq. No.
                   LIB3175-015-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2492519
BLAST score
                   503
                   4.0e-51
E value
                   113
Match length
                   86
% identity
                  26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT
NCBI Description
                   7) >gi_1395191_dbj_BAA13021_ (D86121) 26S proteasome ATPase
                   subunit [Spinacia oleracea]
Seq. No.
                   148684
                   LIB3175-015-P1-K1-D6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539459
BLAST score
                   411
                   3.0e-40
E value
                   135
Match length
                   62
% identity
NCBI Description
                   (AL049500) putative protein [Arabidopsis thaliana]
                   148685
Seq. No.
                   LIB3175-015-P1-K1-D7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4662640
BLAST score
                   367
                   0.0e + 00
E value
                   387
Match length
                   34
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K19 genomic
                   sequence, complete sequence
Seq. No.
                  148686
Seq. ID
                  LIB3175-015-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1169598
BLAST score
                   388
                   1.0e-37
E value
                  85
Match length
```

```
% identity
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  148687
                  LIB3175-015-P1-K1-E10
Seq. ID
                  BLASTN
Method
                  g3047074
NCBI GI
                   389
BLAST score
                  0.0e + 00
E value
                  389
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana BAC F21E10
Seq. No.
                  148688
                  LIB3175-015-P1-K1-E11
Seq. ID
Method
                  BLASTX
                   q1076416
NCBI GI
                   696
BLAST score
                   1.0e-73
E value
                   133
Match length
                   100
% identity
                  sulfite reductase (ferredoxin) (EC 1.8.7.1) precursor -
NCBI Description
                   Arabidopsis thaliana >gi_2129745_pir__S71437 sulfite
                   reductase (ferredoxin) (EC 1.8.7.1) precursor - Arabidopsis
                   thaliana >gi_804953_emb_CAA89154_ (Z49217) sulfite
                   reductase [Arabidopsis thaliana]
Seq. No.
                   148689
                   LIB3175-015-P1-K1-E12
Seq. ID
                   BLASTN
Method
                   g2191126
NCBI GI
                   395
BLAST score
                   0.0e + 00
E value
                   395
Match length
                   100
% identity
NCBI Description Arabidopsis thaliana BAC IG002N01
Seq. No.
                   148690
                   LIB3175-015-P1-K1-E3
Seq. ID
                   BLASTN
Method
                   q4760411
NCBI GI
BLAST score
                   340
                   0.0e + 00
E value
                   408
Match length
                   96
% identity
                  Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
NCBI Description
                   complete sequence
Seq. No.
                   148691
                   LIB3175-015-P1-K1-E4
Seq. ID
                   BLASTX
Method
                   g2921094
NCBI GI
                   604
BLAST score
                   6.0e-63
E value
                   129
Match length
```

Seq. No.

148697

```
% identity
                   (AF018174) thioredoxin-f [Brassica napus]
NCBI Description
Seq. No.
                   148692
                  LIB3175-015-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3434969
BLAST score
                   165
                   2.0e-11
E value
                   37
Match length
% identity
                   76
                   (AB008104) ethylene responsive element binding factor 2
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   148693
                   LIB3175-015-P1-K1-E7
Seq. ID
Method
                   BLASTX
                   g2407800
NCBI GI
                                                             1
                   349
BLAST score
                   4.0e-33
E value
                   71
Match length
                   100
% identity
                   (Y12575) histone H2A.F/Z [Arabidopsis thaliana]
NCBI Description
                   148694
Seq. No.
                   LIB3175-015-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3924615
BLAST score
                   157
E value
                   2.0e-10
                   95
Match length
% identity
NCBI Description
                   (AF069442) hypothetical protein [Arabidopsis thaliana]
                   148695
Seq. No.
                   LIB3175-015-P1-K1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2760172
BLAST score
                   387
                   0.0e + 00
E value
Match length
                   387
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148696
                  LIB3175-015-P1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4584531
BLAST score
                   102
E value
                   4.0e-50
Match length
                   404
                   93
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8
NCBI Description
                   (ESSA project)
```

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Seq. ID
                  LIB3175-015-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2118220
BLAST score
                  334
                  2.0e-31
E value
Match length
                  86
                  51
% identity
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
NCBI Description
                  (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana] >gi_926933 (L44583) vacuolar H+-pumping ATPase 16
                  kDa proteolipid [Arabidopsis thaliana]
                  >gi 3096941_emb_CAA18851.1_ (AL023094) vacuolar
                  H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                  >gi 4539311 emb CAB38812.1 (AL035679) H+-transporting
                  ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
                  >gi 4589976 gb AAD26493.1 AC007195 7 (AC007195) vacuolar
                  H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.
                  148698
                  LIB3175-015-P1-K1-F11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3063438
BLAST score
                  400
                  0.0e+00
E value
                  407
Match length
                  100
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                  [Arabidopsis thaliana]
                  148699
Seq. No.
                  LIB3175-015-P1-K1-F2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3123745
                  390
BLAST score
                  8.0e-38
E value
                  96
Match length
% identity
NCBI Description
                  (AB013447) aluminum-induced [Brassica napus]
Seq. No.
                  148700
                  LIB3175-015-P1-K1-F3
Seq. ID
Method
                  BLASTN
                  g4335744
NCBI GI
BLAST score
                  335
                  0.0e+00
E value
                  359
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T4M8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148701
                  LIB3175-015-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678226
BLAST score
                  480
```

2.0e-48

E value

```
Match length
                   97
% identity
                   (ACO07135) putative 40S ribosomal protein S14 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148702
                  LIB3175-015-P1-K1-F6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g99752
                  507
BLAST score
                  2.0e-51
E value
Match length
                  125
% identity
                  86
                  protochlorophyllide reductase (EC 1.3.1.33) precursor -
NCBI Description
                  Arabidopsis thaliana
Seq. No.
                  148703
Seq. ID
                  LIB3175-015-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  q4586265
BLAST score
                  510
                  7.0e-52
E value
Match length
                  135
% identity
                  74
                   (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  148704
Seq. No.
Seq. ID
                  LIB3175-015-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g4678266
BLAST score
                   309
                  1.0e-173
E value
                  350
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8
NCBI Description
                   (ESSA project)
                  148705
Seq. No.
Seq. ID
                  LIB3175-015-P1-K1-F9
Method
                  BLASTX
                  g4678288
NCBI GI
                   231
BLAST score
                  3.0e-19
E value
Match length
                  132
% identity
                  46
                   (AL049660) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148706
                  LIB3175-015-P1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g556473
BLAST score
                  223
E value
                  1.0e-122
                  377
Match length
                  99
% identity
NCBI Description Arabidopsis thaliana mRNA for ERD14 protein, complete cds
```

```
Seq. No.
                  148707
                  LIB3175-015-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  567
                  1.0e-58
E value
Match length
                  131
% identity
                  84
                  12S SEED STORAGE PROTEIN PRECURSOR >qi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  148708
Seq. ID
                  LIB3175-015-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  q1773330
BLAST score
                  543
                  8.0e-56
E value
Match length
                  125
% identity
                  (U80071) glycolate oxidase [Mesembryanthemum crystallinum]
NCBI Description
                  148709
Seq. No.
                  LIB3175-015-P1-K1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q807576
BLAST score
                  236
E value
                  1.0e-130
Match length
                  272
                  98
% identity
NCBI Description
                  Arabidopsis thaliana GTP-binding protein mRNA, complete cds
Seq. No.
                  148710
Seq. ID
                  LIB3175-015-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g132102
BLAST score
                  151
E value
                   6.0e-10
Match length
                  41
% identity
                  71
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 2B) >gi 68061 pir_RKMUB2
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                  B2 precursor - Arabidopsis thaliana >qi 16194 emb CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  148711
Seq. ID
                  LIB3175-015-P1-K1-G6
Method
                  BLASTN
NCBI GI
                  g16244
BLAST score
                  55
                  2.0e-22
E value
Match length
                  87
                  91
% identity
```

```
NCBI Description Arabidopsis thaliana Csr 1.2 gene for acetolactate synthase
                  (EC 4.1.3.18)
                  148712
Seq. No.
                  LIB3175-015-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  q2145356
NCBI GI
                  423
BLAST score
                  1.0e-41
E value
                  81
Match length
                  99
% identity
                  (Y11122) HD-Zip protein [Arabidopsis thaliana] >gi 3132474
NCBI Description
                   (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
Seq. No.
                  148713
Seq. ID
                  LIB3175-015-P1-K1-G8
Method
                  BLASTN
                  g1209241
NCBI GI
                                                           6
BLAST score
                  387
                  0.0e + 00
E value
Match length
                  387
% identity
                  100
                  Arabidopsis thaliana metallothionein mRNA sequence
NCBI Description
Seq. No.
                  148714
                  LIB3175-015-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3176668
BLAST score
                  665
                  4.0e-70
E value
                  131
Match length
% identity
                   (AC004393) Similar to ribosomal protein L17 gb X62724 from
NCBI Description
                  Hordeum vulgare. ESTs gb Z34728, gb F19974, gb T75677 and
                  gb_Z33937 come from this gene. [Arabidopsis thaliana]
                  148715
Seq. No.
                  LIB3175-015-P1-K1-H1
Seq. ID
Method
                  BLASTN
                  q3927822
NCBI GI
BLAST score
                  286
                  1.0e-160
E value
                  405
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148716
                  LIB3175-015-P1-K1-H11
Seq. ID
Method
                  BLASTX
                  q1769905
NCBI GI
BLAST score
                  396
E value
                  2.0e-38
Match length
                  118
% identity
                  67
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                   [Arabidopsis thaliana]
```

```
Seq. No.
                  148717
Seq. ID
                  LIB3175-015-P1-K1-H2
                  BLASTN
Method
NCBI GI
                   g1143391
BLAST score
                  106
                   2.0e-52
E value
Match length
                   265
                  88
% identity
                  A.thaliana mRNA for uridine diphosphate glucose epimerase
NCBI Description
                   148718
Seq. No.
Seq. ID
                   LIB3175-015-P1-K1-H4
                   BLASTX
Method
                   q913445
NCBI GI
                   501
BLAST score
E value
                   7.0e-51
Match length
                   134
% identity
                   74
                   (S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase
NCBI Description
                   homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv.
                   red cherry, Peptide, 389 aa] [Lycopersicon esculentum]
Seq. No.
                   148719
                   LIB3175-015-P1-K1-H7
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3492855
BLAST score
                   390
E value
                   0.0e + 00
Match length
                   405
                   99
% identity
                   Genomic sequence for Arabidopsis thaliana BAC F20N2,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   148720
                   LIB3175-015-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1799787
BLAST score
                   281
                   5.0e-25
E value
Match length
                   122
% identity
                   (D90868) OXALYL-COA DECARBOXYLASE (EC 4.1.1.8).
NCBI Description
                   [Escherichia coli]
Seq. No.
                   148721
                   LIB3175-015-P1-K1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4263694
BLAST score
                   398
                   0.0e + 00
E value
                   402
Match length
                   100
% identity
                   Arabidopsis thaliana chromosome II BAC F22D22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

Seq. No.

```
Seq. ID
                  LIB3175-016-P1-K1-A10
                  BLASTX
Method
NCBI GI
                  q2642159
BLAST score
                  463
E value
                  1.0e-46
                  101
Match length
                  93
% identity
                  (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                  [Arabidopsis thaliana] >gi 3598958 (AF076484) GDP-mannose
                  pyrophosphorylase [Arabidopsis thaliana] >gi 4151925
                  (AF108660) CYT1 protein [Arabidopsis thaliana]
                  148723
Seq. No.
Seq. ID
                  LIB3175-016-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g2642159
BLAST score
                  262
                  2.0e-23
E value
                  52
Match length
% identity
                   (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                  [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose
                  pyrophosphorylase [Arabidopsis thaliana] >gi 4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
Seq. No.
                  148724
Seq. ID
                  LIB3175-016-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q2642159
BLAST score
                  703
                  2.0e-74
E value
Match length
                  139
% identity
                  99
                  (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                  [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose
                  pyrophosphorylase [Arabidopsis thaliana] >gi 4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
Seq. No.
                  148725
                  LIB3175-016-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16472
BLAST score
                  314
                  1.0e-176
E value
                  388
Match length
% identity
NCBI Description
                  A.thaliana rRNA repeat unit, most frequent IGR type
Seq. No.
                  148726
Seq. ID
                  LIB3175-016-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  q2564044
BLAST score
                  276
E value
                  1.0e-154
Match length
                  413
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
```

## K19P17, complete sequence [Arabidopsis thaliana]

Seq. No. 148727 LIB3175-016-P1-K1-A7 Seq. ID Method BLASTX

NCBI GI q1710581 BLAST score 579 5.0e-60 E value 118 Match length 96 % identity

60S RIBOSOMAL PROTEIN L9 >gi\_2129720\_pir\_\_S71255 ribosomal NCBI Description protein L9 - Arabidopsis thaliana >gi\_1107489\_emb\_CAA63024\_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

148728 Seq. No.

LIB3175-016-P1-K1-A8 Seq. ID

Method BLASTX NCBI GI q3834309 664 BLAST score 6.0e-70 E value 134 Match length

% identity (AC005679) Strong similarity to glycoprotein EP1 gb\_L16983 NCBI Description Daucus carota and a member of S locus glycoprotein family

PF 00954. ESTs gb F13813, gb\_T21052, gb\_R30218 and gb W43262 come from this gene. [Arabidopsis thaliana]

Seq. No. 148729

Seq. ID LIB3175-016-P1-K1-B1

BLASTN Method q3763944 NCBI GI 199 BLAST score 1.0e-108 E value 339 Match length 99

Arabidopsis thaliana DNA chromosome 4, BAC clone F28A23 NCBI Description

(ESSAII project)

Seq. No. 148730

% identity

Seq. ID LIB3175-016-P1-K1-B10

Method BLASTX NCBI GI g2642159 BLAST score 696 E value 1.0e-73 137 Match length 100 % identity

(AC003000) putative mannose-1-phosphate guanyltransferase NCBI Description

[Arabidopsis thaliana] >gi\_3598958 (AF076484) GDP-mannose

pyrophosphorylase [Arabidopsis thaliana] >gi 4151925

(AF108660) CYT1 protein [Arabidopsis thaliana]

148731 Seq. No.

LIB3175-016-P1-K1-B11 Seq. ID

BLASTN Method g3282170 NCBI GI BLAST score 48 6.0e-18 E value

NCBI GI

E value

BLAST score

g1944518

1.0e-19

235

```
Match length
                  144
% identity
                  83
                  Arabidopsis thaliana chromosome 1 BAC F8K4 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  148732
Seq. ID
                  LIB3175-016-P1-K1-B12
Method
                  BLASTX
                  g4490329
NCBI GI
                  531
BLAST score
                  2.0e-54
E value
Match length
                  120
% identity
                  84
                   (AL035656) extensin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148733
                  LIB3175-016-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2275202
BLAST score
                  296
E value
                  7.0e-27
Match length
                  59
% identity
                  98
                   (AC002337) acyl-CoA synthetase isolog [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148734
Seq. ID
                  LIB3175-016-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4827050
BLAST score
                  339
E value
                  8.0e-32
Match length
                  117
% identity
NCBI Description
                  ubiquitin specific protease 14 (tRNA-guanine
                  transglycosylase) >gi 1729927 sp P54578 TGT HUMAN QUEUINE
                  TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE)
                   (GUANINE INSERTION ENZYME) >gi 940182 (U30888) tRNA-Guanine
                  Transglycosylase [Homo sapiens]
Seq. No.
                  148735
                  LIB3175-016-P1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3510346
BLAST score
                  387
                  0.0e + 00
E value
Match length
                  391
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNL12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148736
Seq. ID
                  LIB3175-016-P1-K1-B5
Method
                  BLASTX
```

```
Match length
                  47
                  98
% identity
NCBI Description
                   (Y07822) Shaggy-like kinase tetha [Arabidopsis thaliana]
                  >gi 3047105 (AF058919) protein kinase [Arabidopsis
                  thaliana]
                  148737
Seq. No.
                  LIB3175-016-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3953473
BLAST score
                  637
E value
                  9.0e-67
                  128
Match length
% identity
                  100
NCBI Description
                  (AC002328) F2202.18 [Arabidopsis thaliana]
                  148738
Seq. No.
Seq. ID
                  LIB3175-016-P1-K1-B7
Method
                  BLASTX
                  q416922
NCBI GI
                  292
BLAST score
                  2.0e-26
E value
Match length
                  84
% identity
                  DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE (DUTPASE)
NCBI Description
                   (DUTP PYROPHOSPHATASE) (P18) >gi_282947_pir__JQ1599 dUTP
                  pyrophosphatase (EC 3.6.1.23) - tomato
                  >gi 251897 bbs 109276 (S40549) deoxyuridine triphosphatase,
                  dUTPase, P18 {EC 3.6.1.23} [tomatoes, Tint Tim cultivar
                  LA154, Peptide, 169 aa] [Lycopersicon esculentum]
Seq. No.
                  148739
Seq. ID
                  LIB3175-016-P1-K1-B8
Method
                  BLASTN
                  g972918
NCBI GI
                  62
BLAST score
                  1.0e-26
E value
Match length
                  186
% identity
                  83
                  Arabidopsis thaliana IAA8 (IAA8) gene complete cds
NCBI Description
                  148740
Seq. No.
Seq. ID
                  LIB3175-016-P1-K1-B9
Method
                  BLASTN
                  g4191760
NCBI GI
BLAST score
                  43
                  7.0e-15
E value
                  306
Match length
                  84
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F17F8,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  148741
Seq. No.
                  LIB3175-016-P1-K1-C1
Seq. ID
Method
                  BLASTX
                  g4662641
NCBI GI
```

282

BLAST score

```
E value
                  4.0e-25
Match length
                  71
                  79
% identity
NCBI Description
                  (AC006429) putative auxin down-regulated protein
                  [Arabidopsis thaliana]
Seq. No.
                  148742
                  LIB3175-016-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585350
BLAST score
                  362
                  2.0e-34
E value
Match length
                  92
                  77
% identity
                  CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
NCBI Description
                  >gi 419753 pir S31099 casein kinase II (EC 2.7.1.-)
                  alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
                  >gi 391605 dbj BAA01091 (D10247) casein kinase II
                  catalytic subunit [Arabidopsis thaliana]
                  148743
Seq. No.
                  LIB3175-016-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115767
                  622
BLAST score
E value
                  4.0e-65
Match length
                  118
% identity
                  100
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  148744
Seq. ID
                  LIB3175-016-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g4538959
BLAST score
                  593
                  1.0e-61
E value
Match length
                  110
% identity
                  100
                  (AL049488) putative protein [Arabidopsis thaliana]
NCBI Description
                  148745
Seq. No.
                  LIB3175-016-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4454036
BLAST score
                  695
                  1.0e-73
E value
                  127
Match length
                  100
% identity
                  (AL035394) putative major latex protein [Arabidopsis
NCBI Description
```

thaliana]

```
Seq. No.
                  148746
Seq. ID
                  LIB3175-016-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q2829899
BLAST score
                   405
E value
                   1.0e-39
Match length
                  116
% identity
                   66
                   (AC002311) similar to ripening-induced protein,
NCBI Description
                   gp AJ001449 2465015 and major#latex protein,
                   gp X91961 1107495 [Arabidopsis thaliana]
                  148747
Seq. No.
                  LIB3175-016-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2342717
BLAST score
                  141
E value
                   2.0e-73
Match length
                   426
% identity
                   100
                  Arabidopsis thaliana chromosome II BAC T14G11 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148748
                  LIB3175-016-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2979555
BLAST score
                   371
                   1.0e-35
E value
Match length
                  138
% identity
                   53
                   (AC003680) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148749
                  LIB3175-016-P1-K1-C6
Seq. ID
Method
                  BLASTN
                   g4220633
NCBI GI
BLAST score
                   336
E value
                   0.0e + 00
Match length
                   384
% identity
                   96
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K7J8, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148750
                  LIB3175-016-P1-K1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g928809
                  66
BLAST score
E value
                  2.0e-29
                  89
Match length
% identity
                  100
NCBI Description
                  Arabidopsis thaliana polyubiquitin (ubq3) gene
                  148751
Seq. No.
                  LIB3175-016-P1-K1-C8
Seq. ID
Method
                  BLASTX
```

```
g2507421
NCBI GI
BLAST score
                  554
                  5.0e-57
E value
                  113
Match length
                  96
% identity
                  PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG >gi 1800277
NCBI Description
                  (U81042) translation initiation factor [Arabidopsis
                  thaliana] >gi_4490709_emb_CAB38843.1_ (AL035680)
                  translation initiation factor [Arabidopsis thaliana]
                  148752
Seq. No.
                  LIB3175-016-P1-K1-C9
Seq. ID
                  BLASTX
Method
                  g267073
NCBI GI
                  487
BLAST score
                  3.0e-49
E value
                  89
Match length
                  100
% identity
                  TUBULIN BETA-2/BETA-3 CHAIN >gi 320184 pir JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi_1-668\overline{98} (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi_166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  148753
                  LIB3175-016-P1-K1-D1
Seq. ID
                  BLASTN
Method
                  q3510339
NCBI GI
BLAST score
                  44
E value
                  1.0e-15
                  90
Match length
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3K7, complete sequence [Arabidopsis thaliana]
                  148754
Seq. No.
                  LIB3175-016-P1-K1-D10
Seq. ID
                  BLASTX
Method
                  q2529229
NCBI GI
BLAST score
                  524
                  2.0e-53
E value
Match length
                  112
% identity
                   (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                  148755
                  LIB3175-016-P1-K1-D11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1644427
                  500
BLAST score
E value
                   1.0e-50
Match length
                  109
% identity
                   (U74610) glyoxalase II [Arabidopsis thaliana]
NCBI Description
                  148756
Seq. No.
                  LIB3175-016-P1-K1-D12
Seq. ID
Method
                  BLASTX
```

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```
g4584255
NCBI GI
BLAST score
                  238
                  5.0e-20
E value
Match length
                  56
                  79
% identity
                  (Y18471) SINA1p [Vitis vinifera]
NCBI Description
                  148757
Seq. No.
                  LIB3175-016-P1-K1-D2
Seq. ID
                  BLASTX
Method
                  g974294
NCBI GI
                  244
BLAST score
                  1.0e-20
E value
                  92
Match length
                  54
% identity
                  (U31309) LP6 [Pinus taeda]
NCBI Description
Seq. No.
                  148758
                  LIB3175-016-P1-K1-D3
Seq. ID
                  BLASTX
Method
                  g1946367
NCBI GI
BLAST score
                  155
                  3.0e-10
E value
                  70
Match length
                  47
% identity
                   (U93215) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148759
                  LIB3175-016-P1-K1-D4
Seq. ID
                  BLASTX
Method
                  q4314363
NCBI GI
                  725
BLAST score
                   4.0e-77
E value
Match length
                  140
                  100
% identity
                   (AC006340) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  148760
Seq. No.
Seq. ID
                  LIB3175-016-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q2501056
                   661
BLAST score
                  1.0e-69
E value
Match length
                  132
                  100
% identity
                  SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS)
NCBI Description
                  >gi 2129737 pir S71293 seryl-tRNA synthetase - Arabidopsis
                  thaliana >gi 1359497 emb_CAA94388_ (Z70313) seryl-tRNA
                  Synthetase [Arabidopsis thaliana]
                  148761
Seq. No.
                  LIB3175-016-P1-K1-D6
Seq. ID
Method
                  BLASTX
                  q4586249
NCBI GI
                  718
BLAST score
                  3.0e-76
E value
                  140
Match length
```

. .

Seq. No.

Seq. ID

```
% identity
                  (AL049640) putative pollen surface protein [Arabidopsis
NCBI Description
                  thaliana]
                  148762
Seq. No.
Seq. ID
                  LIB3175-016-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g4371282
                  604
BLAST score
                  6.0e-63
E value
Match length
                  121
                  100
% identity
                  (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148763
                  LIB3175-016-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q231586
BLAST score
                  289
E value
                  6.0e-26
Match length
                  118
% identity
                  56
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 82027 pir_S20504 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >qi 18831 emb CAA41401 (X58498) mitochondrial ATP synthase
                  beta-subunit [Hevea brasiliensis]
Seq. No.
                  148764
Seq. ID
                  LIB3175-016-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q4689386
BLAST score
                  549
E value
                  2.0e-56
Match length
                  117
% identity
                  (AF139468) photosystem I reaction center subunit III [Vigna
NCBI Description
                  radiata]
Seq. No.
                  148765
                  LIB3175-016-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730864
BLAST score
                  162
E value
                  4.0e-11
Match length
                  130
% identity
                  SPORULATION PROTEIN SPS19 (SPORULATION-SPECIFIC PROTEIN
NCBI Description
                  SPX19) >gi 2117442 pir S50729 sporulation protein SPS19 -
                  yeast (Saccharomyces cerevisiae) >gi 600063 emb CAA55506
                  (X78898) N1362 [Saccharomyces cerevisiae]
```

18840

[Saccharomyces cerevisiae]

LIB3175-016-P1-K1-E10

148766

>gi\_1302205\_emb\_CAA96103\_ (Z71479) ORF YNL202w

```
BLASTX
Method
NCBI GI
                   q2829899
BLAST score
                   410
                   4.0e-40
E value
Match length
                   118
% identity
                   65
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp_AJ001449_2465015 and major#latex protein,
                   gp_X91961_1107495 [Arabidopsis thaliana]
                   148767
Seq. No.
                  LIB3175-016-P1-K1-E12
Seq. ID
Method
                   BLASTX
                   g4006915
NCBI GI
BLAST score
                   234
                   2.0e-19
E value
                   119
Match length
                   45
% identity
                  (Z99708) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   148768
Seq. No.
                  LIB3175-016-P1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4467148
BLAST score
                   691
                   4.0e-73
E value
Match length
                   138
                   100
% identity
                   (AL035540) putative protein [Arabidopsis thaliana]
NCBI Description
                   148769
Seq. No.
                   LIB3175-016-P1-K1-E4
Seq. ID
Method
                   BLASTN
                   g1657620
NCBI GI
BLAST score
                   387
                   0.0e + 00
E value
Match length
                   395
% identity
                   Arabidopsis thaliana putative acyl-coA dehydrogenase G6p
NCBI Description
                   (AtG6) mRNA, complete cds
                   148770
Seq. No.
                   LIB3175-016-P1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3402692
BLAST score
                   305
E value
                   7.0e-28
Match length
                   77
                   75
% identity
NCBI Description
                   (AC004697) putative
                   CDP-diacylglycerol--glycerol-3-phosphate
                   3-phosphatidyltransferase [Arabidopsis thaliana]
Seq. No.
                   148771
                   LIB3175-016-P1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3236234
```

```
BLAST score
                    0.0e + 00
E value
Match length
                    393
% identity
                    95
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F13M22 genomic
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    148772
Seq. ID
                   LIB3175-016-P1-K1-E7
Method
                   BLASTN
NCBI GI
                    g1931636
BLAST score
                    265
E value
                    1.0e-147
Match length
                    416
% identity
                    100
NCBI Description
                   Arabidopsis thaliana BAC T19D16 genomic sequence
                    148773
Seq. No.
Seq. ID
                    LIB3175-016-P1-K1-E8
Method
                    BLASTX
NCBI GI
                    q4567268
BLAST score
                   586
E value
                    8.0e-61
Match length
                    124
% identity
                    99
NCBI Description
                    (AC006841) putative fructose biphosphate aldolase
                    [Arabidopsis thaliana]
Seq. No.
                    148774
Seq. ID
                    LIB3175-016-P1-K1-F1
Method
                    BLASTX
NCBI GI
                    g2225877
BLAST score
                    368
E value
                    3.0e - 35
Match length
                    99
% identity
                    70
NCBI Description
                    (AB002406) TIP49 [Rattus norvegicus] >qi 4106528 (AF100694)
                   Pontin52 [Mus musculus] >gi_4521276_dbj_BAA76313.1_(AB001581) DNA helicase p50 [Rattus norvegicus]
Seq. No.
                    148775
                   LIB3175-016-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                    g4432856
BLAST score
                    410
E value
                    2.0e-40
Match length
                   84
% identity
                   (AC006300) putative 2A6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    148776
Seq. ID
                   LIB3175-016-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g4512675
BLAST score
                   699
E value
                   5.0e-74
Match length
                   138
```

```
% identity
NCBI Description
                    (AC006931) putative citrate synthase [Arabidopsis thaliana]
Seq. No.
                    148777
Seq. ID
                    LIB3175-016-P1-K1-F12
Method
                    BLASTX
NCBI GI
                    q119143
BLAST score
                    730
E value
                    1.0e-77
Match length
                    138
                    100
% identity
                    ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                   >gi_81606_pir__S06724 translation elongation factor eEF-1
alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                    (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                    >gi 1369927 emb CAA34454 (X16431) elongation factor
                    1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                    (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                   >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
>gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                    >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                    148778
Seq. ID
                    LIB3175-016-P1-K1-F2
Method
                    BLASTX
NCBI GI
                    g3445416
BLAST score
                    168
E value
                    9.0e-12
                    39
Match length
% identity
                    92
NCBI Description (Y11154) DEAD box-like RNA helicase [Arabidopsis thaliana]
Seq. No.
                    148779
Seq. ID
                    LIB3175-016-P1-K1-F3
Method
                    BLASTX
NCBI GI
                    q1172599
BLAST score
                    598
E value
                    3.0e-62
Match length
                    118
% identity
                    97
                    PROTEASOME COMPONENT C5 (MULTICATALYTIC ENDOPEPTIDASE
NCBI Description
                    COMPLEX SUBUNIT C5) (TAS-F22/FAFP98)
                    >gi_600387_emb_CAA47753_ (X67338) proteosome subunit
                    [Arabidopsis thaliana]
Seq. No.
                    148780
Seq. ID
                   LIB3175-016-P1-K1-F4
                   BLASTX
Method
NCBI GI
                   q112681
                    739
BLAST score
E value
                    1.0e-78
Match length
                   138
                    99
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                    >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
```

```
storage protein [Arabidopsis thaliana]
Seq. No.
                   148781
Seq. ID
                   LIB3175-016-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   q3236248
BLAST score
                   530
E value
                   3.0e-54
Match length
                   133
                                            · <u>A</u> ·
% identity
NCBI Description (AC004684) unknown protein [Arabidopsis thaliana]
                   148782
Seq. No.
                   LIB3175-016-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q113334
BLAST score
                   419
E value
                   3.0e-41
                   131
Match length
% identity
                  ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2
NCBI Description
                   ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A)
                   (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT)
                   >gi_90291_pir__A30111 alpha-adaptin A - mouse
                   >gi_49878_emb_CAA33096_ (X14971) alpha-adaptin (A) (AA
                   1-977) [Mus musculus]
                   148783
Seq. No.
                   LIB3175-016-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3522946
BLAST score
                   501
                   8.0e-51
E value
                   105
Match length
% identity
NCBI Description
                   (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
                   148784
Seq. No.
                   LIB3175-016-P1-K1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3201608
BLAST score
                   228
E value
                   1.0e-125
Match length
                   409
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148785
Seq. ID
                   LIB3175-016-P1-K1-G1
Method
                   BLASTN
NCBI GI
                   q3319365
BLAST score
                   113
E value
                   1.0e-56
Match length
                   349
                   98
% identity
```

40.

18844

NCBI Description Arabidopsis thaliana BAC T24M8

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148786
Seq. No.
                   LIB3175-016-P1-K1-G10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4580384
BLAST score
                   246
                   7.0e-21
E value
                   138
Match length
% identity
                   (AC007184) putative histone H2B [Arabidopsis thaliana]
NCBI Description
                   148787
Seq. No.
                   LIB3175-016-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   a4587552
                   512
BLAST score
                   4.0e-52
E value
                   99
Match length
                   100
% identity
                   (AC006577) Strong similarity to gb_S77096 aldehyde
NCBI Description
                   dehydrogenase homolog from Brassica napus and is a member
                   of PF_00171 Aldehyde dehydrogenase family. ESTs gb_T46213,
                   gb T42164, gb_T43682, gb_N96380, gb_T42973, gb
                   148788
Seq. No.
                   LIB3175-016-P1-K1-G2
Seq. ID
Method
                   BLASTN
NCBI GI
                   a3421122
                   141
BLAST score
                   9.0e-74
E value
Match length
                   181
% identity
                   Arabidopsis thaliana 20S proteasome beta subunit PBG1
NCBI Description
                   (PBG1) mRNA, complete cds
                   148789
Seq. No.
Seq. ID
                   LIB3175-016-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q3834310
BLAST score
                   522
                   3.0e - 53
E value
Match length
                   99
% identity
                   100
                   (AC005679) Similar to Ubiquitin-conjugating enzyme E2-17 KD
NCBI Description
                   gb D83004 from Homo sapiens. ESTs gb_T88233, gb_Z24464,
                   gb_N37265, gb_H36151, gb_Z34711, gb_AAO40983, and gb_T22122 come from this gene. [Arabidopsis thaliana]
                   148790
Seq. No.
Seq. ID
                   LIB3175-016-P1-K1-G4
Method
                   BLASTX
                   q541858
NCBI GI
BLAST score
                   495
                   3.0e-50
E value
                   100
Match length
% identity
                   endoxyloglucan transferase - Arabidopsis thaliana
NCBI Description
```

Seq. No. Seq. ID

BLAST score

Match length

% identity

Method NCBI GI

E value

Seq. No. Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

Seq. No. Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

```
>gi_469484_dbj_BAA03921_ (D16454) endo-xyloglucan
transferase [Arabidopsis thaliana] >gi_4063757 (AC005561)
                   endo-xyloglucan transferase [Arabidopsis thaliana]
                   148791
                   LIB3175-016-P1-K1-G5
                   BLASTN
                   g1297184
                   222
                   1.0e-121
                   376
                   100
NCBI Description
                   Arabidopsis thaliana chromosome I cosmid q8261 DNA
                   (cytosine-5-) methyltransferase, zinc finger protein 1,
                   nucleoporin 98, poly A+ RNA export protein, plasma membrane
                   ATPase 2, and serine/threonine protein kinase genes, co
                   148792
                   LIB3175-016-P1-K1-G6
                   BLASTX
                   q3600059
                   726
                   3.0e-77
                   139
                   100
NCBI Description
                   (AF080120) contains similarity to WB domains, G-beta
                   repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03)
                   [Arabidopsis thaliana]
                   148793
                   LIB3175-016-P1-K1-G8
                   BLASTX
                   q1172873
                   672
                   7.0e-71
                   133
                   100
                   CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
NCBI Description
                   drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                   precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                   (D13043) thiol protease [Arabidopsis thaliana]
                   148794
                   LIB3175-016-P1-K1-H10
                   BLASTX
                   q2909781
```

Seq. No.

Seq. ID

Method NCBI GI BLAST score 270 E value 2.0e-24 Match length 53 % identity

(AF020288) MgATP-energized glutathione S-conjugate pump NCBI Description

[Arabidopsis thaliana]

Seq. No. 148795

Seq. ID LIB3175-016-P1-K1-H11

Method BLASTX NCBI GI q4689386

18846

Sign of

```
BLAST score
                    318
E value
                    2.0e-29
Match length
                   143
% identity
                    52
                    (AF139468) photosystem I reaction center subunit III [Vigna
NCBI Description
                   radiata]
Seq. No.
                    148796
Seq. ID
                   LIB3175-016-P1-K1-H12
Method
                   BLASTX
NCBI GI
                    g4753651
BLAST score
                   638
E value
                    7.0e-67
Match length
                    129
% identity
NCBI Description
                    (AL049751) ribosomal protein L13a like protein [Arabidopsis
                    thaliana]
                    148797
Seq. No.
Seq. ID
                    LIB3175-016-P1-K1-H2
Method
                   BLASTX
NCBI GI
                    g132074
BLAST score
                    733
E value
                    5.0e-78
Match length
                    136
% identity
                    100
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir_RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                    148798
Seq. ID
                    LIB3175-016-P1-K1-H4
Method
                    BLASTX
NCBI GI
                    g112681
BLAST score
                    102
E value
                    2.0e-35
Match length
                    122
                    70
% identity
                   12S SEED STORAGE PROTEIN PRECURSOR >gi_81604_pir_ $08509
NCBI Description
                    cruciferin precursor (CRA1) - Arabidopsis thaliana
                    >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                    thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                    storage protein [Arabidopsis thaliana]
Seq. No.
                    148799
Seq. ID
                   LIB3175-016-P1-K1-H5
Method
                   BLASTX
NCBI GI
                    g2129550
BLAST score
                    308
E value
                    3.0e-28
Match length
                   134
                    57
% identity
                   calcium-dependent protein kinase (EC 2.7.1.-) CDPK6 -
NCBI Description
                   Arabidopsis thaliana >gi_2129554_pir__S71901 calcium-dependent protein kinase 6 - Arabidopsis thaliana
                    >gi_836940 (U20623) calcium-dependent protein kinase
```

```
calcium-dependent protein kinase [Arabidopsis thaliana]
                   >gi 4454034 emb CAA23031.1 (AL035394) calcium-dependent
                  protein kinase (CDPK6) [Arabidopsis thaliana]
Seq. No.
                   148800
Seq. ID
                  LIB3175-016-P1-K1-H6
Method
                  BLASTX
NCBI GI
                   q4753651
BLAST score
                   306
E value
                   4.0e-28
                   81
Match length
% identity
                   73
NCBI Description
                   (AL049751) ribosomal protein L13a like protein [Arabidopsis
                   thaliana]
Seq. No.
                   148801
                   LIB3175-016-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3184082.
BLAST score
                   287
E value
                   1.0e-25
                   95
Match length
% identity
                   52
NCBI Description
                   (AL023781) N-terminal acetyltransferase 1
                   [Schizosaccharomyces pombe]
Seq. No.
                   148802
                   LIB3175-016-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4454467
BLAST score
                   218
E value
                   1.0e-17
Match length
                   135
% identity
                   33
NCBI Description
                   (AC006234) unknown protein [Arabidopsis thaliana]
Seq. No.
                   148803
Seq. ID
                   LIB3175-016-P1-K1-H9
Method
                   BLASTN
NCBI GI
                   g4106339
BLAST score
                   387
E value
                   0.0e + 00
Match length
                   415
                   98
% identity
NCBI Description
                  Arabidopsis thaliana protein phosphatase 2A regulatory
                   subunit isoform B' delta mRNA, complete cds
Seq. No.
                   148804
                  LIB3175-017-P1-K1-A1
Seq. ID
Method
                  BLASTN
NCBI GI
                   q4263753
BLAST score
                  170
E value
                   1.0e-90
                  353
Match length
% identity
                   100
```

[Arabidopsis thaliana] >qi 836944 (U20625)

18848

NCBI Description Arabidopsis thaliana chromosome V map near 60.5 cM,



complete sequence [Arabidopsis thaliana] Seq. No. 148805 Seq. ID LIB3175-017-P1-K1-A10 Method BLASTX NCBI GI g2795803 BLAST score 425 E value 6.0e-42Match length 124 % identity 63 (AC003674) putative beta-1,3-endoglucanase [Arabidopsis NCBI Description thaliana] >gi 3355491 (AC004218) putative beta-1,3-endoglucanase [Arabidopsis thaliana] Seq. No. 148806 LIB3175-017-P1-K1-A12 Seq. ID Method BLASTN NCBI GI g4662640 BLAST score 172 E value 7.0e-92 Match length 410 31 % identity Arabidopsis thaliana chromosome II BAC F15K19 genomic NCBI Description sequence, complete sequence Seq. No. 148807 Seq. ID LIB3175-017-P1-K1-A2 Method BLASTX NCBI GI g3834312 BLAST score 681 E value 5.0e-72 Match length 126 % identity NCBI Description (AC005679) Strong similarity to glycoprotein EP1 gb\_L16983 Daucus carota and a member of S locus glycoprotein family PF\_00954. ESTs gb\_AA067487, gb\_Z35737, gb\_Z30815, gb\_Z35350, gb\_AA713171, gb\_AI100553, gb\_Z34248, gb AA728536, gb Z30816 an Seq. No. 148808 Seq. ID LIB3175-017-P1-K1-A4 Method BLASTX NCBI GI g2497539 BLAST score 155 E value

2.0e-10 Match length 39 % identity 85

PYRUVATE KINASE, CHLOROPLAST ISOZYME A PRECURSOR >gi 169703 NCBI Description (M64736) ATP:pyruvate phosphotransferase [Ricinus communis]

Seq. No. 148809

Seq. ID LIB3175-017-P1-K1-A5

Method BLASTX NCBI GI g2129608 BLAST score 705 1.0e-74 E value Match length 142

```
% identity
NCBI Description
                  GTP-binding protein, 68K - Arabidopsis thaliana >qi 807577
                   (L38614) GTP-binding protein [Arabidopsis thaliana]
                  148810
Seq. No.
Seq. ID
                  LIB3175-017-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q2894612
BLAST score
                  213
E value
                  1.0e-19
                  95
Match length
                  54
% identity
                  (AL021889) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  148811
                  LIB3175-017-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4220612
BLAST score
                  531
E value
                  2.0e-54
Match length
                  114
% identity
                  89
NCBI Description
                  (AB021934) nicotianamine synthase [Arabidopsis thaliana]
Seq. No.
                  148812
                  LIB3175-017-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4544458
BLAST score
                  193
E value
                  8.0e-15
Match length
                  123
% identity
                  41
NCBI Description
                  (AC006592) unknown protein [Arabidopsis thaliana]
Seq. No.
                  148813
Seq. ID
                  LIB3175-017-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q4510360
BLAST score
                  405
E value
                  0.0e + 00
Match length
                  417
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F11F19 genomic
                  sequence, complete sequence
Seq. No.
                  148814
Seq. ID
                  LIB3175-017-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g542157
BLAST score
                  559
E value
                  1.0e-57
Match length
                  128
                  82
% identity
NCBI Description
                 ribosomal 5S RNA-binding protein - Rice
Seq. No.
                  148815
Seq. ID
                  LIB3175-017-P1-K1-B4
```

```
Method
                  BLASTX
NCBI GI
                  q2398679
BLAST score
                  184
E value
                   1.0e-13
Match length
                   119
% identity
NCBI Description
                   (Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate
                  synthase [Morinda citrifolia]
                  148816
Seq. No.
Seq. ID
                  LIB3175-017-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q4454447
BLAST score
                  345
E value
                  0.0e + 00
Match length
                   425
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  148817
Seq. No.
                  LIB3175-017-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                   662
E value
                  1.0e-69
                  126
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  148818
Seq. ID
                  LIB3175-017-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q2829911
BLAST score
                  402
E value
                  3.0e-39
Match length
                  115
% identity
NCBI Description
                   (AC002291) Unknown protein [Arabidopsis thaliana]
Seq. No.
                  148819
Seq. ID
                  LIB3175-017-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q2454184
BLAST score
                  546
E value
                  3.0e-56
Match length
                  110
% identity
NCBI Description
                   (U80186) pyruvate dehydrogenase El beta subunit
                   [Arabidopsis thaliana]
```

```
Seq. No.
                  148820
Seq. ID
                  LIB3175-017-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g166867
BLAST score
                  602
E value
                  1.0e-62
Match length
                  133
                  87
% identity
                   (J05216) ribosomal protein S11 (probable start codon at bp
NCBI Description
                  67) [Arabidopsis thaliana]
                  148821
Seq. No.
Seq. ID
                  LIB3175-017-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g126962
BLAST score
                  576
                  1.0e-59
E value
Match length
                  116
                  100
% identity
                  TONOPLAST INTRINSIC PROTEIN, ROOT-SPECIFIC RB7
NCBI Description
                  >gi_99747_pir__S13718 probable membrane channel protein -
                  Arabidopsis thaliana >gi_16492_emb_CAA38633_ (X54854)
                  possible membrane channel protein [Arabidopsis thaliana]
Seq. No.
                  148822
                  LIB3175-017-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245093
BLAST score
                  485
                  5.0e-49
E value
Match length
                  117
                  51
% identity
NCBI Description (Z97343) membrane channel protein [Arabidopsis thaliana]
                  148823
Seq. No.
Seq. ID
                  LIB3175-017-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g4567237
                  108
BLAST score
E value
                  1.0e-53
Match length
                  329
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T22F11 genomic
                  sequence, complete sequence
                  148824
Seq. No.
Seq. ID
                  LIB3175-017-P1-K1-C2
Method
                  BLASTN
NCBI GI
                  g4589446
BLAST score
                  241
E value
                  1.0e-133
Match length
                  2.86
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  T12B11, complete sequence
Seq. No.
                  148825
```

```
Seq. ID
                   LIB3175-017-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g2842477
BLAST score
                   589
                   4.0e-61
E value
Match length
                   122
% identity
NCBI Description
                   (AL021749) copper-binding protein-like [Arabidopsis
                   thaliana]
                                                     . : :
Seq. No.
                   148826
                   LIB3175-017-P1-K1-C6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1161926
BLAST score
                   559
E value
                   1.0e-57
                   136
Match length
% identity
                   79
                   (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
NCBI Description
                   148827
Seq. No.
Seq. ID
                   LIB3175-017-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g115385
BLAST score
                   686
                   1.0e-72
E value
                   132
Match length
                   97
 % identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                    (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
                   148828
 Seq. No.
                   LIB3175-017-P1-K1-D1
 Seq. ID
Method
                   BLASTX
NCBI GI
                   q1710780
 BLAST score
                   453
                   3.0e-45
E value
Match length
                   121
                   72
 % identity
                   40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
NCBI Description
                    (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
                   148829
 Seq. No.
 Seq. ID
                   LIB3175-017-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q4454032
 BLAST score
                   303
 E value
                   1.0e-27
Match length
                   110
 % identity
                    (AL035394) putative protein [Arabidopsis thaliana]
NCBI Description
 Seq. No.
                   148830
 Seq. ID
                   LIB3175-017-P1-K1-D4
```

```
BLASTN
Method
NCBI GI
                   q3046855
BLAST score
                   231
E value
                   1.0e-127
Match length
                   380
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MSL1, complete sequence [Arabidopsis thaliana]
                   148831
Seq. No.
Seq. ID
                  LIB3175-017-P1-K1-D5
                  BLASTX
Method
                   q100490
NCBI GI
BLAST score
                  583
E value
                   2.0e-60
                   117
Match length
                   28
% identity
NCBI Description
                  polyubiquitin - garden snapdragon (fragment)
                   >gi_16071_emb_CAA48140_ (X67957) ubiquitin [Antirrhinum
                  majus]
                   148832
Seq. No.
Seq. ID
                   LIB3175-017-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   q3128142
BLAST score
                   393
                   0.0e + 00
E value
                   413
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQN23, complete sequence [Arabidopsis thaliana]
                   148833
Seq. No.
                   LIB3175-017-P1-K1-D7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4314354
BLAST score
                   113
                   1.0e-56
E value
                   357
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC T9I22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   148834
Seq. No.
                   LIB3175-017-P1-K1-D9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1628583
BLAST score
                   625
E value
                   2.0e-65
                   120
Match length
                   100
% identity
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                   thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                   cruciferin seed storage protein [Arabidopsis thaliana]
                   148835
Seq. No.
Seq. ID
                   LIB3175-017-P1-K1-E1
```

```
Method
                  BLASTX
NCBI GI
                  a1173103
BLAST score
                  506
E value
                  2.0e-51
Match length
                  87
                  99
% identity
                  RIBONUCLEASE 1 PRECURSOR >gi_561998 (U05206) ribonuclease
NCBI Description
                  [Arabidopsis thaliana] >gi_3461823 (AC004138) ribonuclease,
                  RNS1 [Arabidopsis thaliana]
Seq. No.
                  148836
                  LIB3175-017-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2244750
BLAST score
                  429
E value
                  3.0e-45
Match length
                  116
                  78
% identity
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                  >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
Seq. No.
                  148837
Seq. ID
                  LIB3175-017-P1-K1-E11
Method
                  BLASTX
                  g1717949
NCBI GI
                  355
BLAST score
E value
                  7.0e-34
                  72
Match length
                  85
% identity
NCBI Description
                  UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1
                  PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1)
                  >gi_100375_pir__B41607 ubiquinol--cytochrome-c reductase
                  (EC 1.10.2.2) iron-sulfur protein precursor - common
                  tobacco (fragment) >gi_170322 (M77225) Rieske Fe-S protein
                  [Nicotiana tabacum]
                  148838
Seq. No.
                  LIB3175-017-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  a4544419
BLAST score
                  443
                  5.0e-44
E value
Match length
                  118
                  79
% identity
NCBI Description
                  (AC006955) unknown protein [Arabidopsis thaliana]
Seq. No.
                  148839
Seq. ID
                  LIB3175-017-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q3660469
BLAST score
                  558
E value
                  2.0e-57
Match length
                  113
% identity
                  (AJ001808) succinyl-CoA-ligase beta subunit [Arabidopsis
NCBI Description
                  thaliana] >gi 4512693 gb AAD21746.1 (AC006569)
```

```
succinyl-CoA ligase beta subunit [Arabidopsis thaliana]
Seq. No.
                  148840
Seq. ID
                  LIB3175-017-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q1617013
BLAST score
                  334
                  3.0e-31
E value
Match length
                  67
% identity
                  100
NCBI Description
                  (Y07745) histone H2B like protein [Arabidopsis thaliana]
Seq. No.
                  148841
                  LIB3175-017-P1-K1-E4
Seq. ID
Method
                  BLASTN
                  g4263774
NCBI GI
                  278
BLAST score
E value
                  1.0e-155
Match length
                  366
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T20F21 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148842
                  LIB3175-017-P1-K1-E6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129473
BLAST score
                  295
E value
                  1.0e-26
Match length
                  92
% identity
                  60
                  arabinogalactan-like protein - loblolly pine >gi_607774
NCBI Description
                   (U09556) arabinogalactan-like protein [Pinus taeda]
Seq. No.
                  148843
Seq. ID
                  LIB3175-017-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4741940
BLAST score
                  516
E value
                  1.0e-52
Match length
                  95
% identity
NCBI Description
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.
                  148844
Seq. ID
                  LIB3175-017-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g2129543
                  706
BLAST score
E value
                  7.0e-75
Match length
                  130
% identity
                  100
                  beta-fructofuranosidase (EC 3.2.1.26) - Arabidopsis
NCBI Description
                  thaliana (fragment) >gi_1183868_emb_CAA64781_ (X95537)
                  beta-fructosidase [Arabidopsis thaliana]
```

148845

Seq. No.

```
LIB3175-017-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1709825
BLAST score
                   590
E value
                   3.0e-61
Match length
                  123
                   99
% identity
NCBI Description
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR
                   (PSI-N) >gi 1237124 (U32176) PSI-N [Arabidopsis thaliana]
Seq. No.
                  148846
                  LIB3175-017-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432856
BLAST score
                   358
E value
                   5.0e - 34
                  71
Match length
% identity
                   99
NCBI Description
                 (AC006300) putative 2A6 protein [Arabidopsis thaliana]
                   148847
Seq. No.
Seq. ID
                  LIB3175-017-P1-K1-F3
Method
                  BLASTN
NCBI GI
                   q2760170
BLAST score
                  250
E value
                   1.0e-138
Match length
                   346
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIO24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148848
Seq. ID
                  LIB3175-017-P1-K1-F4
Method
                  BLASTX
NCBI GI
                   g1561730
BLAST score
                   153
E value
                   5.0e-10
                   58
Match length
% identity
                  (U65491) Dreg-3 protein [Drosophila melanogaster]
NCBI Description
Seq. No.
                  148849
                  LIB3175-017-P1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449329
BLAST score
                  23
E value
                   6.0e-03
Match length
                   409
% identity
                   85
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148850
                  LIB3175-017-P1-K1-F7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g2088638
BLAST score
                  34
```

```
E value
                   6.0e-10
Match length
                   70
% identity
                   87
                   Arabidopsis thaliana chromosome II BAC T28M21 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148851
Seq. ID
                   LIB3175-017-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g3511285
BLAST score
                   609
E value
                   2.0e-63
Match length
                   125
                   88
% identity
NCBI Description
                   (AF081534) cellulose synthase [Populus alba x Populus
                   tremulal
                   148852
Seq. No.
                   LIB3175-017-P1-K1-G1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3319365
BLAST score
                   307
E value
                   1.0e-172
Match length
                   410
% identity
                   Arabidopsis thaliana BAC T24M8
NCBI Description
Seq. No.
                   148853
                   LIB3175-017-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q132074
BLAST score
                   668
                   2.0e-70
E value
                   124
Match length
                   100
% identity
NCBI Description
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                   Al precursor - Arabidopsis thaliana
                   148854
Seq. No.
Seq. ID
                   LIB3175-017-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q2506443
BLAST score
                   476
                   6.0e-48
E value
Match length
                   124
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                   CHLOROPLAST >gi_2117520_pir__JQ1285
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                   Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                   3-phosphate dehydrogenase [Arabidopsis thaliana]
                   >gi_1402885_emb_CAA66816_ (X98130)
                   glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) [Arabidopsis thaliana]
```

```
Seq. No.
                   148855
Seq. ID
                   LIB3175-017-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g2605769
BLAST score
                   237
E value
                   4.0e-20
Match length
                   87
% identity
NCBI Description
                   (AF027288) NADH dehydrogenase [Olea europaea]
                   148856
Seq. No.
Seq. ID
                   LIB3175-017-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   q3859606
BLAST score
                   460
E value
                   5.0e-46
Match length
                   111
% identity
NCBI Description
                   (AF104919) contains similarity to cysteine proteases (Pfam:
                   PF00112, E=1.3e-79, N=1) [Arabidopsis thaliana]
Seq. No.
                   148857
Seq. ID
                   LIB3175-017-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   q3075394
BLAST score
                   656
E value
                   5.0e-69
Match length
                   130
% identity
                   98
NCBI Description
                   (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
                   thaliana] >gi_3559809_emb_CAA09311_ (AJ010713) fiddlehead
                   protein [Arabidopsis thaliana]
Seq. No.
                   148858
Seq. ID
                   LIB3175-017-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g544242
BLAST score
                   332
E value
                   5.0e-36
Match length
                   123
% identity
                   69
                   ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG)
NCBI Description
                   >gi 485498 pir S33533 heat shock protein 90 homolog
                   precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94
                   homologue [Hordeum vulgare]
                   148859
Seq. No.
Seq. ID
                   LIB3175-017-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q125576
BLAST score
                   338
E value
                   9.0e-32
                   92
Match length
                   76
% identity
NCBI Description
                   PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE)
                   (PRK) >gi_99744_pir__S16583 phosphoribulokinase (EC
```

```
2.7.1.19) precursor - Arabidopsis thaliana
                  >gi 16441 emb CAA41155 (X58149) Ribulose-5-phosphate
                  kinase [Arabidopsis thaliana]
Seq. No.
                  148860
Seq. ID
                  LIB3175-017-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g3449334
BLAST score
                  98
                  8.0e-48
E value
                  228
Match length
                   97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148861
                  LIB3175-017-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3157928
BLAST score
                  559
E value
                  1.0e-57
Match length
                  115
% identity
                   99
                   (AC002131) Similar to fumarylacetoacetate hydrolase,
NCBI Description
                  qb L41670 from Emericella nidulans. [Arabidopsis thaliana]
Seq. No.
                  148862
Seq. ID
                  LIB3175-017-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g82677
BLAST score
                  254
                  8.0e-29
E value
Match length
                  81
% identity
                  75
NCBI Description
                  catalase (EC 1.11.1.6) chain 1 - maize
                  >gi 22232 emb CAA31056 (X12538) catalase-1 (AA 1-492) [Zea
                  mays]
                  148863
Seq. No.
Seq. ID
                  LIB3175-017-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2924777
BLAST score
                  201
E value
                  1.0e-15
Match length
                  132
% identity
NCBI Description
                   (AC002334) putative receptor protein kinase [Arabidopsis
                  thaliana]
                  148864
Seq. No.
Seq. ID
                  LIB3175-017-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g131211
BLAST score
                  176
E value
                  9.0e-13
Match length
                  36
% identity
                  94
```

```
PHOTOSYSTEM I REACTION CENTRE SUBUNIT IX (PSI-J)
NCBI Description
                   >gi_1363533_pir__S58571 photosystem I protein psaJ - maize
chloroplast >gi_552734 (J04502) ORF42 [Zea mays]
                   >gi_902241 emb CAA60305_ (X86563) psaJ [Zea mays]
Seq. No.
                   148865
                   LIB3175-017-P1-K1-H9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3176695
BLAST score
                   364
E value
                   0.0e + 00
                   372
Match length
% identity
                   Arabidopsis thaliana chromosome I BAC F14J9 genomic
NCBI Description
                   sequence contains phyA marker, complete sequence
                   [Arabidopsis thaliana]
                   148866
Seq. No.
                   LIB3175-018-P1-K1-A1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1350680
BLAST score
                   611
E value
                   1.0e-63
Match length
                   123
                   94
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L1
                   148867
Seq. No.
                   LIB3175-018-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3522945
BLAST score
                   689
E value
                   7.0e-73
Match length
                   133
                   100
% identity
                   (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148868
                   LIB3175-018-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3522945
BLAST score
                   659
                   2.0e-69
E value
Match length
                   129
% identity
                   (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148869
Seq. ID
                   LIB3175-018-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g3522945
BLAST score
                   593
E value
                   1.0e-61
Match length
                   114
                   99
% identity
```

NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]

```
Seq. No.
                   148870
Seq. ID
                   LIB3175-018-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g322571
BLAST score
                   303
E value
                   1.0e-27
Match length
                   77
                   79
% identity
                   proteinase inhibitor II - Arabidopsis thaliana
NCBI Description
                   >gi_16427_emb_CAA48892_ (X69139) protease inhibitor II
[Arabidopsis thaliana] >gi_4038041 (AC005936) proteinase
                   inhibitor II [Arabidopsis thaliana]
Seq. No.
                   148871
Seq. ID
                   LIB3175-018-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g2781354
BLAST score
                   615
E value
                   3.0e-64
Match length
                   118
                   97
% identity
NCBI Description
                   (AC003113) F2401.10 [Arabidopsis thaliana]
                   148872
Seq. No.
Seq. ID
                   LIB3175-018-P1-K1-A4
Method
                   BLASTX
NCBI GI
                   g1172872
BLAST score
                   281
E value
                   4.0e-25
Match length
                   82
                   70
% identity
NCBI Description
                   CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718
                   drought-inducible cysteine proteinase (\overline{EC} \ 3.4.\overline{22.-)} \ RD19A
                   precursor - Arabidopsis thaliana >gi 435618 dbj BAA02373
                   (D13042) thiol protease [Arabidopsis thaliana]
                   >gi 4539328 emb CAB38829.1 (AL035679) drought-inducible
                   cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                   148873
                   LIB3175-018-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1710530
BLAST score
                   145
E value
                   4.0e-74
Match length
                   140
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L27A >gi 2129719 pir S71256
                   ribosomal protein L27a - Arabidopsis thaliana
                   >gi 1107487 emb CAA63025 (X91959) 60S ribosomal protein
                   L27a [Arabidopsis thaliana]
Seq. No.
                   148874
Seq. ID
                   LIB3175-018-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   q4220446
BLAST score
                   547
E value
                   2.0e-56
```

```
Match length
                  111
% identity
                  (AC006216) Strong similarity to gi 2062155 T02004.2
NCBI Description
                  mitochondrial processing peptidase alpha subunit precusor
                  isolog from Arabidopsis thaliana BAC gb_AC001645. ESTs
                  gb_Z18504 and gb_AA395715 come from this gene. [Arabidopsis
                  thaliana]
Seq. No.
                  148875
                  LIB3175-018-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1710581
BLAST score
                  594
E value
                  9.0e-62
Match length
                  123
% identity
                  94
                  60S RIBOSOMAL PROTEIN L9 >gi_2129720_pir__S71255 ribosomal
NCBI Description
                  protein L9 - Arabidopsis thaliana >gi 1107489 emb_CAA63024_
                  (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]
Seq. No.
                  148876
Seq. ID
                  LIB3175-018-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  g1914683
BLAST score
                  223
E value
                  3.0e-18
                  73
Match length
% identity
                  (Y12013) RAD23, isoform I [Daucus carota]
NCBI Description
Seq. No.
                  148877
                  LIB3175-018-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g417381
BLAST score
                  585
E value
                  9.0e-61
Match length
                  114
% identity
                  99
                  NITRILASE 1 >gi_99738_pir__S22398 nitrilase (EC 3.5.5.1) -
NCBI Description
                  Arabidopsis thaliana >qi 16400 emb CAA45041 (X63445)
                  nitrilase I [Arabidopsis thaliana]
Seq. No.
                  148878
                  LIB3175-018-P1-K1-B10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2493122
BLAST score
                  180
E value
                  2.0e-13
                  73
Match length
% identity
                  VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A (V-ATPASE 69 KD
NCBI Description
```

SUBUNIT) (TONOPLAST ATPASE 70 KD SUBUNIT) (BN59)

>gi\_1362024\_pir\_\_S57790 H+-transporting ATPase (EC
3.6.1.35), vacuolar, 70K chain (clone BN59) - rape

>gi\_558479 (U15604) tonoplast ATPase 70 kDa subunit

[Brassica napus]

```
Seq. No.
                   148879
Seq. ID
                  LIB3175-018-P1-K1-B12
Method
                  BLASTX
NCBI GI
                   g3522945
BLAST score
                   653
E value
                   1.0e-68
                   127
Match length
% identity
                   98
NCBI Description
                   (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   148880
                   LIB3175-018-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q899608
BLAST score
                   591
                   2.0e-61
E value
Match length
                   120
% identity
NCBI Description (U29158) polyubiquitin [Zea mays]
                   148881
Seq. No.
Seq. ID
                   LIB3175-018-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   q1755162
BLAST score
                   209
E value.
                   9.0e-55
Match length
                   108
                   90
% identity
NCBI Description (U75192) germin-like protein [Arabidopsis thaliana]
Seq. No.
                   148882
Seq. ID
                   LIB3175-018-P1-K1-B8
Method
                   BLASTN
NCBI GI
                   q4678705
BLAST score
                   384
E value
                   0.0e + 00
Match length
                   384
% identity
                   100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                   (ESSA project)
Seq. No.
                   148883
Seq. ID
                   LIB3175-018-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g3522945
BLAST score
                   487
E value
                   3.0e-49
Match length
                   117
% identity
NCBI Description
                   (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   148884
Seq. ID
                  LIB3175-018-P1-K1-C1
Method
                  BLASTN
NCBI GI
                   g2618677
BLAST score
                   428
E value
                   0.0e + 00
```

```
Match length
                   435
                   100
% identity
                  Arabidopsis thaliana BAC F21B7 chromosome 1, complete
NCBI Description
                   sequence [Arabidopsis thaliana]
                   148885
Seq. No.
Seq. ID
                  LIB3175-018-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  g2244879
BLAST score
                   456
E value
                   1.0e-45
                  103
Match length
% identity
                   88
                   (Z97338) Nucleotide sequence of a cDNA clone encoding a
NCBI Description
                  beta-amylase from Arabidopsis thaliana
Seq. No.
                   148886
                   LIB3175-018-P1-K1-C11
Seq. ID
Method
                  BLASTX -
NCBI GI
                   g1175014
BLAST score
                  567
E value
                   1.0e-58
                  125
Match length
                   90
% identity
NCBI Description
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2B >qi 629543 pir $44085
                   plasma membrane intrinsic protein 2b - Arabidopsis thaliana
                   >gi 472879 emb CAA53478 (X75884) plasma membrane intrinsic
                  protein 2b [Arabidopsis thaliana]
Seq. No.
                   148887
Seq. ID
                  LIB3175-018-P1-K1-C3
Method
                  BLASTX
NCBI GI
                   g3080435
BLAST score
                  298
E value
                   4.0e-27
Match length
                   78
% identity
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148888
Seq. ID
                  LIB3175-018-P1-K1-C4
Method
                  BLASTN
NCBI GI
                  g3695372
BLAST score
                  49
E value
                   2.0e-18
Match length
                  53
% identity
                   98
NCBI Description
                  Arabidopsis thaliana BAC F1104
Seq. No.
                   148889
Seq. ID
                  LIB3175-018-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4559346
BLAST score
                  594
E value
                  1.0e-61
Match length
                  112
% identity
                  100
```

Seq. ID

```
NCBI Description (AC006585) early nodulin 16 [Arabidopsis thaliana]
Seq. No.
                  148890
Seq. ID
                  LIB3175-018-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g113782
BLAST score
                  718
E value
                  3.0e-76
Match length
                  136
% identity
                  100
NCBI Description
                  BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE)
                  >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) -
                  Arabidopsis thaliana >gi_166602 (M73467) beta-amylase
                  [Arabidopsis thaliana] >gi 228699 prf 1808329A beta
                  amylase [Arabidopsis thaliana]
                  148891
Seq. No.
Seq. ID
                  LIB3175-018-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  626
                  1.0e-65
E value
Match length
                  118
% identity
                  99
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                  (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  148892
Seq. No.
Seq. ID
                  LIB3175-018-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q2462824
BLAST score
                  409
E value
                  4.0e-40
Match length
                  81
% identity
                  (AF000657) similar to Jun activation domain binding protein
NCBI Description
                  [Arabidopsis thaliana] >gi_2791885 (AF042334) JAB1
                  [Arabidopsis thaliana]
                  148893
Seq. No.
Seq. ID
                  LIB3175-018-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  q4417264
BLAST score
                  324
                  0.0e + 00
E value
Match length
                  421
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148894
```

18866

LIB3175-018-P1-K1-D10

BLAST score

551

```
BLASTX
Method
NCBI GI
                   g3738335
BLAST score
                   312
                   1.0e-28
E value
Match length
                   113
% identity
                   58
                   (AC005170) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   148895
Seq. ID
                   LIB3175-018-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   q464621
BLAST score
                   602
E value
                   1.0e-62
Match length
                   140
% identity
                   83
                   60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
NCBI Description
                   ribosomal protein ML16 - common ice plant >gi_19539_emb_CAA49175_ (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
Seq. No.
                   148896
Seq. ID
                   LIB3175-018-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q3522945
BLAST score
                   582
E value
                   2.0e-60
Match length
                   111
% identity
                   100
NCBI Description
                   (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
                   148897
Seq. No.
Seq. ID
                   LIB3175-018-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q1619300
BLAST score
                   310
E value
                   2.0e-28
Match length
                   67
% identity
NCBI Description
                   (X95269) LRR protein [Lycopersicon esculentum]
Seq. No.
                   148898
Seq. ID
                   LIB3175-018-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   g4185505
BLAST score
                   356
E value
                   8.0e-34
Match length
                   103
% identity
                   67
                    (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                   [Brassica napus]
                   148899
Seq. No.
                   LIB3175-018-P1-K1-D4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g126985
```

```
E value 1.0e-56
Match length 115
% identity 94
NCBI Description MERI-5 PROTEIN >gi_166778 (M63166) meri-5 [Arabidopsis thaliana]
Seq. No. 148900
```

Seq. ID LIB3175-018-P1-K1-D5
Method BLASTX

Method BLASTX
NCBI GI g231586
BLAST score 248
E value 3.0e-21
Match length 127
% identity 50

NCBI Description ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR

>gi\_82027\_pir\_\_S20504 H+-transporting ATP synthase (EC
3.6.1.34) beta chain, mitochondrial - Para rubber tree
>gi\_18831\_emb\_CAA41401\_ (X58498) mitochondrial ATP synthase

beta-subunit [Hevea brasiliensis]

Seq. No. 148901

Seq. ID LIB3175-018-P1-K1-D6

Method BLASTX
NCBI GI g1531762
BLAST score 195
E value 6.0e-15
Match length 51
% identity 75

NCBI Description (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis

thaliana]

Seq. No. 148902

Seq. ID LIB3175-018-P1-K1-D7

Method BLASTX
NCBI GI g1346113
BLAST score 488
E value 2.0e-49
Match length 103
% identity 90

NCBI Description GTP CYCLOHYDROLASE II >gi\_1084339\_pir\_\_JC4209 GTP

cyclohydrolase II (EC 3.5.4.25) - Arabidopsis thaliana >gi\_940383\_dbj\_BAA08113\_ (D45165) GTP cyclohydrolase II

[Arabidopsis thaliana]

Seq. No. 148903

Seq. ID LIB3175-018-P1-K1-D9

Method BLASTX
NCBI GI g1169598
BLAST score 461
E value 4.0e-46
Match length 98
% identity 87

NCBI Description OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM

(DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12

desaturase [Arabidopsis thaliana]

Seq. No. 148904

```
Seq. ID
                   LIB3175-018-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   q1209756
BLAST score
                   159
E value
                   8.0e-11
Match length
                   35
% identity
NCBI Description
                   (U43629) integral membrane protein [Beta vulgaris]
Seq. No.
                   148905
Seq. ID
                   LIB3175-018-P1-K1-E2
Method
                   BLASTN
NCBI GI
                   q4519195
BLAST score
                   366
E value
                   0.0e + 00
Match length
                   404
                   97
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MQC12, complete sequence
                   148906
Seq. No.
Seq. ID
                   LIB3175-018-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q4185515
BLAST score
                   422
E value
                   1.0e-41
Match length
                   81
                   100
% identity
NCBI Description
                   (AF102824) actin depolymerizing factor 6 [Arabidopsis
                   thaliana]
Seq. No.
                   148907
Seq. ID
                   LIB3175-018-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g2565009
BLAST score
                   495
E value
                   4.0e-50
Match length
                   124
% identity
NCBI Description
                   (AC002983) putative zinc finger protein [Arabidopsis
                   thaliana]
Seq. No.
                   148908
Seq. ID
                   LIB3175-018-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   q2739359
BLAST score
                   364
E value
                   0.0e + 00
Match length
                   364
                   100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T9J22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   148909
Seq. No.
Seq. ID
                   LIB3175-018-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q2494320
```

```
BLAST score
                   450
E value
                   7.0e-45
Match length
                  107
% identity
                   80
NCBI Description
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5)
                   >gi 1806575 emb CAA67868 (X99517) Eukaryotic initiation
                   factor-5 [Zea mays]
                  148910
Seq. No.
Seq. ID
                  LIB3175-018-P1-K1-E8
Method
                  BLASTX
                  g2924779
NCBI GI
BLAST score
                   615
                   3.0e-64
E value
                  123
Match length
% identity
NCBI Description
                   (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
                  thaliana] >gi 2981616 dbj BAA25248 (AB008854)
                   3-ketoacyl-Co\overline{A} thiolase [Arabidopsis thaliana]
                  >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
Seq. No.
                  148911
                  LIB3175-018-P1-K1-E9
Seq. ID
Method
                  BLASTN
                  g4220644
NCBI GI
BLAST score
                  271
                  1.0e-151
E value
                   423
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MXL8, complete sequence [Arabidopsis thaliana]
                  148912
Seq. No.
                  LIB3175-018-P1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4567237
                  33
BLAST score
E value
                   6.0e-09
                  295
Match length
                  90
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T22F11 genomic
                  sequence, complete sequence
Seq. No.
                  148913
                  LIB3175-018-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1346263
                  398
BLAST score
                  8.0e-39
E value
Match length
                  81
% identity
                  GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR)
NCBI Description
                  >gi_2146736_pir__S65773 glutamyl-tRNA reductase 2 precursor
```

reductase [Arabidopsis thaliana]

- Arabidopsis thaliana >gi 1049057 (U27118) glutamyl-tRNA

```
148914
Seq. No.
Seq. ID
                   LIB3175-018-P1-K1-F11
Method
                   BLASTN
NCBI GI
                   g4584841
BLAST score
                   157
                   6.0e-83
E value
                   416
Match length
% identity
                   Genomic sequence for Arabidopsis thaliana BAC T23E23,
NCBI Description
                   complete sequence
                   148915
Seq. No.
Seq. ID
                   LIB3175-018-P1-K1-F2
Method
                   BLASTX
                   g1864017
NCBI GI
                   210
BLAST score
                   3.0e-17
E value
                   43
Match length
                   93
% identity
                   (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
Seq. No.
                   148916
                   LIB3175-018-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3413716
BLAST score
                   581
E value
                   3.0e-60
                   139
Match length
                   57
% identity
                    (AC004747) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi 3643589 (AC005395) unknown protein [Arabidopsis
                   thaliana]
                   148917
Seq. No.
                   LIB3175-018-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g119350
BLAST score
                   657
                   4.0e-69
E value
                   130
Match length
                   99
% identity
NCBI Description
                   ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                   thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                    [Arabidopsis thaliana]
                   >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
                    (2-phospho-D-glycerate hydroylase); identical to P25696
                    [Arabidopsis thaliana]
Seq. No.
                   148918
                   LIB3175-018-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2129759
BLAST score
                   543
                   9.0e-56
E value
                   110
Match length
```

```
% identity
                  UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana
NCBI Description
                   >qi 1143392 emb CAA90941 (Z54214) uridine diphosphate
                   glucose epimerase [Arabidopsis thaliana]
Seq. No.
                   148919
Seq. ID
                   LIB3175-018-P1-K1-F8
Method
                  BLASTX
NCBI GI
                   g2894574
BLAST score
                   616
E value
                   2.0e-64
Match length
                   118
% identity
                   99
NCBI Description
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
                   >gi_2961341 emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
                   148920
Seq. No.
Seq. ID
                   LIB3175-018-P1-K1-G1
Method
                   BLASTN
NCBI GI
                   g3426057
BLAST score
                   398
E value
                   0.0e + 00
Match length
                   398
                   100
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for IB1P8-4 protein
                   148921
Seq. No.
                  LIB3175-018-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3522945
BLAST score
                   624
E value
                   3.0e-65
Match length
                   120
% identity
                   99
NCBI Description
                   (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                   148922
                  LIB3175-018-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3522945
BLAST score
                   637
E value
                   8.0e-67
Match length
                  122
% identity
                   100
NCBI Description
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  148923
                  LIB3175-018-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4586265
BLAST score
                  512
E value
                   4.0e-52
Match length
                  117
                  81
% identity
```

NCBI Description (ALO49640) putative protein [Arabidopsis thaliana]

```
148924
Seq. No.
Seq. ID
                  LIB3175-018-P1-K1-G3
Method
                  BLASTX
NCBI GI
                   g1304227
BLAST score
                   290
E value
                   4.0e-26
Match length
                   107
% identity
                   50
NCBI Description
                   (D63781) Epoxide hydrolase [Glycine max]
                   >gi 2764804_emb_CAA55293_ (X78547) epoxide hydrolase
                   [Glycine max]
Seq. No.
                   148925
Seq. ID
                  LIB3175-018-P1-K1-G4
Method
                  BLASTX
NCBI GI
                   g4741923
BLAST score
                   368
E value
                   3.0e-35
Match length
                   92
% identity
NCBI Description
                  (AF130849) PIT1 [Arabidopsis thaliana]
Seq. No.
                   148926
Seq. ID
                   LIB3175-018-P1-K1-G5
Method
                  BLASTX
NCBI GI
                   q4680661
BLAST score
                   149
E value
                   2.0e-09
Match length
                   107
                   27
% identity
NCBI Description
                   (AF132945) CGI-11 protein [Homo sapiens]
                   148927
Seq. No.
Seq. ID
                   LIB3175-018-P1-K1-G6
Method
                   BLASTN
NCBI GI
                   q972937
BLAST score
                   223
E value
                   1.0e-122
Match length
                   436
                   100
% identity
NCBI Description
                  Arabidopsis thaliana putative chlorophyll synthetase (G4)
                   gene, complete cds
Seq. No.
                   148928
Seq. ID
                   LIB3175-018-P1-K1-G7
Method
                  BLASTX
NCBI GI
                   g2129769
BLAST score
                   669
E value
                   2.0e-70
Match length
                   122
                   99
% identity
NCBI Description
                  xyloglucan endo-transglycosylase precursor - Arabidopsis
                   thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan
                  transferase [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3175-018-P1-K1-G8
```

```
BLASTN
Method
NCBI GI
                  g3449329
                  353
BLAST score
                  0.0e+00
E value
                  377
Match length
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDH9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148930
Seq. ID
                  LIB3175-018-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q4115387
BLAST score
                  393
E value
                   4.0e-38
                  78
Match length
                   99
% identity
                   (AC005967) putative NADP-dependent
NCBI Description
                   glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana]
Seq. No.
                  148931
                  LIB3175-018-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q584998
BLAST score
                  265
E value
                   4.0e-23
                  96
Match length
                   50
% identity
NCBI Description
                  FLAVONOID 3',5'-HYDROXYLASE (F3'5'H) (CYTOCHROME P450
                  LXXVA2) (P-450EG1) >gi_629713_pir__S43342 flavonoid
                  hydroxylase cytochrome P450 - eggplant
                  >gi 395261_emb_CAA50155_ (X70824) flavonoid hydroxylase
                   (P450) [Solanum melongena]
Seq. No.
                  148932
                  LIB3175-018-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2914700
BLAST score
                  563
E value
                   4.0e-58
Match length
                  111
% identity
                   100
                   (ACO03974) tRNA-processing protein SEN3-like [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  148933
                  LIB3175-018-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522945
BLAST score
                  672
E value
                  8.0e-71
Match length
                  137
% identity
NCBI Description (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  148934
```

```
LIB3175-018-P1-K1-H2
Seq. ID
                   BLASTX
Method
                   g2832629
NCBI GI
BLAST score
                   164
                   2.0e-11
E value
Match length
                   104
% identity
                   37
                   (AL021711) 4-coumarate-CoA ligase - like [Arabidopsis
NCBI Description
                   thaliana]
                   148935
Seq. No.
                   LIB3175-018-P1-K1-H3
Seq. ID
                   BLASTN
Method
                   q3449330
NCBI GI
                   321
BLAST score
                   0.0e+00
E value
                   400
Match length
                   94
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MDJ14, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148936
                   LIB3175-018-P1-K1-H5
Seq. ID
                   BLASTX
Method
NCBI GI
                   q282865
BLAST score
                   638
                   6.0e-67
E value
                   133
Match length
                   69
% identity
NCBI Description
                   chlorophyll a/b-binding protein - Arabidopsis thaliana
                   >gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
                   chlorophyll a/b-binding protein [Arabidopsis thaliana]
                   >gi 4678304 emb_CAB41095.1_ (AL049655) chlorophyll
                   a/b-binding protein [Arabidopsis thaliana]
                   148937
Seq. No.
                   LIB3175-018-P1-K1-H7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4006899
                   375
BLAST score
                   5.0e-36
E value
                   121
Match length
% identity
                   56
NCBI Description
                   (Z99708) putative protein [Arabidopsis thaliana]
Seq. No.
                   148938
                   LIB3175-018-P1-K1-H9
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4585882
BLAST score
                   496
                   3.0e-50
E value
                   95
Match length
                   100
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
```

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```
Seq. No.
                  148939
Seq. ID
                  LIB3175-019-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g4415905
BLAST score
                  184
E value
                  5.0e-99
Match length
                  451
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13K3 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148940
Seq. ID
                  LIB3175-019-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  q119723
BLAST score
                  800
E value
                  8.0e-86
Match length
                  153
                  100
% identity
NCBI Description
                  FRUCTOSE-1, 6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR
                  (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
                  >gi_99693_pir__S16582 fructose-bisphosphatase (EC 3.1.3.11)
                  precursor, chloroplast - Arabidopsis thaliana
                  >gi_11242_emb_CAA41154_ (X58148) fructose-bisphosphatase
                  [Arabidopsis thaliana]
Seq. No.
                  148941
Seq. ID
                  LIB3175-019-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1542941
BLAST score
                  288
E value
                  2.0e-26
Match length
                  61
% identity
NCBI Description (X78116) Acetoacetyl-coenzyme A thiolase [Raphanus sativus]
Seq. No.
                  148942
Seq. ID
                  LIB3175-019-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q1076389
BLAST score
                  540
E value
                  2.0e-55
Match length
                  125
% identity
                  protein phosphatase 2A pDF1 - Arabidopsis thaliana
NCBI Description
                  >gi_683502_emb_CAA57528_ (X82002) protein phosphatase 2A 65
                  kDa regulatory subunit [Arabidopsis thaliana]
Seq. No.
                  148943
Seq. ID
                  LIB3175-019-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q1402904
BLAST score
                  513
E value
                  2.0e-52
                  100
Match length
% identity
                  98
NCBI Description
                  (X98313) peroxidase [Arabidopsis thaliana]
```

```
Seq. No.
                  148944
Seq. ID
                  LIB3175-019-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4206206
BLAST score
                   305
E value
                   7.0e-28
Match length
                  74
% identity
NCBI Description
                   (AF071527) putative M-type thioredoxin [Arabidopsis
                  thaliana] >gi_4263039_gb_AAD15308_ (AC005142) putative
                  M-type thioredoxin [Arabidopsis thaliana]
                  148945
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-A9
Method
                  BLASTX
NCBI GI
                   g2583126
BLAST score
                   527
                   9.0e-54
E value
Match length
                   109
% identity
NCBI Description
                   (AC002387) putative DNA repair protein (RAD57) [Arabidopsis
                  thaliana]
                   148946
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q2829899
BLAST score
                   468
E value
                   7.0e-47
Match length
                   136
% identity
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                  gp X91961 1107495 [Arabidopsis thaliana]
Seq. No.
                   148947
                  LIB3175-019-P1-K1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2828278
BLAST score
                   66
E value
                   9.0e-29
Match length
                  118
% identity
                  89
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16
                   (ESSAII project)
Seq. No.
                  148948
Seq. ID
                  LIB3175-019-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1173187
BLAST score
                  579
E value
                   6.0e-60
Match length
                  121
% identity
                  93
                  40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673
NCBI Description
                  ribosomal protein S23.e, cytosolic (clone RJ3) - garden
```

```
strawberry >gi 643074 (U19940) putative 40S ribosomal
                  protein s12 [Fragaria x ananassa]
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q4200165
BLAST score
                  342
E value
                  4.0e-32
Match length
                  130
% identity
                  62
NCBI Description
                  (Y16262) neutral invertase [Daucus carota]
                  148950
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q584892
BLAST score
                  506
E value
                  2.0e-51
Match length
                  145
% identity
NCBI Description
                  SERINE CARBOXYPEPTIDASE I PRECURSOR (CARBOXYPEPTIDASE C)
                  >gi_629805_pir__S43516 serine carboxypeptidase I - rice
                  >gi_409580_dbj_BAA04510_ (D17586) serine carboxypeptidase I
                  [Oryza sativa]
Seq. No.
                  148951
Seq. ID
                  LIB3175-019-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  q4753195
BLAST score
                  54
E value
                  2.0e-21
Match length
                  360
% identity
NCBI Description
                  Arabidopsis thaliana BAC F15A18 from chromosome V near 68.5
                  cM, complete sequence
Seq. No.
                  148952
Seq. ID
                  LIB3175-019-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g2564049
BLAST score
                  171
E value
                  3.0e-91
                  210
Match length
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  148953
                  LIB3175-019-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g127041
BLAST score
                  445
E value
                  2.0e-44
Match length
                  86
                  99
% identity
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
```

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi\_81647\_pir\_\_JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi\_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No. 148954

Seq. ID LIB3175-019-P1-K1-C12

Method BLASTX
NCBI GI g2645971
BLAST score 697
E value 8.0e-74
Match length 130
% identity 99

NCBI Description (AF034255) reversibly glycosylated polypeptide-3

[Arabidopsis thaliana]

Seq. No. 148955

Seq. ID LIB3175-019-P1-K1-C4

Method BLASTN
NCBI GI g2828278
BLAST score 278
E value 1.0e-155
Match length 423
% identity 98

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 148956

Seq. ID LIB3175-019-P1-K1-C6

Method BLASTX
NCBI GI g2645971
BLAST score 305
E value 5.0e-28
Match length 61
% identity 93

NCBI Description (AF034255) reversibly glycosylated polypeptide-3

[Arabidopsis thaliana]

Seq. No. 148957

Seq. ID LIB3175-019-P1-K1-C7

Method BLASTX
NCBI GI 94538963
BLAST score 362
E value 1.0e-34
Match length 100
% identity 72

NCBI Description (AL049488) chlorophyll a/b-binding protein-like

[Arabidopsis thaliana] >gi\_4741958\_gb\_AAD28776.1\_AF134129\_1

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

Seq. No. 148958

Seq. ID LIB3175-019-P1-K1-C9

Method BLASTX
NCBI GI g2213590
BLAST score 184
E value 1.0e-13
Match length 82

```
% identity
NCBI Description
                   (AC000348) T7N9.10 [Arabidopsis thaliana]
Seq. No.
                   148959
Seq. ID
                  LIB3175-019-P1-K1-D1
Method
                  BLASTX
NCBI GI
                   q4204300
BLAST score
                   615
E value
                   4.0e-64
Match length
                   120
% identity
                   100
NCBI Description
                   (AC003027) Unknown protein [Arabidopsis thaliana]
                   148960
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-D10
Method
                  BLASTN
NCBI GI
                   q3548797
BLAST score
                   339
                   0.0e+00
E value
Match length
                   455
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T18E12 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   148961
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-D11
Method
                  BLASTX
NCBI GI
                   q4154281
BLAST score
                   434
                   6.0e-43
E value
Match length
                   106
% identity
NCBI Description (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
Seq. No.
                  148962
Seq. ID
                  LIB3175-019-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  g2130051
BLAST score
                   489
E value
                  2.0e-49
Match length
                  123
% identity
NCBI Description
                  xylose isomerase (EC 5.3.1.5) - barley
                  >gi_1296807_emb_CAA64544_ (X95256) xylose isomerase
                   [Hordeum vulgare] >gi_1588664_prf__2209268A xylose
                  isomerase [Hordeum vulgare]
Seq. No.
                  148963
Seq. ID
                  LIB3175-019-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  q1172872
BLAST score
                  703
E value
                  2.0e-74
Match length
                  131
% identity
                  100
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
```



precursor - Arabidopsis thaliana >gi\_435618\_dbj\_BAA02373\_ (D13042) thiol protease [Arabidopsis thaliana] >gi\_4539328\_emb\_CAB38829.1\_ (AL035679) drought-inducible cysteine proteinase RD19A precursor [Arabidopsis thaliana]

Seq. No. 148964

Seq. ID LIB3175-019-P1-K1-D3

Method BLASTN
NCBI GI g3269280
BLAST score 356
E value 0.0e+00
Match length 419
% identity 100

NCBI Description Arabidopsis thaliana DNA chromosome 4, P1 clone M4I22

(ESSAII project)

Seq. No.

Seq. ID LIB3175-019-P1-K1-D4

148965

Method BLASTX
NCBI GI g3858939
BLAST score 531
E value 3.0e-54
Match length 129
% identity 86

NCBI Description (AL021636) serine/threonine protein kinase like protein

[Arabidopsis thaliana]

Seq. No. 148966

Seq. ID LIB3175-019-P1-K1-D5

Method BLASTX
NCBI GI g2129532
BLAST score 507
E value 2.0e-51
Match length 126
% identity 79

NCBI Description acyl-[acyl-carrier-protein] desaturase (EC 1.14.99.6) -

Arabidopsis thaliana >gi\_1107507\_emb\_CAA63746\_ (X93461) acyl-[acyl-carrier protein] desaturase [Arabidopsis

thaliana]

Seq. No. 148967

Seq. ID LIB3175-019-P1-K1-D6

Method BLASTX
NCBI GI g2129675
BLAST score 686
E value 2.0e-72
Match length 158
% identity 84

NCBI Description probable chlorophyll synthetase G4 - Arabidopsis thaliana

>gi\_972938 (U19382) putative chlorophyll synthetase
[Arabidopsis thaliana] >gi\_3068709 (AF049236) putative

chlorophyll synthetase [Arabidopsis thaliana]

Seq. No. 148968

Seq. ID LIB3175-019-P1-K1-D8

Method BLASTN NCBI GI g4757400

```
BLAST score
E value
                   2.0e-92
Match length
                   404
% identity
                   98
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MFJ20, complete sequence
                   148969
Seq. No.
Seq. ID
                   LIB3175-019-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q4406753
BLAST score
                   495
E value
                   5.0e-50
Match length
                   106
% identity
NCBI Description
                   (AC006836) hypothetical protein [Arabidopsis thaliana]
                   148970
Seq. No.
                   LIB3175-019-P1-K1-E1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3309170
BLAST score
                   245
E value
                   1.0e-20
Match length
                   133
% identity
                   42
                   (AF071314) COP9 complex subunit 4 [Mus musculus]
NCBI Description
                   148971
Seq. No.
Seq. ID
                   LIB3175-019-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   q4757411
BLAST score
                   243
E value
                   1.0e-134
Match length
                   446
                   100
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MXC7, complete sequence
Seq. No.
                   148972
Seq. ID
                   LIB3175-019-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g4158221
BLAST score
                   630
E value
                   7.0e-66
Match length
                   139
% identity
                   80
NCBI Description
                   (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
Seq. No.
                   148973
Seq. ID
                   LIB3175-019-P1-K1-E2
Method
                   BLASTN
NCBI GI
                   g2160132
BLAST score
                   165
E value
                   1.0e-87
Match length
                   921
                   56
% identity
NCBI Description
                   Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
```

Seq. No.

Seq. ID

Method

NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

BLAST score E value

Match length

% identity

Seq. No.

Seq. ID

NCBI GI

E value

BLAST score

Match length

% identity

Method

BLAST score

Match length

% identity

```
1, complete sequence [Arabidopsis thaliana]
                  148974
                  LIB3175-019-P1-K1-E3
                  BLASTX
                  q3859591
                  330
                  7.0e-31
                  108
                  55
NCBI Description
                  (AF104919) No definition line found [Arabidopsis thaliana]
                  148975
                  LIB3175-019-P1-K1-E5
                  BLASTX
                  q3892712
                  500
                  1.0e-50
                  97
                  100
                  (AL033545) adenine phosphoribosyltransferase (EC
NCBI Description
                  2.4.2.7)-like protein [Arabidopsis thaliana]
                  148976
                  LIB3175-019-P1-K1-E6
                  BLASTX
                  q2244759
                  771
                  2.0e-82
                  157
                  92
                  (Z97335) selenium-binding protein [Arabidopsis thaliana]
NCBI Description
                  148977
                  LIB3175-019-P1-K1-E7
                  BLASTN
                  q4734003
                  377
                  0.0e + 00
                  381
                  68
```

```
Seq. No.
Seq. ID
Method
NCBI GI
BLAST score
E value
Match length
% identity
```

NCBI Description Arabidopsis thaliana chromosome II BAC F3L12 genomic sequence, complete sequence

Seq. No. 148978 Seq. ID LIB3175-019-P1-K1-E8 Method BLASTX NCBI GI q3123745 BLAST score 510 E value 7.0e-52 107 Match length

% identity NCBI Description (AB013447) aluminum-induced [Brassica napus]

148979 Seq. No.

LIB3175-019-P1-K1-E9 Seq. ID

Method BLASTN

Seq. ID

```
NCBI GI
                   q4220633
BLAST score
                   41
E value
                   1.0e-13
Match length
                   287
% identity
                   88
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K7J8, complete sequence [Arabidopsis thaliana]
                   148980
Seq. No.
                   LIB3175-019-P1-K1-F1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3449326
BLAST score
                   377
                   0.0e+00
E value
                   377
Match length
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19M22, complete sequence [Arabidopsis thaliana]
                   148981
Seq. No.
                   LIB3175-019-P1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1169278
BLAST score
                   283
E value
                   3.0e-25
                   71
Match length
% identity
                   83
                   DEHYDRIN ERD14 >gi 556474 dbj BAA04569 (D17715) ERD14
NCBI Description
                   protein [Arabidopsis thaliana]
                   148982
Seq. No.
Seq. ID
                   LIB3175-019-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g3157924
BLAST score
                   309
E value
                   3.0e-28
Match length
                   80
% identity
NCBI Description
                   (AC002131) Contains homology to extensin-like protein
                   gb D83227 from Populus nigra. ESTs gb H76425, gb T13883,
                   gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb_Z25951
                   come from this gene. There is a similar ORF on the opposite strand. [... >gi_4063707 (AF104327) extensin-like
                   protein [Arabidopsis thaliana]
Seq. No.
                   148983
Seq. ID
                   LIB3175-019-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q2827699
BLAST score
                   457
E value
                   1.0e-45
Match length
                   159
% identity
                   (AL021684) predicted protein [Arabidopsis thaliana]
NCBI Description
                   148984
Seq. No.
```

LIB3175-019-P1-K1-F3

```
Method
                   BLASTN
NCBI GI
                   g3449322
BLAST score
                   438
E value
                   0.0e + 00
Match length
                   441
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXC17, complete sequence [Arabidopsis thaliana]
                   148985
Seq. No.
                  LIB3175-019-P1-K1-F4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4589396
BLAST score
                   330
E value
                   1.0e-30
Match length
                   146
% identity
NCBI Description
                   (D89971) asparaginyl endopeptidase (VmPE-1) [Vigna mungo]
Seq. No.
                   148986
                  LIB3175-019-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2196466
BLAST score
                   443
E value
                   4.0e-44
Match length
                   104
                   90
% identity
NCBI Description
                   (Y13673) TATA binding protein-associated factor
                   [Arabidopsis thaliana]
Seq. No.
                   148987
Seq. ID
                   LIB3175-019-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   g2244750
BLAST score
                   799
E value
                   1.0e-85
Match length
                   155
% identity
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
Seq. No.
                   148988
                  LIB3175-019-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3600053
BLAST score
                  337
E value
                   1.0e-31
Match length
                  116
% identity
                   (AF080120) contains similarity to HMG (high mobility group)
NCBI Description
                  box (Pfam: HMG box.hmm, scores: 70.67, 53.09 and 80.15)
                   [Arabidopsis thaliana]
                  148989
Seq. No.
                  LIB3175-019-P1-K1-F8
Seq. ID
Method
                  BLASTN
```

```
q3426033
NCBI GI
BLAST score
                   123
E value
                   1.0e-62
Match length
                   443
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F12C20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   148990
Seq. ID
                   LIB3175-019-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q1706368
BLAST score
                   773
E value
                   1.0e-82
Match length
                   148
                   99
% identity
NCBI Description
                   DIHYDROFLAVONOL-4-REDUCTASE (DFR) (DIHYDROKAEMPFEROL
                   4-REDUCTASE) >gi_320557_pir__JQ1688 dihydrokaempferol
4-reductase (EC 1.1.1.219) - Arabidopsis thaliana
                   >gi 166686 (M86359) dihydroflavonol 4-reductase
                   [Arabidopsis thaliana]
Seq. No.
                   148991
Seq. ID
                   LIB3175-019-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   q2529229
BLAST score
                   536
E value
                   7.0e-55
Match length
                   116
% identity
NCBI Description
                   (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
                   148992
Seq. No.
Seq. ID
                   LIB3175-019-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q3138972
BLAST score
                   680
E value
                   9.0e-72
Match length
                   142
% identity
NCBI Description
                   (AF038505) dihydrolipoylacyltransferase subunit of the
                   branched-chain alpha-keto acid dehydrogenase complex
                   [Arabidopsis thaliana]
Seq. No.
                   148993
Seq. ID
                   LIB3175-019-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q3157947
BLAST score
                   570
E value
                   6.0e-59
Match length
                   111
% identity
NCBI Description
                   (AC002131) Similar to protein gb Z74962 from Brassica
                   oleracea which is similar to bacterial YRN1 and HEAHIO
                   proteins. ESTs gb_T21954, gb_T04283, gb_Z37609, gb_N37366,
                   gb_R90704, gb_F15500 and gb_F14353 come from this gene.
```

[Arabidopsis tha

```
148994
Seq. No.
                  LIB3175-019-P1-K1-G3
Seq. ID
                  BLASTX
Method
                  g3420049
NCBI GI
                  443
BLAST score
                  6.0e-44
E value
                  129
Match length
                  69
% identity
                   (AC004680) putative protein phosphatase 2C [Arabidopsis
NCBI Description
                  thaliana]
                  148995
Seq. No.
                  LIB3175-019-P1-K1-G4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2245031
BLAST score
                  141
                  3.0e-73
E value
                  495
Match length
                  98
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  148996
Seq. No.
                  LIB3175-019-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2258135
                  188
BLAST score
E value
                   4.0e-14
                  46
Match length
                   67
% identity
NCBI Description
                  (Z83830) porin [Picea abies]
                  148997
Seq. No.
                  LIB3175-019-P1-K1-G6
Seq. ID
                  BLASTX
Method
                  g1724100
NCBI GI
BLAST score
                   520
E value
                   6.0e-53
                  134
Match length
                   74
% identity
                  (U79765) porin [Mesembryanthemum crystallinum]
NCBI Description
                  148998
Seq. No.
                  LIB3175-019-P1-K1-G9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g132110
BLAST score
                   729
E value
                   2.0e-77
Match length
                  139
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
```

```
148999
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g2407802
BLAST score
                  186
E value
                  7.0e-16
Match length
                  66
% identity
                  69
NCBI Description
                  (Y12576) histone H2B [Arabidopsis thaliana]
                  149000
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  q136251
BLAST score
                  505
E value
                  2.0e-51
Match length
                  119
                  83
% identity
NCBI Description
                  TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR
                  >gi_99767_pir__A31393 tryptophan synthase (EC 4.2.1.20)
                  beta chain - Arabidopsis thaliana >gi_166892 (M23872)
                  tryptophan synthase beta subunit [Arabidopsis thaliana]
                  149001
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q2454184
BLAST score
                  436
E value
                  3.0e-43
Match length
                  108
% identity
                   (U80186) pyruvate dehydrogenase El beta subunit
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  149002
Seq. ID
                  LIB3175-019-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q3273196
BLAST score
                  538
E value
                  3.0e-55
Match length
                  109
% identity
                  98
NCBI Description
                   (AB010915) responce regulator1 [Arabidopsis thaliana]
                  >gi 3323583 (AF057282) two-component response regulator
                  homolog [Arabidopsis thaliana] >gi_3953597_dbj_BAA34726_
                   (AB008487) response regulator 4 [Arabidopsis thaliana]
Seq. No.
                  149003
Seq. ID
                  LIB3175-019-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q3063465
BLAST score
                  684
E value
                  3.0e-72
Match length
                  133
% identity
NCBI Description
                  (AC003981) F22013.27 [Arabidopsis thaliana]
```

```
149004
Seq. No.
                  LIB3175-019-P1-K1-H4
Seq. ID
Method
                  BLASTN
                  g2760169
NCBI GI
BLAST score
                  246
                   1.0e-136
E value
                  410
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFB13, complete sequence [Arabidopsis thaliana]
                  149005
Seq. No.
                  LIB3175-019-P1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2264313
                  82
BLAST score
E value
                   4.0e-38
Match length
                  242
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOP10, complete sequence [Arabidopsis thaliana]
                  149006
Seq. No.
                  LIB3175-019-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4455302
BLAST score
                   438
                   2.0e-43
E value
Match length
                  122
                   66
% identity
                   (AL035528) putative protein [Arabidopsis thaliana]
NCBI Description
                  149007
Seq. No.
                  LIB3175-019-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1353163
BLAST score
                   237
E value
                   8.0e-20
                   75
Match length
                   60
% identity
NCBI Description
                  HYPOTHETICAL 19.6 KD PROTEIN C23G10.2 IN CHROMOSOME III
                   PRECURSOR >gi_1055071 (U39851) C23G10.2 gene product
                   [Caenorhabditis elegans]
                   149008
Seq. No.
Seq. ID
                  LIB3175-019-P1-K1-H9
Method
                  BLASTX
NCBI GI
                   q421929
BLAST score
                  587
                   7.0e-63
E value
Match length
                  134
% identity
                   15
                  ubiquitin - tomato >gi 312160_emb_CAA51679_ (X73156)
NCBI Description
                  ubiquitin [Lycopersicon esculentum]
Seq. No.
                   149009
```

```
LIB3175-020-P1-K1-A1
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3335331
BLAST score
                   238
                   1.0e-131
E value
                   297
Match length
                   95
% identity
                   Arabidopsis thaliana chromosome 1 BAC T8F5 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   149010
                   LIB3175-020-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2245087
BLAST score
                   427
                   3.0e-42
E value
                   110
Match length
                                                             5
                   73
% identity
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   149011
Seq. No.
                   LIB3175-020-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2286069
BLAST score
                   623
E value
                   4.0e-65
Match length
                   120
% identity
                   (U72155) beta-glucosidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149012
Seq. ID
                   LIB3175-020-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   g2245087
BLAST score
                   511
E value
                   5.0e-52
Match length
                   122
% identity
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   149013
                   LIB3175-020-P1-K1-A2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3643607
BLAST score
                   531
E value
                   2.0e-54
Match length
                   120
% identity
                   (AC005395) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149014
Seq. ID
                   LIB3175-020-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   g112741
BLAST score
                   526
E value
                   6.0e-54
Match length
                   97
```

```
100
% identity
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
                   149015
Seq. No.
Seq. ID
                   LIB3175-020-P1-K1-A4
Method
                   BLASTX
                   a4585882
NCBI GI
BLAST score
                   476
                   7.0e-48
E value
Match length
                   91
                   100
% identity
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   149016
                   LIB3175-020-P1-K1-A5
Seq. ID
Method
                   BLASTN
                   g4510408
NCBI GI
                   53
BLAST score
E value
                   6.0e-21
                   73
Match length
% identity
                   Arabidopsis thaliana chromosome II BAC T1E2 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   149017
                   LIB3175-020-P1-K1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4376087
BLAST score
                   114
                   2.0e-57
E value
                   190
Match length
                   90
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
                   149018
Seq. No.
Seq. ID
                   LIB3175-020-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g541848
BLAST score
                   542
                   1.0e-55
E value
Match length
                   123
```

% identity
NCBI Description

amino acid transport protein I - Arabidopsis thaliana  $>gi_22641$  emb\_CAA47603\_ (X67124) amino acid permease I [Arabidopsis thaliana]  $>gi_404019$  (L16240) amino acid

transporter [Arabidopsis thaliana]

Seq. No. 149019

Seq. ID LIB3175-020-P1-K1-A8

```
Method
                   BLASTN
NCBI GI
                   g2894591
BLAST score
                   413
                   0.0e + 00
E value
Match length
                   416
                   100
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21
NCBI Description
                   (ESSAII project)
Seq. No.
                   149020
Seq. ID
                  LIB3175-020-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   q2245087
BLAST score
                   509
E value
                   1.0e-51
Match length
                   126
% identity
NCBI Description
                   (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   149021
Seq. ID
                   LIB3175-020-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   q1531758
BLAST score
                   388
E value
                   1.0e-37
Match length
                   84
% identity
                   85
NCBI Description
                   (X98772) AUX1 [Arabidopsis thaliana] >gi 3335360 (AC003028)
                   unknown protein [Arabidopsis thaliana]
Seq. No.
                   149022
Seq. ID
                   LIB3175-020-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g130759
BLAST score
                   185
E value
                   2.0e-23
Match length
                   110
% identity
NCBI Description
                   PROLYL ENDOPEPTIDASE (POST-PROLINE CLEAVING ENZYME) (PE)
                   >gi_108383_pir__A37942 prolyl oligopeptidase (EC 3.4.21.26)
                   - pig >gi 164621 (M64227) prolyl endopeptidase [Sus scrofa]
Seq. No.
                   149023
Seq. ID
                  LIB3175-020-P1-K1-B4
Method
                  BLASTX
NCBI GI
                   g2244979
BLAST score
                   712
E value
                   1.0e-75
Match length
                   143
% identity
NCBI Description
                   (Z97340) similarity to enoyl-CoA hydratase [Arabidopsis
                   thaliana]
                   149024
Seq. No.
                  LIB3175-020-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3132475
```

Seq. No.

```
BLAST score
E value
                   3.0e-56
Match length
                   120
% identity
                   87
NCBI Description
                   (AC003096) similar to proline-rich protein [Arabidopsis
                   thaliana]
                   149025
Seq. No.
Seq. ID
                   LIB3175-020-P1-K1-B6
Method
                   BLASTX
NCBI GI
                   g585536
BLAST score
                   473
E value
                   1.0e-47
Match length
                   85
% identity
                   99
NCBI Description
                   MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
                   >gi_1362006_pir__S56653 thioglucosidase (EC 3.2.3.1) -
                   Arabidopsis thaliana >gi_304115 (L11454) thioglucosidase
                   [Arabidopsis thaliana] >gi_871990_emb_CAA55786_ (X79194)
                   thioglucosidase [Arabidopsis thaliana]
Seq. No.
                   149026
Seq. ID
                   LIB3175-020-P1-K1-B7
Method
                   BLASTX
NCBI GI
                   q2829275
BLAST score
                   461
E value
                   4.0e-46
Match length
                   132
% identity
NCBI Description
                   (AF044265) nucleoside diphosphate kinase 3 (Arabidopsis
                   thaliana] >gi_3513740 (AF080118) contains similarity to
                   nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_
                   (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                   [Arabidopsis thaliana]
Seq. No.
                   149027
Seq. ID
                   LIB3175-020-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   q2245087
BLAST score
                   536
E value
                   7.0e-55
Match length
                   125
% identity
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   149028
Seq. ID
                   LIB3175-020-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g2627433
BLAST score
                   258
E value
                   3.0e-22
Match length
                   118
% identity
NCBI Description
                   (AF012129) putative DNA methyltransferase [Mus musculus]
```

```
LIB3175-020-P1-K1-C10
Seq. ID
Method
                  BLASTX
NCBI GI
                   q567893
BLAST score
                   176
E value
                   8.0e-13
Match length
                  87
                   49
% identity
NCBI Description
                   (L37382) beta-galactosidase-complementation protein
                   [Cloning vector]
Seq. No.
                   149030
                  LIB3175-020-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3043415
BLAST score
                   641
E value
                   3.0e-67
Match length
                   123
                   100
% identity
NCBI Description
                   (Y17053) At-hsc70-3 [Arabidopsis thaliana]
                   149031
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q4454032
BLAST score
                   258
E value
                   2.0e-22
Match length
                   101
% identity
                   52
NCBI Description
                   (AL035394) putative protein [Arabidopsis thaliana]
Seq. No.
                   149032
Seq. ID
                   LIB3175-020-P1-K1-C2
Method
                   BLASTN
NCBI GI
                   q2150022
BLAST score
                   93
E value
                   7.0e-45
Match length
                   265
% identity
                   95
NCBI Description
                  Arabidopsis thaliana receptor-like kinase LECRK1 (LECRK1)
                   gene, complete cds
Seq. No.
                   149033
Seq. ID
                   LIB3175-020-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   g3869075
BLAST score
                   260
E value
                   1.0e-144
Match length
                   423
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149034
                  LIB3175-020-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2351065
BLAST score
                  243
```

```
E value
                  1.0e-134
Match length
                  255
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149035
Seq. ID
                  LIB3175-020-P1-K1-C5
Method
                  BLASTN
NCBI GI
                  g2828186
BLAST score
                  161
E value
                  3.0e-85
Match length
                  443
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18I23, complete sequence [Arabidopsis thaliana]
                  149036
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g2760164
BLAST score
                  412
E value
                  0.0e+00
Match length
                  428
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18P6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149037
Seq. ID
                  LIB3175-020-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g3913871
BLAST score
                  756
E value
                  1.0e-80
Match length
                  146
% identity
                  100
                  FERROCHELATASE, CHLOROPLAST PRECURSOR (PROTOHEME
NCBI Description
                  FERRO-LYASE) (HEME SYNTHETASE) (FERROCHELATASE-II)
                  >gi 1946377 (U93215) ferrochelatase precusor isolog
                   [Arabidopsis thaliana] >gi 2347202 (AC002338)
                  ferrochelatase precusor isolog [Arabidopsis thaliana]
                  149038
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q2498731
BLAST score
                  487
E value
                  3.0e-49
                  126
Match length
                  74
% identity
                  PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1
NCBI Description
                  >gi 1362013 pir S57611 zeta-crystallin homolog -
                  Arabidopsis thaliana >gi 886428 emb CAA89838 (Z49768)
                  zeta-crystallin homologue [Arabidopsis thaliana]
Seq. No.
                  149039
Seq. ID
                  LIB3175-020-P1-K1-C9
```

```
Method
                  BLASTX
NCBI GI
                  q2160133
BLAST score
                  393
E value
                  4.0e-38
Match length
                  128
% identity
NCBI Description
                  (AC000375) Strong similarity to Arabidopsis
                  gb X91953,F19K23.3,F19K23.15. ESTs
                  gb T21984,gb ATTS0219,gb ATTS0207,gb T21984 come from this
                  gene. [Arabidopsis thaliana]
                  149040
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  449
E value
                  7.0e-45
Match length
                  84
                  100
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  149041
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  a4589398
BLAST score
                  412
E value
                  2.0e-40
Match length
                  95
                  77
% identity
                  (D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]
NCBI Description
                  149042
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q4582459
BLAST score
                  639
E value
                  6.0e-67
Match length
                  147
% identity
NCBI Description
                  (AC007071) putative RanBP7/importin protein [Arabidopsis
                  thaliana]
                  149043
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q1351082
BLAST score
                  593
E value
                  1.0e-61
Match length
                  146
% identity
                  79
NCBI Description
                  SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) >qi 166700
                  (M55910) Fe-superoxide dismutase [Arabidopsis thaliana]
Seq. No.
                  149044
```

Seq. ID

```
LIB3175-020-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115767
                  703
BLAST score
                  2.0e-74
E value
Match length
                  133
% identity
                  100
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603_pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >qi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  149045
Seq. ID
                  LIB3175-020-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  q4757391
BLAST score
                  255
E value
                  1.0e-141
Match length
                  255
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  F2C19, complete sequence
Seq. No.
                  149046
Seq. ID
                  LIB3175-020-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g461550
BLAST score
                  403
                  2.0e-39
E value
Match length
                  115
                  73
% identity
NCBI Description
                  ATP SYNTHASE GAMMA CHAIN 1, CHLOROPLAST PRECURSOR
                  >gi 81635 pir B39732 H+-transporting ATP synthase (EC
                  3.6.1.34) gamma-1 chain precursor, chloroplast -
                  Arabidopsis thaliana >gi 166632 (M61741) ATP synthase
                  gamma-subunit [Arabidopsis thaliana]
                  149047
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2252825
BLAST score
                  649
E value
                  4.0e-68
Match length
                  124
% identity
                  (AF013293) Similar to transmembrane protein; coded for by
NCBI Description
                  A. thaliana cDNA H37637; coded for by A. thaliana cDNA
                  T41850; coded for by A. thaliana cDNA T13717; coded for by
                  A. thaliana cDNA T04371; coded for by A. thaliana cDNA
                  T43789; coded
Seq. No.
                  149048
```

Method BLASTN

LIB3175-020-P1-K1-E1

```
g3892698
NCBI GI
BLAST score
                  175
E value
                  6.0e-94
Match length
                  175
                  100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2
                   (ESSAII project)
Seq. No.
                  149049
Seq. ID
                  LIB3175-020-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  q886427
BLAST score
                  52
E value
                  2.0e-20
Match length
                  183
% identity
NCBI Description A.thaliana mRNA for zeta-crystallin homologue
                  149050
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  q4191771
BLAST score
                  157
E value
                  6.0e-83
Match length
                  430
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3P11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149051
Seq. ID
                  LIB3175-020-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q267073
BLAST score
                  373
E value
                  6.0e-36
Match length
                  74
% identity
                  TUBULIN BETA-2/BETA-3 CHAIN >gi_320184_pir__JQ1587 tubulin
NCBI Description
                  beta chain - Arabidopsis thaliana >gi_166898 (M84700)
                  beta-2 tubulin [Arabidopsis thaliana] >gi 166900 (M84701)
                  beta-3 tubulin [Arabidopsis thaliana]
Seq. No.
                  149052
Seq. ID
                  LIB3175-020-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g4589409
BLAST score
                  261
E value
                  1.0e-145
Match length
                  337
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F17P19, complete sequence
Seq. No.
                  149053
                  LIB3175-020-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4063749
```

```
176
BLAST score
                   1.0e-12
E value
                   85
Match length
% identity
                   24
                   (AC005851) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   149054
Seq. No.
                   LIB3175-020-P1-K1-E7
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3928074
BLAST score
                   236
                   1.0e-130
E value
                   438
Match length
                   100
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T7F6 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   149055
Seq. No.
                   LIB3175-020-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2117612
BLAST score
                   803
                   3.0e-86
E value
Match length
                   143
                   100
% identity
NCBI Description
                   catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
                   149056
Seq. No.
                   LIB3175-020-P1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4581207
BLAST score
                   488
E value
                   2.0e-49
                   93
Match length
                   100
% identity
                   (Y17914) cyclic nucleotide and calmodulin-regulated ion
NCBI Description
                   channel [Arabidopsis thaliana]
                   149057
Seq. No.
                   LIB3175-020-P1-K1-F10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q1086460
BLAST score
                   188
                   1.0e-101
E value
                   316
Match length
% identity
NCBI Description
                   Arabidopsis thaliana Columbia ecotype metallothionein
                   (MT1c) gene, complete cds
Seq. No.
                   149058
                   LIB3175-020-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   a267069
BLAST score
                   669
E value
                   2.0e-70
Match length
                   124
                   100
% identity
```

1.8899

% identity

100

```
TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >qi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >qi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  149059
Seq. No.
                  LIB3175-020-P1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g495728
                  303
BLAST score
                  1.0e-170
E value
Match length
                  315
                  99
% identity
NCBI Description
                  Arabidopsis thaliana small Ras-like GTP-binding protein
                  (Ran-1) mRNA, complete cds. >gi 2058277 emb X97379 ATRRAN1
                  A.thaliana mRNA for AtRanl protein
                  149060
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g2160296
BLAST score
                  186
E value
                  4.0e-14
                  106
Match length
% identity
                  42
                  (D61395) gamma-VPE [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  149061
                  LIB3175-020-P1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2459406
BLAST score
                  99
E value
                  2.0e-48
Match length
                  312
% identity
                  92
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F4P9 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149062
Seq. ID
                  LIB3175-020-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4835233
BLAST score
                  591
                  2.0e-61
E value
Match length
                  122
% identity
                  97
                  (AL049862) putative protein 1 photosystem II
NCBI Description
                  oxygen-evolving complex [Arabidopsis thaliana]
Seq. No.
                  149063
Seq. ID
                  LIB3175-020-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  g3869075
BLAST score
                  277
E value
                  1.0e-154
Match length
                  417
```

BLAST score

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MXK3, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149064
Seq. ID
                   LIB3175-020-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q115767
BLAST score
                   499
E value
                   8.0e-51
Match length
                   95
% identity
                   100
NCBI Description
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-165/180) (LHCP) >gi_81603_pir_A29280 chlorophyll a/b-binding protein ab165 - Arabidopsis thaliana
                   >gi 16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                   protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   149065
Seq. ID
                   LIB3175-020-P1-K1-G10
Method
                   BLASTN
NCBI GI
                   q4589440
BLAST score
                   212
E value
                   1.0e-116
Match length
                   212
                   100
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MSD21, complete sequence
Seq. No.
                   149066
                   LIB3175-020-P1-K1-G11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3036793
BLAST score
                   154
E value
                   4.0e-10
Match length
                   119
% identity
                   36
NCBI Description
                   (AL022373) putative protein [Arabidopsis thaliana]
                   >gi 3805855 emb CAA21475 (AL031986) putative protein
                   [Arabidopsis thaliana]
                   149067
Seq. No.
Seq. ID
                   LIB3175-020-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g4585919
BLAST score
                   143
E value
                   5.0e-09
Match length
                   103
% identity
                   41
                  (AC007211) aSPF1 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149068
Seq. ID
                   LIB3175-020-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g3831446
```

```
E value
                   6.0e-69
Match length
                   130
% identity
                   (AC005819) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   149069
Seq. No.
Seq. ID
                   LIB3175-020-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   g4510430
BLAST score
                   757
E value
                   8.0e-81
Match length
                   144
                   99
% identity
                   (AC006929) unknown protein, 3' partial [Arabidopsis
NCBI Description
                   thalianal
                   149070
Seq. No.
                   LIB3175-020-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2529229
BLAST score
                   342
E value
                   5.0e - 34
                   87
Match length
% identity
                   (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
                   149071
Seq. No.
                   LIB3175-020-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1709970
BLAST score
                   193
E value
                   1.0e-14
Match length
                   49
% identity
                   84
NCBI Description
                  60S RIBOSOMAL PROTEIN L10A
Seq. No.
                   149072
                   LIB3175-020-P1-K1-G9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4519188
BLAST score
                   20
E value
                   3.7e-01
                   423
Match length
                   76
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21L19, complete sequence
                   149073
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-H10
                  BLASTX
Method
NCBI GI
                   g2262167
                   747
BLAST score
E value
                   1.0e-79
                   142
Match length
% identity
                   (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
```

```
thaliana]
```

```
149074
Seq. No.
                   LIB3175-020-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4056493
BLAST score
                   440
E value
                   1.0e-43
Match length
                   140
% identity
                   63
                   (AC005896) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149075
Seq. ID
                   LIB3175-020-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g543841
                   620
BLAST score
E value
                   9.0e-65
Match length
                   123
% identity
                   98
                   ADP-RIBOSYLATION FACTOR 1 >gi 322518 pir S28875
NCBI Description
                   ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                   >gi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                   thaliana] >gi 4630747 gb AAD26597.1 AC007236 2 (AC007236)
                   ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                   149076
                   LIB3175-020-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g112741
BLAST score
                   550
E value
                   1.0e-56
Match length
                   102
% identity
                   100
NCBI Description
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
Seq. No.
                   149077
Seq. ID
                   LIB3175-020-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   g4006871
BLAST score
                   417
E value
                   3.0e-41
Match length
                   101
% identity
                   85
NCBI Description
                   (Z99707) patatin-like protein [Arabidopsis thaliana]
```

Seq. No. 149078

Seq. ID LIB3175-020-P1-K1-H5

Method BLASTN NCBI GI g3128141

NCBI GI

g116464

```
BLAST score
                  222
                  1.0e-122
E value
                  322
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQD22, complete sequence [Arabidopsis thaliana]
                  149079
Seq. No.
                  LIB3175-020-P1-K1-H6
Seq. ID
                  BLASTX
Method
                  g2864602
NCBI GI
BLAST score
                   402
                   4.0e-39
E value
                  119
Match length
                   67
% identity
                   (Y12071) thylakoid lumen rotamase [Spinacia oleracea]
NCBI Description
                  149080
Seq. No.
                  LIB3175-020-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1363489
BLAST score
                   392
                   6.0e-49
E value
                   107
Match length
                   92
% identity
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                   thaliana >gi_984052_emb_CAA61592_ (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
                   149081
Seq. No.
                  LIB3175-020-P1-K1-H8
Seq. ID
                   BLASTN
Method
NCBI GI
                   g2264367
BLAST score
                   389
                   0.0e + 00
E value
                   389
Match length
                   100
% identity
NCBI Description
                  Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm,
                   complete sequence [Arabidopsis thaliana]
                   149082
Seq. No.
Seq. ID
                  LIB3175-020-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   g132074
                   618
BLAST score
                   1.0e-64
E value
                   112
Match length
                   100
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
                   149083
Seq. No.
                  LIB3175-021-P1-K1-A1
Seq. ID
Method
                  BLASTX
```

```
BLAST score
                   8.0e-29
E value
Match length
                   8.3
                   86
% identity
                  CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi 68230_pir__YKMUM citrate (si)-synthase (EC 4.1.3.7)
                  precursor, mitochondrial - Arabidopsis thaliana
                   >gi 2652924 emb CAA35570 (X17528) citrate synthetase
                   [Arabidopsis thaliana]
                  <sup>~</sup>149084
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-A10
Method
                  BLASTX
NCBI GI
                   q4335750
                   493
BLAST score
                   6.0e-50
E value
                   90
Match length
                   98
% identity
                   (ACO06284) putative beta-1,3-endoglucanase [Arabidopsis
NCBI Description
                   thaliana]
                   149085
Seq. No.
                  LIB3175-021-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4544399
BLAST score
                   439
                   1.0e-43
E value
Match length
                   101
% identity
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   149086
Seq. ID
                  LIB3175-021-P1-K1-A12
Method
                  BLASTX
NCBI GI
                   q3157931
BLAST score
                   689
                   7.0e-73
E value
Match length
                  133
% identity
                   100
                   (AC002131) Similar to pyrophosphate-dependent
NCBI Description
                  phosphofuctokinase beta subunit gb_Z32850 from Ricinus
                  communis. ESTs gb_N65773, gb_N64925 and gb_F15232 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                   149087
Seq. ID
                  LIB3175-021-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g1865681
BLAST score
                   651
E value
                   2.0e-68
Match length
                  133
                   95
% identity
                   (Z83320) Related sequences: ATH1 genomic clone, acc. no.
NCBI Description
                  X80127; cDNA ATH1 clone, acc. no. X80126 [Arabidopsis
                  thaliana]
```

```
149088
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-A4
                  BLASTX
Method
NCBI GI
                  g2645971
                  707
BLAST score
                  5.0e-75
E value
Match length
                  131
% identity
                  100
                  (AF034255) reversibly glycosylated polypeptide-3
NCBI Description
                  [Arabidopsis thaliana]
                  149089
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-A5
Method
                  BLASTN
                  g2979540
NCBI GI
BLAST score
                  404
E value
                  0.0e+00
                  404
Match length
                  100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17K2 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  149090
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q3913410
                  589
BLAST score
E value
                  4.0e-61
Match length
                  134
% identity
                  86
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME 2 (ADOMETDC 2)
NCBI Description
                   (SAMDC 2) >gi_2662406 (U80916) S-adenosyl-L-methionine
                  decarboxylase [Brassica juncea]
Seq. No.
                  149091
Seq. ID
                  LIB3175-021-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  q3892722
BLAST score
                  309
                  1.0e-28
E value
                  74
Match length
% identity
NCBI Description (AL033545) putative protein [Arabidopsis thaliana]
Seq. No.
                  149092
Seq. ID
                  LIB3175-021-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  q4678371
                  388
BLAST score
E value
                  0.0e+00
Match length
                  403 .
% identity
                  100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T6G15
NCBI Description
                  (ESSA project)
Seq. No.
                  149093
Seq. ID
                  LIB3175-021-P1-K1-A9
```

```
Method
                  BLASTN
NCBI GI
                  q2618602
BLAST score
                  20
E value
                  3.3e-01
Match length
                  389
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149094
                  LIB3175-021-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g729477
BLAST score
                  314
E value
                  6.0e-29
Match length
                  119
                  55
% identity
                  FERREDOXIN--NADP REDUCTASE PRECURSOR (FNR)
NCBI Description
                  >gi 320548_pir_ A44974 ferredoxin--NADP+ reductase (EC
                  1.18.1.2) precursor - common ice plant >gi_167256 (M25528)
                  ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
                  [Mesembryanthemum crystallinum] >gi_226768_prf__1604475A
                  ferredoxin NADP reductase [Mesembryanthemum crystallinum]
Seq. No.
                  149095
Seq. ID
                  LIB3175-021-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  q4519191
BLAST score
                  294
E value
                  1.0e-164
Match length
                  341
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K9P8, complete sequence
Seq. No.
                  149096
Seq. ID
                  LIB3175-021-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q2264318
BLAST score
                  399
E value
                  0.0e + 00
Match length
                  403
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149097
Seq. ID
                  LIB3175-021-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q3377844
BLAST score
                  212
E value
                  6.0e-17
Match length
                  67
% identity
                  76
                  (AF076274) contains similarity to DNA
NCBI Description
                   (cytosine-5-)-methyltransferases [Arabidopsis thaliana]
```

```
Seq. No.
                   149098
Seq. ID
                  LIB3175-021-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4432856
                  205
BLAST score
E value
                   4.0e-16
                  89
Match length
                   53
% identity
NCBI Description
                   (AC006300) putative 2A6 protein [Arabidopsis thaliana]
Seq. No.
                  149099
Seq. ID
                  LIB3175-021-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  q3789706
BLAST score
                  229
E value
                  1.0e-126
Match length
                   413
                  100
% identity
                  Arabidopsis thaliana chromosome 1 BAC F15K9 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  149100
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q2500130
BLAST score
                  694
E value
                  2.0e-73
Match length
                  134
% identity
                  100
NCBI Description
                  THIOREDOXIN REDUCTASE 2 (NADPH-DEPENDENT THIOREDOXIN
                  REDUCTASE 2) (NTR 2) >gi_1076358_pir__S44026 thioredoxin
                  reductase (NADPH) (EC 1.6.4.5) A - Arabidopsis thaliana
                   (fragment) >gi_468524_emb_CAA80655_ (Z23108) NADPH
                  thioredoxin reductase [Arabidopsis thaliana]
Seq. No.
                  149101
Seq. ID
                  LIB3175-021-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q3980254
BLAST score
                  676
E value
                  2.0e-71
Match length
                  133
% identity
                  100
NCBI Description
                   (AJ006053) peroxisomal membrane protein [Arabidopsis
                  thaliana] >gi_4773886_gb_AAD29759.1_AF076243_6 (AF076243)
                  pmp22 peroxisomal membrane protein [Arabidopsis thaliana]
Seq. No.
                  149102
Seq. ID
                  LIB3175-021-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q1169476
BLAST score
                  607
E value
                  3.0e-63
Match length
                  117
                  99
% identity
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
```

```
vitronectin-like adhesion protein [Nicotiana tabacum]
                   149103
Seq. No.
Seq. ID
                   LIB3175-021-P1-K1-B8
                   BLASTX
Method
NCBI GI
                   g687677
BLAST score
                   172
                   3.0e-12
E value
                   34
Match length
                   97
% identity
                   (U19925) unknown [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149104
Seq. ID
                   LIB31-75-021-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g82200
BLAST score
                   309
E value
                   2.0e-28
Match length
                   121
                   58
% identity
NCBI Description hypothetical protein 1244 - common tobacco chloroplast
                   149105
Seq. No.
Seq. ID
                   LIB3175-021-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   g2618602
BLAST score
                   171
                   3.0e-91
E value
Match length
                   418
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
                   149106
Seq. No.
Seq. ID
                   LIB3175-021-P1-K1-C10
Method
                   BLASTN
NCBI GI
                   g4757414
BLAST score
                   400
E value
                   0.0e+00
Match length
                   400
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYF24, complete sequence
Seq. No.
                   149107
                  LIB3175-021-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2828267
BLAST score
                   432
E value
                   9.0e-43
                   108
Match length
```

NCBI Description

% identity

Seq. No. 149108

Seq. ID LIB3175-021-P1-K1-C12

81

Method BLASTX

18909

(Y14044) geranylgeranyl reductase [Arabidopsis thaliana]

```
NCBI GI
                  q2828267
BLAST score
                  239
E value
                   3.0e-20
Match length
                  97
                   61
% identity
NCBI Description
                   (Y14044) geranylgeranyl reductase [Arabidopsis thaliana]
                  149109
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q1362162
BLAST score
                  579
E value
                   5.0e-60
Match length
                  137
% identity
                   76
                  beta-glucosidase BGQ60 precursor - barley >gi 804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
                  149110
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q1362162
BLAST score
                  283
E value
                   6.0e-34
Match length
                  115
% identity
                  beta-glucosidase BGQ60 precursor - barley >gi 804656
NCBI Description
                   (L41869) beta-glucosidase [Hordeum vulgare]
Seq. No.
                  149111
Seq. ID
                  LIB3175-021-P1-K1-C4
Method
                  BLASTX
NCBI GI
                   q2738248
BLAST score
                   491
E value
                   1.0e-49
Match length
                   103
% identity
                   90
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   149112
Seq. ID
                   LIB3175-021-P1-K1-C5
Method
                  BLASTN
NCBI GI
                   q2618602
BLAST score
                  20
E value
                   3.5e-01
Match length
                   401
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSJ1, complete sequence [Arabidopsis thaliana]
                   149113
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q4415930
BLAST score
                  534
E value
                   1.0e-54
```

```
Match length
                  127
                  80
% identity
                  (AC006418) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 4559389 gb_AAD23049.1_AC006526_14 (AC006526) unknown
                  protein [Arabidopsis thaliana]
                  149114
Seq. No.
                  LIB3175-021-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2119846
BLAST score
                  672
                  7.0e-71
E value
Match length
                  127
                  100
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  149115
Seq. ID
                  LIB3175-021-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q1345592
BLAST score
                  681
                  6.0e-72
E value
Match length
                  136
                  100
% identity
NCBI Description
                  14-3-3-LIKE PROTEIN GF14 EPSILON >qi 1022778 (U36446) GF14
                  epsilon isoform [Arabidopsis thaliana]
Seq. No.
                  149116
Seq. ID
                  LIB3175-021-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q3927831
BLAST score
                  720
E value
                  2.0e-76
Match length
                  136
% identity
NCBI Description
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
                  thaliana]
                  149117
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  q4097949
BLAST score
                  322
                  0.0e + 00
E value
Match length
                  357
                  100
% identity
NCBI Description
                  Arabidopsis thaliana plant IF-like protein mRNA, complete
                  cds
                  149118
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-D10
```

```
Method
                   BLASTX
NCBI GI
                   g1335862
BLAST score
                   532
                   2.0e-54
E value
                   133
Match length
                   78
% identity
NCBI Description
                  (U42608) clathrin heavy chain [Glycine max]
                   149119
Seq. No.
Seq. ID
                   LIB3175-021-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   q4741952
BLAST score
                   630
                   6.0e-66
E value
Match length
                   118
                   75
% identity
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149120
Seq. ID
                   LIB3175-021-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q4583542
BLAST score
                   331
E value
                   7.0e-31
                   130
Match length
                   60
% identity
                   (Y16847) 16 kDa polypeptide of oxygen-evolving complex
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   149121
                   LIB3175-021-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1170159
BLAST score
                   326
E value
                   3.0e-30
Match length
                   66
% identity
                   100
NCBI Description HISTONE H2B
Seq. No.
                   149122
Seq. ID
                   LIB3175-021-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   g1931639
BLAST score
                   244
E value
                   1.0e-20
Match length
                   106
% identity
                   43
NCBI Description
                  (U95973) lysophospholipase isolog [Arabidopsis thaliana]
Seq. No.
                   149123
Seq. ID
                   LIB3175-021-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   g3319349
BLAST score
                   646
E value
                   7.0e-68
Match length
                   126
% identity
                   100
```

```
(AF077407) No definition line found [Arabidopsis thaliana]
NCBI Description
                  149124
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g1169277
BLAST score
                  460
                  5.0e-46
E value
Match length
                  106
                  87
% identity
NCBI Description
                  DEHYDRIN ERD10 (LOW-TEMPERATURE-INDUCED PROTEIN LTI45)
                  >gi 2129638 pir S60480 low temperature-induced protein
                  lit29 - Arabidopsis thaliana >gi_556472_dbj_BAA04568_
                  (D17714) ERD10 protein [Arabidopsis thaliana]
                  >gi 975648 emb_CAA62448_ (X90958) lti29 [Arabidopsis
                  thaliana]
                  149125
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g2501102
BLAST score
                  585
E value
                  1.0e-60
Match length
                  119
                  100
% identity
NCBI Description
                  SYNTAXIN-RELATED PROTEIN KNOLLE >gi 1184165 (U39451)
                  syntaxin-related [Arabidopsis thaliana] >gi 1184167
                  (U39452) syntaxin-related [Arabidopsis thaliana]
                  >gi_3063443 (AC003981) F22013.4 [Arabidopsis thaliana]
                  >gi_1587182_prf__2206310A syntaxin-related protein
                  [Arabidopsis thaliana]
Seq. No.
                  149126
Seq. ID
                  LIB3175-021-P1-K1-E1
Method
                  BLASTN
NCBI GI
                  g704396
BLAST score
                  373
E value
                  0.0e + 00
Match length
                  412
% identity
NCBI Description
                  Arabidopsis thaliana cystathionine beta-lyase mRNA,
                  complete cds
                  149127
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q1345595
BLAST score
                  598
E value
                  3.0e-62
Match length
                  122
% identity
                  100
NCBI Description
                  14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
                  >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) -
                  Arabidopsis thaliana >gi 953221 (U02565) 14-3-3-like
                  protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14
```

lambda [Arabidopsis thaliana]

```
Seq. No.
                   149128
                   LIB3175-021-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244837
BLAST score
                   507
                   1.0e-51
E value
                   100
Match length
                   100
% identity
NCBI Description
                    (Z97337) proteasome chain protein [Arabidopsis thaliana]
                   >gi_2511572_emb_CAA73618.1_ (Y13175) multicatalytic
endopeptidase [Arabidopsis thaliana] >gi_3421114 (AF043535)
                   20S proteasome beta subunit PBD2 [Arabidopsis thaliana]
                   149129
Seq. No.
Seq. ID
                   LIB3175-021-P1-K1-E3
Method
                   BLASTX
NCBI GI
                   q4678332
BLAST score
                   430
                   2.0e-42
E value
Match length
                   135
% identity
                    (AL049658) putative peptide transporter [Arabidopsis
NCBI Description
                   thaliana]
                   149130
Seq. No.
Seq. ID
                   LIB3175-021-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   q1009234
BLAST score
                   591
                   3.0e-64
E value
Match length
                   135
% identity
                   93
NCBI Description
                   (L38829) SUP2 gene product [Nicotiana tabacum]
                   149131
Seq. No.
Seq. ID
                   LIB3175-021-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   q3096935
BLAST score
                   221
E value
                   5.0e-18
Match length
                   85
% identity
NCBI Description
                   (AL023094) putative protein [Arabidopsis thaliana]
Seq. No.
                   149132
Seq. ID
                   LIB3175-021-P1-K1-E6
Method
                   BLASTN
NCBI GI
                   q2739359
BLAST score
                   404
E value
                   0.0e + 00
Match length
                   404
% identity
                   100
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T9J22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149133
Seq. ID
                   LIB3175-021-P1-K1-E7
```

```
Method
                    BLASTX
NCBI GI
                    g3482979
BLAST score
                    457
                    1.0e-45
E value.
                    85
Match length
                    100
% identity
                    (AL031369) putative protein [Arabidopsis thaliana]
NCBI Description
                    >gi 4567258 gb AAD23672.1 AC007070 21 (AC007070)
                    hypothetical protein [Arabidopsis thaliana]
                    149134
Seq. No.
                    LIB3175-021-P1-K1-E8
Seq. ID
                    BLASTX
Method
NCBI GI
                    q131336
BLAST score
                    339
E value
                    7.0e-32
                    73
Match length
                    93
% identity
NCBI Description
                    PHOTOSYSTEM II 10 KD PHOSPHOPROTEIN >gi 72715 pir F2NT0P
                    photosystem II phosphoprotein psbH - common tobacco chloroplast >gi_11857_emb_CAA77374_ (Z00044) PSII 10kD phosphoprotein [Nicotiana tabacum]
                    >gi_225225_prf__1211235BG photosystem II 10kD
phosphoprotein [Nicotiana tabacum]
Seq. No.
                    149135
Seq. ID
                    LIB3175-021-P1-K1-E9
                    BLASTX
Method
NCBI GI
                    g2275196
BLAST score
                    629
E value
                    7.0e-66
                    122
Match length
                    100
% identity
NCBI Description
                     (AC002337) water stress-induced protein, WSI76 isolog
                    [Arabidopsis thaliana] >gi 4630746 gb AAD26596.1 AC007236 1
                     (AC007236) water stress-induced protein [Arabidopsis
                    thaliana]
Seq. No.
                    149136
                    LIB3175-021-P1-K1-F1
Seq. ID
Method
                    BLASTX
NCBI GI
                    g1177320
BLAST score
                    197
E value
                    3.0e-15
Match length
                    84
% identity
                    (X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza
NCBI Description
                    sativa]
                    149137
Seq. No.
Seq. ID
                    LIB3175-021-P1-K1-F10
Method
                    BLASTX
NCBI GI
                    g132110
BLAST score
                    598
E value
                    3.0e-62
Match length
                    111
% identity
                    99
```

NCBI GI

```
NCBI Description RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   149138
Seq. ID
                  LIB3175-021-P1-K1-F11
Method
                  BLASTX
NCBI GI
                   g2979544
BLAST score
                   587
E value
                   6.0e-61
Match length
                   110
% identity
                   100
NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]
Seq. No.
                   149139
Seq. ID
                  LIB3175-021-P1-K1-F2
Method
                  BLASTX
NCBI GI
                   g1346106
BLAST score
                   589
E value
                   4.0e-61
Match length
                   128
% identity
                   89
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT >gi 557694
NCBI Description
                   (U12232) GTP binding protein beta subunit [Arabidopsis
                   thaliana] >gi 3096915 emb CAA18825.1 (AL023094) GTP
                  binding protein beta subunit [Arabidopsis thaliana]
Seq. No.
                   149140
                  LIB3175-021-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3335333
BLAST score
                   488
E value
                   3.0e-49
Match length
                   124
                   82
% identity
                   (AC004512) Similar to chloroplast membrane-associated 30KD
NCBI Description
                   protein precursor (IM30) gb M73744 from Pisum sativum.
                   ESTs gb N37557, gb W43887 and gb AA042479 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                   149141
Seq. ID
                  LIB3175-021-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3201613
BLAST score
                   415
E value
                   9.0e-41
                  78
Match length
% identity
NCBI Description (AC004669) glutathione S-transferase [Arabidopsis thaliana]
Seq. No.
                  149142
Seq. ID
                  LIB3175-021-P1-K1-F5
Method
                  BLASTX
```

18916

g3183088

```
BLAST score
                  3.0e-17
E value
                   68
Match length
                  54
% identity
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                   (LTP) >gi 629658 pir S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
                  149143
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-F6
                  BLASTX
Method
NCBI GI
                  g166834
BLAST score
                  521
E value
                  3.0e-53
Match length
                  116
                  90
% identity
                   (M86720) ribulose bisphosphate carboxylase/oxygenase
NCBI Description
                  activase [Arabidopsis thaliana] >gi 2642155 (AC003000)
                  Rubisco activase [Arabidopsis thaliana]
Seq. No.
                  149144
                  LIB3175-021-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741940
                  567
BLAST score
E value
                  1.0e~58
                  103
Match length
                  66
% identity
NCBI Description
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.
                  149145
Seq. ID
                  LIB3175-021-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2827627
BLAST score
                  538
E value
                  3.0e-55
Match length
                  101
                  100
% identity
NCBI Description
                  (AL021636) hypothetical protein [Arabidopsis thaliana]
                  149146
Seq. No.
                  LIB3175-021-P1-K1-F9
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4262221
BLAST score
                  323
                  0.0e + 00
E value
                  323
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F10A8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  149147
Seq. No.
                  LIB3175-021-P1-K1-G1
Seq. ID
Method
                  BLASTX
                  g4688596
NCBI GI
BLAST score
```

```
E value
                  4.0e-49
Match length
                  90
                  100
% identity
NCBI Description
                   (AJ005682) inositol 1,4,5-trisphosphate 5-phosphatase
                   [Arabidopsis thaliana]
                  149148
Seq. No.
                  LIB3175-021-P1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2264308
BLAST score
                  204
                  1.0e-111
E value
                  404
Match length
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIK22, complete sequence [Arabidopsis thaliana]
                  149149
Seq. No.
                  LIB3175-021-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4580460
BLAST score
                  531
E value
                  2.0e-54
Match length
                  122
% identity
NCBI Description
                   (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
                  thaliana]
                  149150
Seq. No.
                  LIB3175-021-P1-K1-G3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3582315
BLAST score
                  241
                   1.0e-133
E value
                   338
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T27A16 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   149151
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-G4
Method
                  BLASTX
NCBI GI
                   g549893
BLAST score
                   193
E value
                   8.0e-15
Match length
                   37
% identity
                   100
NCBI Description
                   (U09342) homeobox protein [Arabidopsis thaliana]
                   149152
Seq. No.
Seq. ID
                  LIB3175-021-P1-K1-G5
Method
                  BLASTX
NCBI GI
                   q2459424
BLAST score
                   687
E value
                   1.0e-72
Match length
                   135
% identity
                   100
```

```
NCBI Description (AC002332) unknown protein [Arabidopsis thaliana]
 Seq. No.
                    149153
                    LIB3175-021-P1-K1-G6
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4538943
                    496
 BLAST score
 E value
                    3.0e-50
 Match length
                    122
% identity
                    78
                    (AL049483) putative beta-galactosidase [Arabidopsis
 NCBI Description
                    thaliana
 Seq. No.
                    149154
 Seq. ID
                    LIB3175-021-P1-K1-G7
 Method
                    BLASTX
 NCBI GI
                    g1402906
 BLAST score
                    402
 E value
                    2.0e-53
 Match length
                    127
 % identity
                    87
 NCBI Description
                    (X98314) peroxidase [Arabidopsis thaliana]
                    >gi_4468977 emb CAB38291_ (AL035605) peroxidase, prxr2
                    [Arabidopsis thaliana]
 Seq. No.
                    149155
                    LIB3175-021-P1-K1-G8
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    g3953473
 BLAST score
                    545
 E value
                    4.0e-56
 Match length
                    110
 % identity
                    100
 NCBI Description
                   (AC002328) F2202.18 [Arabidopsis thaliana]
 Seq. No.
                    149156
 Seq. ID
                    LIB3175-021-P1-K1-H1
 Method
                    BLASTX
 NCBI GI
                    q4490732
 BLAST score
                    358
 E value
                    4.0e-34
                    90
 Match length
                    78
 % identity
                    (AL035709) phosphoenolpyruvate carboxykinase (ATP)-like
 NCBI Description
                    protein [Arabidopsis thaliana]
 Seq. No.
                    149157
                    LIB3175-021-P1-K1-H10
 Seq. ID
 Method
                    BLASTX
 NCBI GI
                    q4585882
 BLAST score
                    442
 E value
                    6.0e-44
 Match length
                    86
 % identity
                    (AC005850) PSI type III chlorophyll a/b-binding protein
 NCBI Description
```

[Arabidopsis thaliana]

```
149158
Seq. No.
                  LIB3175-021-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g134976
BLAST score
                  681
                  6.0e-72
E value
Match length
                  131
% identity
NCBI Description
                  GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi_81619_pir__S12042
                  glucose transport protein STP1 - Arabidopsis thaliana
                  >gi_16520_emb_CAA39037_ (X55350) glucose transporter
                  [Arabidopsis thaliana]
                  149159
Seq. No.
                  LIB3175-021-P1-K1-H12
Seq. ID
                  BLASTX
Method
                  q4539307
NCBI GI
BLAST score
                  294
E value
                  1.0e-26
                  120
Match length
                  53
% identity
                  (AL049480) putative acidic ribosomal protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  149160
                  LIB3175-021-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g1628583
NCBI GI
BLAST score
                  351
E value
                  2.0e-33
Match length
                  72
% identity
                  100
                  (U66916) 12S cruciferin seed storage protein [Arabidopsis
NCBI Description
                  thaliana] >gi_2842495_emb_CAA16892_ (AL021749) 12S
                  cruciferin seed storage protein [Arabidopsis thaliana]
Seq. No.
                  149161
Seq. ID
                  LIB3175-021-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  q3941543
BLAST score
                  345
E value
                  1.0e-32
Match length
                  68
                  100
% identity
NCBI Description
                  (AF069497) pelota [Arabidopsis thaliana]
                  >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
                  [Arabidopsis thaliana]
                  149162
Seq. No.
                  LIB3175-021-P1-K1-H5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g16519
BLAST score
                  66
E value
                  9.0e-29
Match length
                  66
% identity
                  100
NCBI Description A.thaliana STP1 mRNA for glucose transporter
```

```
Seq. No.
                   149163
Seq. ID
                   LIB3175-021-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g267079
BLAST score
                   646
                   7.0e-68
E value
Match length
                   118
% identity
                   100
                   TUBULIN BETA-6 CHAIN >gi_320187_pir__JQ1590 tubulin beta-6
NCBI Description
                   chain - Arabidopsis thaliana >gi_166904 (M84703) beta-6
                   tubulin [Arabidopsis thaliana]
Seq. No.
                   149164
                   LIB3175-021-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244750
BLAST score
                   685
E value
                   2.0e-72
Match length
                   134
                   100
% identity
NCBI Description
                   (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                   >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                   [Arabidopsis thaliana]
Seq. No.
                   149165
                   LIB3175-021-P1-K1-H8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1732570
BLAST score
                   732
E value
                   6.0e-78
Match length
                   132
                   100
% identity
NCBI Description
                   (U72153) beta-glucosidase [Arabidopsis thaliana]
Seq. No.
                   149166
                   LIB3175-021-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2244772
BLAST score
                   698
E value
                   6.0e-74
Match length
                   125
                   100
% identity
NCBI Description
                   (Z97335) transport protein [Arabidopsis thaliana]
Seq. No.
                   149167
Seq. ID
                   LIB3175-022-P1-K1-A1
Method
                   BLASTN
NCBI GI
                   g3059018
BLAST score
                   260
E value
                   1.0e-144
                   298
Match length
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12
NCBI Description
                   (ESSAII project)
Seq. No.
                   149168
```

```
LIB3175-022-P1-K1-A10
Seq. ID
Method
                  BLASTX
                  q1363488
NCBI GI
BLAST score
                  481
                  2.0e-48
E value
                  94
Match length
                  100
% identity
                  IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410)
NCBI Description
                  IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_
                  (AC006340) auxin-induced IAA8 protein [Arabidopsis
                  thaliana]
                  149169
Seq. No.
                  LIB3175-022-P1-K1-A11
Seq. ID
                  BLASTX
Method
                  g1172658
NCBI GI
BLAST score
                  166
                  8.0e-12
E value
                  35
Match length
                  97
% identity
                  PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2
NCBI Description
                  >gi 1262705_dbj_BAA04420.1_ (D17510) PSI P700 apoprotein A2
                  [Pinus thunbergii]
                  149170
Seq. No.
                  LIB3175-022-P1-K1-A2
Seq. ID
Method
                  BLASTN
                  g3738275
NCBI GI
                  347
BLAST score
                  0.0e + 00
E value
                  403
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F17A22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  149171
Seq. No.
Seq. ID
                  LIB3175-022-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g2213607
BLAST score
                  475
                  9.0e-48
E value
                  92
Match length
                  67
% identity
                   (AC000103) F21J9.1 [Arabidopsis thaliana]
NCBI Description
                  149172
Seq. No.
                  LIB3175-022-P1-K1-A5
Seq. ID
Method
                  BLASTX
                  g4191796
NCBI GI
BLAST score
                  231
E value
                   4.0e-19
Match length
                  65
                  60
% identity
NCBI Description
                   (AC005917) putative senescence-associated protein 5
                   [Arabidopsis thaliana]
                  149173
Seq. No.
```

```
Seq. ID
                  LIB3175-022-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g4105798
                  378
BLAST score
                  2.0e-36
E value
                  82
Match length
                   71
% identity
NCBI Description
                   (AF049930) PGP237-11 [Petunia x hybrida]
Seq. No.
                  149174
                  LIB3175-022-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1345595
BLAST score
                  638
E value
                   7.0e-67
Match length
                  130
                  100
% identity
                  14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
NCBI Description
                  >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) -
                  Arabidopsis thaliana >gi 953221 (U02565) 14-3-3-like
                  protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14
                  lambda [Arabidopsis thaliana]
                  149175
Seq. No.
Seq. ID
                  LIB3175-022-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g498038
BLAST score
                  474
E value
                  1.0e-47
Match length
                  143
% identity
                  57
                  (L33792) lipid transfer protein [Senecio odorus]
NCBI Description
Seq. No.
                  149176
Seq. ID
                  LIB3175-022-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q2651314
BLAST score
                  384
E value
                  4.0e-37
Match length
                  110
% identity
                   (AC002336) putative ribosomal protein S26 [Arabidopsis
NCBI Description
                  thaliana]
                  149177
Seq. No.
Seq. ID
                  LIB3175-022-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  q2500082
BLAST score
                  600
                  2.0e-62
E value
Match length
                  120
                  97
% identity
                  PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN)
NCBI Description
                   (PHOTOSYSTEM II PROTEIN D1) >gi 984735_emb_CAA56907_
                  (X80932) photosystem II D1 protein [Vigna unguiculata]
                  149178
Seq. No.
```

```
Seq. ID
                   LIB3175-022-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   q1710780
BLAST score
                   430
E value
                   1.0e-42
Match length
                   116
                   72
% identity
NCBI Description
                   40S RIBOSOMAL PROTEIN S9 (S7) >gi 1321917 emb CAA65433
                   (X96613) cytoplasmic ribosomal protein S7 [Podospora
                   anserina]
                   149179
Seq. No.
Seq. ID
                   LIB3175-022-P1-K1-B6
Method
                   BLASTN
NCBI GI
                   q2618605
BLAST score
                   295
E value
                   1.0e-165
Match length
                   418
% identity
                   99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUK11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149180
Seq. ID
                   LIB3175-022-P1-K1-B8
Method
                   BLASTN
NCBI GI
                   g1402874
BLAST score
                   181
                   3.0e-97
E value
Match length
                   324
% identity
                   97
NCBI Description A.thaliana 81kb genomic sequence
Seq. No.
                   149181
Seq. ID
                   LIB3175-022-P1-K1-B9
Method
                 BLASTN
                   g3510336
NCBI GI
BLAST score
                   384
                   0.0e + 00
E value
Match length
                   416
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18J17, complete sequence [Arabidopsis thaliana]
                   149182
Seq. No.
Seq. ID
                   LIB3175-022-P1-K1-C1
Method
                  BLASTN
                  g3702728
NCBI GI
BLAST score
                   260
E value
                   1.0e-144
Match length
                  397
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19M13, complete sequence [Arabidopsis thaliana]
                   149183
Seq. No.
Seq. ID
                  LIB3175-022-P1-K1-C10
Method
                  BLASTX
```

```
NCBI GI
                   g2864617
                   432
BLAST score
E value
                   1.0e-42
                   112
Match length
                   79
% identity
NCBI Description
                   (AL021811) H+-transporting ATP synthase chain9 - like
                   protein [Arabidopsis thaliana]
                   149184
Seq. No.
                   LIB3175-022-P1-K1-C11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1486472
BLAST score
                   453
                   3.0e-45
E value
Match length
                   103
% identity
                   86
                   (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                   tuberosum]
                   149185
Seq. No.
                   LIB3175-022-P1-K1-C12
Seq. ID
                   BLASTN
Method
                   g4589414
NCBI GI
                   50
BLAST score
                   3.0e-19
E value
Match length
                   224
                   84
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                   K14B15, complete sequence
                   149186
Seq. No.
                   LIB3175-022-P1-K1-C2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2760169
BLAST score
                   379
                   0.0e+00
E value
                   421
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MFB13, complete sequence [Arabidopsis thaliana]
                   149187
Seq. No.
                   LIB3175-022-P1-K1-C3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4589412
BLAST score
                   174
E value
                   5.0e-93
Match length
                   420
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F6N7, complete sequence
                   149188
Seq. No.
Seq. ID
                   LIB3175-022-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q4651202
BLAST score
                   169
```

```
E value
                  7.0e-12
                  99
Match length
                  35
% identity
NCBI Description
                  (AB026253) copper amine oxidase [Pisum sativum]
                  149189
Seq. No.
                  LIB3175-022-P1-K1-C5
Seq. ID
                  BLASTX
Method
                  g3935181
NCBI GI
                  721
BLAST score
                  1.0e-76
E value
                  131
Match length
                  100
% identity
                  (AC004557) F17L21.24 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  149190
                  LIB3175-022-P1-K1-C6
Seq. ID
Method -
                  BLASTN
NCBI GI
                  g3335356
BLAST score
                  320
                  1.0e-180
E value
Match length
                  402
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149191
                  LIB3175-022-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169598
BLAST score
                  417
                  5.0e-41
E value
                  89
Match length
                  87
% identity
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                  (DELTA-12 DESATURASE) >gi_438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
Seq. No.
                  149192
                  LIB3175-022-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1169201
BLAST score
                  527
                  7.0e-54
E value
Match length
                  130
                  84
% identity
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
NCBI Description
                  >gi_421830_pir__S33707 DRT112 protein - Arabidopsis
                  thaliana >gi_166696 (M98456) DRT112 [Arabidopsis thaliana]
                  149193
Seq. No.
                  LIB3175-022-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  g4455248
NCBI GI
                  278
BLAST score
                  1.0e-24
E value
Match length
```

```
% identity
                  (AL035523) acyl carrier-like protein [Arabidopsis thaliana]
NCBI Description
                  149194
Seq. No.
                  LIB3175-022-P1-K1-D4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2213610
                  271
BLAST score
                  7.0e-24
E value
                  115
Match length
                  49
% identity
                  (AC000103) F21J9.4 [Arabidopsis thaliana]
NCBI Description
                  149195
Seq. No.
                  LIB3175-022-P1-K1-D5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1732411
                  68
BLAST score
                  7.0e-18
E value
                  140
Match length
                  24
% identity
                  (U47924) isopeptidase T [Homo sapiens]
NCBI Description
                  149196
Seq. No.
                  LIB3175-022-P1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2558511
BLAST score
                  291
                  1.0e-163
E value
                  307
Match length
                  99
% identity
                  Arabidopsis thaliana mRNA for proton pump interactor,
NCBI Description
                  partial
Seq. No.
                  149197
                  LIB3175-022-P1-K1-D7
Seq. ID
Method
                  BLASTX
                  g131289
NCBI GI
BLAST score
                  749
                  7.0e-80
E value
Match length
                  141
                  100
% identity
                  PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN)
NCBI Description
                   (CP43) >gi_72709_pir__F2NT44 photosystem II chlorophyll
                  a-binding protein psbC - common tobacco chloroplast
                  >gi_225285_prf__1211235W photosystem II 44kD protein
                   [Nicotiana tabacum]
Seq. No.
                  149198
                  LIB3175-022-P1-K1-D8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1107500
BLAST score
                  379
                  0.0e + 00
E value
Match length
                  383
% identity
NCBI Description A.thaliana mRNA for unknown protein (clone YAP037)
```

```
Seq. No.
                  149199
                  LIB3175-022-P1-K1-D9
Seq. ID
                  BLASTN
Method
                  g2182287
NCBI GI
                  265
BLAST score
                  1.0e-147
E value
                  383
Match length
                  99
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T7N9,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  149200
Seq. No.
                  LIB3175-022-P1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1399273
                  702
BLAST score
                  2.0e-74
E value
                  140
Match length
                  72
% identity
                   (U31834) calmodulin-domain protein kinase CDPK isoform 5
NCBI Description
                   [Arabidopsis thaliana] >gi_3080419_emb_CAA18738.1
                   (AL022604) calmodulin-domain protein kinase CDPK isoform 5
                   (CPK5) [Arabidopsis thaliana]
Seq. No.
                  149201
Seq. ID
                  LIB3175-022-P1-K1-E12
Method
                  BLASTX
                  q3695412
NCBI GI
                   691
BLAST score
                   4.0e-73
E value
Match length
                  139
                   100
% identity
                   (AF096373) contains similarity to group 1 glycosyl
NCBI Description
                   transferases (Pfam: PF00534, E=2.1e-11) [Arabidopsis
                  thaliana]
Seq. No.
                  149202
                  LIB3175-022-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3695023
BLAST score
                   319
E value
                   2.0e-29
Match length
                  113
                   54
% identity
                   (AF055850) unknown [Arabidopsis thaliana]
NCBI Description
                  149203
Seq. No.
                  LIB3175-022-P1-K1-E4
Seq. ID
Method
                  BLASTN
                  g2618720
NCBI GI
                   319
BLAST score
E value
                  1.0e-179
                   340
Match length
                  100
% identity
                  Arabidopsis thaliana early auxin-induced (IAA16) mRNA,
NCBI Description
                  complete cds
```

E value Match length

149204 Seq. No. LIB3175-022-P1-K1-E6 Seq. ID BLASTN \_Method NCBI GI g3319339 BLAST score 54 2.0e-21 E value 154 Match length 96 % identity NCBI Description Arabidopsis thaliana BAC F9D12 149205 Seq. No. LIB3175-022-P1-K1-E7 Seq. ID Method BLASTN NCBI GI q443696 BLAST score 254 1.0e-141 E value 349 Match length 100 % identity Arabidopsis thaliana mRNA for ERD1 protein, complete cds NCBI Description 149206 Seq. No. LIB3175-022-P1-K1-E8 Seq. ID BLASTX Method g2501056 NCBI GI BLAST score 731 E value 8.0e-78Match length 140 100 % identity SERYL-TRNA SYNTHETASE (SERINE--TRNA LIGASE) (SERRS) NCBI Description >gi\_2129737\_pir\_\_S71293 seryl-tRNA synthetase - Arabidopsis thaliana >gi 1359497\_emb\_CAA94388\_ (Z70313) seryl-tRNA Synthetase [Arabidopsis thaliana] Seq. No. 149207 Seq. ID LIB3175-022-P1-K1-E9 Method BLASTX NCBI GI q2119846 693 BLAST score 2.0e-73 E value 130 Match length % identity chlorophyll a/b-binding protein type I precursor Lhb1B2 -NCBI Description Arabidopsis thaliana >gi\_16364\_emb\_CAA45790\_ (X64460) photosystem II type I chlorophyll a /b binding protein  $[Arabidopsis\ thaliana]\ > gi\_3128230\ (AC004077)\ photosystem$ II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi\_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] 149208 Seq. No. Seq. ID LIB3175-022-P1-K1-F1 Method BLASTX NCBI GI g4056456 BLAST score 281

18929

5.0e-25



dehydrogenase family PF\_00107. ESTs gb\_T43674, gb\_H77006 and gb AA395179 come from this gene. [Arabidopsis thaliana]

Seq. No. 149209

Seq. ID LIB3175-022-P1-K1-F10

Method BLASTX
NCBI GI g2342687
BLAST score 544
E value 7.0e-56
Match length 108
% identity 99

NCBI Description (AC000106) Similar to Beta integral membrane protein

(gb U43629). EST gb W43122 comes from this gene.

[Arabidopsis thaliana]

Seq. No. 149210

Seq. ID LIB3175-022-P1-K1-F11

Method BLASTX
NCBI GI g115783
BLAST score 601
E value 1.0e-62
Match length 113
% identity 100

NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR

(CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)

chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis

thaliana]

Seq. No. 149211

Seq. ID LIB3175-022-P1-K1-F12

Method BLASTX
NCBI GI g1737218
BLAST score 365
E value 7.0e-35
Match length 69
% identity 100

NCBI Description (U79959) vacuolar sorting receptor homolog [Arabidopsis

thaliana]

Seq. No. 149212

Seq. ID LIB3175-022-P1-K1-F2

Method BLASTX
NCBI GI g4580393
BLAST score 257
E value 3.0e-22
Match length 99
% identity 55

NCBI Description (AC007171) hypothetical protein [Arabidopsis thaliana]

Seq. No. 149213

Seq. ID LIB3175-022-P1-K1-F3

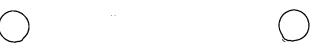
Method BLASTX NCBI GI g140299 BLAST score 349

```
E value
                   5.0e-33
Match length
                   142
                   55
% identity
NCBI Description
                   CYTOCHROME C BIOGENESIS PROTEIN CCSA >gi 82213 pir A05213
                   hypothetical protein 313 - common tobacco chloroplast >gi_1223666_emb_CAA77395_ (Z00044) c-type cytochrome
                   synthesis protein [Nicotiana tabacum]
                   >gi_225254_prf__1211235CN ORF 313 [Nicotiana tabacum]
                   149214
Seq. No.
Seq. ID
                   LIB3175-022-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q4586256
BLAST score
                   596
E value
                   6.0e-62
Match length
                   136
                   87
% identity
NCBI Description
                    (AL049640) probable photosystem I chain XI precursor
                   [Arabidopsis thaliana]
                   149215
Seq. No.
Seq. ID
                   LIB3175-022-P1-K1-F6
Method
                   BLASTX
NCBI GI
                   q1575752
BLAST score
                   504
E value
                   3.0e-51
Match length
                   126
                   75
% identity
NCBI Description
                   (U70672) glutathione S-transferase [Arabidopsis thaliana]
Seq. No.
                   149216
Seq. ID
                   LIB3175-022-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   g1657621
BLAST score
                   720
E value
                   2.0e-76
Match length
                   140
% identity
                   (U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236)
NCBI Description
                   putative acyl-coA dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   149217
                   LIB3175-022-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129932
BLAST score
                   549
E value
                   2.0e-56
Match length
                   99
                   97
% identity
NCBI Description
                   myb-related transcription factor TMH1 - tomato
                   >gi_1167486_emb_CAA64615_ (X95297) transcription factor
                   [Lycopersicon esculentum]
Seq. No.
                   149218
                   LIB3175-022-P1-K1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g556473
```

```
BLAST score
                  1.0e-179
E value
Match length
                  408
% identity
                  99
                  Arabidopsis thaliana mRNA for ERD14 protein, complete cds
NCBI Description
Seq. No.
                  149219
                  LIB3175-022-P1-K1-G1
Seq. ID
                  BLASTX
Method
                  g267069
NCBI GI
                  558
BLAST score
                  2.0e-57
E value
                  103
Match length
                  100
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  149220
Seq. No.
                  LIB3175-022-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4056482
BLAST score
                  569
                  7.0e-59
E value
                  126
Match length
                  54
% identity
NCBI Description
                   (AC005896) putative ABC transporter [Arabidopsis thaliana]
                  149221
Seq. No.
                  LIB3175-022-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2914688
                  319
BLAST score
                  1.0e-179
E value
                  405
Match length
                  67
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  149222
Seq. No.
                  LIB3175-022-P1-K1-G2
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2182287
                  422
BLAST score
                  0.0e + 00
E value
                  422
Match length
                  100
% identity
                  Genomic sequence for Arabidopsis thaliana BAC T7N9,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  149223
Seq. No.
                  LIB3175-022-P1-K1-G4
Seq. ID
Method
                  BLASTX
                  g4033349
NCBI GI
BLAST score
                  384
                  3.0e-37
E value
```

```
Match length
                   89
                   85
% identity
NCBI Description
                   (AJ223496) phosphoenolpyrovate carboxylase [Brassica
                   juncea]
                   149224
Seq. No.
                   LIB3175-022-P1-K1-G6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3451055
                   196
BLAST score
                   1.0e-106
E value
Match length
                   415
                   98
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20
                   (ESSAII project)
                   149225
Seq. No.
Seq. ID
                   LIB3175-022-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   q4218535
BLAST score
                   408
E value
                   6.0e - 40
                   105
Match length
% identity
                   66
NCBI Description
                  (AJ010829) GRAB1 protein [Triticum sp.]
                   149226
Seq. No.
                   LIB3175-022-P1-K1-H10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3449312
BLAST score
                   414
E value
                   0.0e + 00
Match length
                   414
% identity
                   35
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K16L22, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149227
Seq. ID
                   LIB3175-022-P1-K1-H12
Method
                   BLASTN
NCBI GI
                   g3492855
BLAST score
                   47
E value
                   3.0e-17
                   253
Match length
% identity
                   90
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F20N2,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                   149228
Seq. ID
                  LIB3175-022-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2108252
BLAST score
                   668
E value
                   2.0e-70
Match length
                  139
% identity
                  (Y10228) P-glycoprotein-2 [Arabidopsis thaliana]
NCBI Description
```

```
>gi_2108254_emb_CAA71276_ (Y10227) P-glycoprotein-2
                  [Arabidopsis thaliana] >gi_4538925_emb_CAB39661.1
                  (AL049483) P-glycoprotein-2 (pgp2) [Arabidopsis thaliana]
                  149229
Seq. No.
                  LIB3175-022-P1-K1-H5
Seq. ID
                  BLASTX
Method
                  g2369714
NCBI GI
                  462
BLAST score
                  3.0e-46
E value
                  109
Match length
                  85
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                  149230
Seq. No.
                  LIB3175-022-P1-K1-H6
Seq. ID
Method
                  BLASTX
                  q1351272
NCBI GI
                  562
BLAST score
                  5.0e-58
E value
                  130
Match length
                  86
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550
NCBI Description
                  (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                  thaliana] >gi 742408_prf__2009415A triose phosphate
                  isomerase [Arabidopsis thaliana]
                  149231
Seq. No.
Seq. ID
                  LIB3175-022-P1-K1-H7
Method
                  BLASTN
NCBI GI
                  q4455262
BLAST score
                  252
E value
                  1.0e-139
                  421
Match length
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                  (ESSAII project)
                  149232
Seq. No.
Seq. ID
                  LIB3175-022-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  q4510345
BLAST score
                  412
                  2.0e-40
E value
                  77
Match length
                  100
% identity
NCBI Description
                  (AC006921) unknown protein [Arabidopsis thaliana]
                  149233
Seq. No.
Seq. ID
                  LIB3175-024-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  g3510342
BLAST score
                  379
                  0.0e + 00
E value
                  401
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
```



## MGN6, complete sequence [Arabidopsis thaliana]

149234 Seq. No. Seq. ID LIB3175-024-P1-K1-A10 Method BLASTN g4756963 NCBI GI 316 BLAST score 1.0e-178 E value 376 Match length % identity Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 NCBI Description (ESSA project) 149235 Seq. No. LIB3175-024-P1-K1-A11 Seq. ID BLASTN Method NCBI GI g3128143 149 BLAST score 2.0e-78 E value 236 Match length 90 % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MTI20, complete sequence [Arabidopsis thaliana] 149236 Seq. No. LIB3175-024-P1-K1-A3 Seq. ID Method BLASTX NCBI GI g1864017 562 BLAST score 5.0e-58 E value 108 Match length % identity 99 (D63396) elongation factor-1 alpha [Nicotiana tabacum] NCBI Description 149237 Seq. No. LIB3175-024-P1-K1-A4 Seq. ID Method BLASTX NCBI GI g3582335 BLAST score 780 E value 2.0e-83 Match length 146 % identity NCBI Description (AC005496) unknown protein [Arabidopsis thaliana] 149238 Seq. No. LIB3175-024-P1-K1-A6 Seq. ID Method BLASTN NCBI GI g4756963 BLAST score 234 E value 1.0e-129 Match length 361 % identity NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23 (ESSA project) 149239 Seq. No. LIB3175-024-P1-K1-A7 Seq. ID

18935

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```
Method
                   BLASTX
NCBI GI
                   q2245125
BLAST score
                   253
E value
                   1.0e-21
                   57
Match length
                   79
% identity
                  (297343) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149240
                   LIB3175-024-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q113512
BLAST score
                   224
                   2.0e-18
E value
Match length
                   54
% identity
                   72
NCBI Description
                   FLORAL HOMEOTIC PROTEIN AGL2 >gi 81610 pir B39534 floral
                   homeotic protein AGL2 - Arabidopsis thaliana >gi 166591
                   (M55551) transcription factor [Arabidopsis thaliana]
Seq. No.
                   149241
                   LIB3175-024-P1-K1-A9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q544424
BLAST score
                   311
E value
                   9.0e-39
                   83
Match length
% identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi 419755 pir S30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                   149242
Seq. ID
                   LIB3175-024-P1-K1-B1
Method
                   BLASTX
NCBI GI
                   a135467
BLAST score
                   576
E value
                   8.0e-60
Match length
                   114
% identity
                   TUBULIN BETA-4 CHAIN >gi_2129546 pir__S68122 beta-tubulin 4
NCBI Description
                   - Arabidopsis thaliana >gi_1 166640 (M21415) beta-tubulin
                   [Arabidopsis thaliana]
Seq. No.
                   149243
Seq. ID
                   LIB3175-024-P1-K1-B10
Method
                   BLASTX
NCBI GI
                   q282865
BLAST score
                   541
E value
                   1.0e-55
Match length
                   110
% identity
                   68
NCBI Description
                   chlorophyll a/b-binding protein - Arabidopsis thaliana
```

```
>gi_16207_emb_CAA39534_ (X56062) chlorophyll A/B-binding
protein [Arabidopsis thaliana] >gi_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi_4678304_emb_CAB41095.1_ (AL049655) chlorophyll
a/b-binding protein [Arabidopsis thaliana]
```

 Seq. No.
 149244

 Seq. ID
 LIB3175-024-P1-K1-B11

 Method
 BLASTN

 NCBI GI
 g4469002

 BLAST score
 129

 E value
 2.0e-66

 Match length
 318

97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15

(ESSA project)

Seq. No. 149245

% identity

Seq. ID LIB3175-024-P1-K1-B12

Method BLASTX
NCBI GI g2979544
BLAST score 511
E value 5.0e-52
Match length 99
% identity 98

NCBI Description (AC003680) putative cytochrome P-450 [Arabidopsis thaliana]

Seq. No. 149246

Seq. ID LIB3175-024-P1-K1-B2

Method BLASTX
NCBI GI g4512712
BLAST score 345
E value 2.0e-32
Match length 92
% identity 72

NCBI Description (AC006569) unknown protein [Arabidopsis thaliana]

Seq. No. 149247

Seq. ID LIB3175-024-P1-K1-B3

Method BLASTX
NCBI GI g112741
BLAST score 713
E value 1.0e-75
Match length 137
% identity 98

NCBI Description 2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE

PROTEIN) >gi\_68855\_pir\_NWMU3 2S albumin 3 precursor - Arabidopsis thaliana >gi\_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi\_395201\_emb\_CAA80868\_

(Z24744) 2S albumin isoform 3 [Arabidopsis thaliana] >gi 4490712 emb CAB38846.1 (AL035680) NWMU3-2S albumin 3

precursor [Arabidopsis thaliana]

Seq. No. 149248

Seq. ID LIB3175-024-P1-K1-B4

Method BLASTN NCBI GI g2828183

```
BLAST score
                  157
                  7.0e-83
E value
                  459
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPL12, complete sequence [Arabidopsis thaliana]
                  149249
Seq. No.
                  LIB3175-024-P1-K1-B5
Seq. ID
                  BLASTX
Method
                  g1709794
NCBI GI
BLAST score
                  504
E value
                  3.0e-51
                  113
Match length
                  88
% identity
                  26S PROTEASOME REGULATORY SUBUNIT S5A (MULTIUBIQUITIN CHAIN
NCBI Description
                  BINDING PROTEIN) >gi 1165206 (U33269) MBP1 [Arabidopsis
                  thaliana] >gi_4467150_emb_CAB37519_ (AL035540)
                  multiubiquitin chain binding protein (MBP1) [Arabidopsis
                  thaliana]
                  149250
Seq. No.
                  LIB3175-024-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4455290
BLAST score
                  176
E value
                  3.0e-94
                  355
Match length
                  88
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F18A5
NCBI Description
                   (ESSAII project)
                  149251
Seq. No.
                  LIB3175-024-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3522932
BLAST score
                  229
E value
                  1.0e-126
Match length
                  328
% identity
                  Arabidopsis thaliana chromosome II BAC F14M4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  149252
Seq. No.
                  LIB3175-024-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1755162
BLAST score
                  647
E value
                  4.0e-69
Match length
                  145
% identity
                  (U75192) germin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  149253
                  LIB3175-024-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g549056
```

NCBI GI

BLAST score

```
BLAST score
                  321
E value
                  1.0e-29
                  87
Match length
                  74
% identity
                  T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA)
NCBI Description
                  >gi_631651_pir__S43059 CCT (chaperonin containing TCP-1)
                  beta chain - mouse >gi_468546_emb_CAA83428_ (Z31553) CCT
                   (chaperonin containing TCP-1) beta subunit [Mus musculus]
Seq. No.
                  149254
Seq. ID
                  LIB3175-024-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  q2564050
                  285
BLAST score
E value
                   1.0e-159
Match length
                   328
                   96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUA22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149255
                  LIB3175-024-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1724100
BLAST score
                   466
E value
                   1.0e-46
                  133
Match length
% identity
                  (U79765) porin [Mesembryanthemum crystallinum]
NCBI Description
                  149256
Seq. No.
                  LIB3175-024-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4691223
                   216
BLAST score
E value
                   1.0e-118
Match length
                   348
% identity
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F4F15
NCBI Description
                   (ESSA project)
Seq. No.
                   149257
                  LIB3175-024-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4733981
BLAST score
                   325
E value
                   3.0e-30
Match length
                  90
% identity
                   72
                   (AC007268) putative serine carboxypeptidase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   149258
Seq. ID
                  LIB3175-024-P1-K1-C4
Method
                  BLASTX
```

18939

g2829899

```
E value
                  4.0e-33
Match length
                  101
                  64
% identity
NCBI Description
                  (AC002311) similar to ripening-induced protein,
                  gp AJ001449 2465015 and major#latex protein,
                  gp X91961 1107495 [Arabidopsis thaliana]
                  149259
Seq. No.
Seq. ID
                  LIB3175-024-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q112741
BLAST score
                  604
                  5.0e-63
E value
Match length
                  116
                  97
% identity
                  2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                  Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit
                  3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                  >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                  precursor [Arabidopsis thaliana]
                  149260
Seq. No.
Seq. ID
                  LIB3175-024-P1-K1-C6
Method
                  BLASTX
                  g1565225
NCBI GI
BLAST score
                  364
E value
                  7.0e-35
Match length
                  67
                  100
% identity
NCBI Description
                  (X95572) salt-tolerance protein [Arabidopsis thaliana]
                  149261
Seq. No.
Seq. ID
                  LIB3175-024-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  q1335862
BLAST score
                  563
E value
                  5.0e-58
Match length
                  148
% identity
                  75
                  (U42608) clathrin heavy chain [Glycine max]
NCBI Description
                  149262
Seq. No.
                  LIB3175-024-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115767
BLAST score
                  604
E value
                  6.0e-63
                  115
Match length
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir_ A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
```

## protein (LHCP AB 180) [Arabidopsis thaliana] Seq. No. 149263 LIB3175-024-P1-K1-C9 Seq. ID Method BLASTX NCBI GI q4583542 607 BLAST score E value 3.0e-63 Match length 145 % identity 88 (Y16847) 16 kDa polypeptide of oxygen-evolving complex NCBI Description [Arabidopsis thaliana] Seq. No. 149264 Seq. ID LIB3175-024-P1-K1-D1 Method BLASTN NCBI GI g2618605 BLAST score 79 E value 8.0e-37 Match length 166 98 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana] Seq. No. 149265 LIB3175-024-P1-K1-D11 Seq. ID Method BLASTX NCBI GI q3123745 BLAST score 353 E value 1.0e-33 Match length 77 % identity (AB013447) aluminum-induced [Brassica napus] NCBI Description Seq. No. 149266 Seq. ID LIB3175-024-P1-K1-D12 Method BLASTX NCBI GI g1304227 BLAST score 207 E value 6.0e-17 Match length 53 % identity 75 (D63781) Epoxide hydrolase [Glycine max] NCBI Description >gi\_2764804 emb\_CAA55293\_ (X78547) epoxide hydrolase [Glycine max] Seq. No. 149267 Seq. ID LIB3175-024-P1-K1-D5 Method BLASTX NCBI GI g1169862 BLAST score 205 E value 3.0e-16 Match length 37 % identity 100 G-BOX BINDING FACTOR 3 >gi 600863 (U17891) G-box binding NCBI Description factor [Arabidopsis thaliana] >gi\_1262922 (U51850) G-box

factor 3 [Arabidopsis thaliana]

```
Seq. No.
                  149268
Seq. ID
                  LIB3175-024-P1-K1-D7
Method
                  BLASTN
NCBI GI
                   g2924734
BLAST score
                   343
E value
                   0.0e+00
Match length
                   378
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXE10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149269
Seq. ID
                  LIB3175-024-P1-K1-D8
Method
                  BLASTX
NCBI GI
                   q4371297
BLAST score
                   597
E value
                   4.0e-62
Match length
                   117
% identity
                   99
NCBI Description
                   (AC006260) phenylalanine ammonia-lyase 1, 3' partial
                   [Arabidopsis thaliana]
Seq. No.
                  149270
Seq. ID
                  LIB3175-024-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4406816
BLAST score
                   616
E value
                   2.0e-64
Match length
                   116
% identity
                   99
NCBI Description
                   (AC006201) 60S ribosomal protein L2 [Arabidopsis thaliana]
                  149271
Seq. No.
Seq. ID
                  LIB3175-024-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q3851636
BLAST score
                   472
E value
                  2.0e-47
Match length
                  113
% identity
                  79
NCBI Description
                   (AF098519) unknown [Avicennia marina] >qi 4128206
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                  149272
Seq. ID
                  LIB3175-024-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  q3883123
BLAST score
                  392
E value
                  0.0e + 00
Match length
                  411
% identity
                  99
NCBI Description
                  Arabidopsis thaliana arabinogalactan-protein (AGP3) mRNA,
                  complete cds
Seq. No.
                  149273
Seq. ID
                  LIB3175-024-P1-K1-E2
```

```
Method
                  BLASTX
                  g3334123
NCBI GI
BLAST score
                  398
E value
                  9.0e-39
Match length
                  101
                  83
% identity
                  ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_1655480_dbj_BAA13599_ (D88374) gamma subunit of
                  mitochondrial F1-ATPase [Arabidopsis thaliana] >gi_2924787
                  (AC002334) mitochondrial F1-ATPase, gamma subunit
                  [Arabidopsis thaliana]
Seq. No.
                  149274
                  LIB3175-024-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2558511
BLAST score
                  261
E value
                  1.0e-145
Match length
                  296
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for proton pump interactor,
                  partial
                  149275
Seq. No.
                  LIB3175-024-P1-K1-E5
Seq. ID
Method
                  BLASTN
                  q4587641
NCBI GI
BLAST score
                  282
                  1.0e-157
E value
Match length
                  368
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
Seq. No.
                  149276
Seq. ID
                  LIB3175-024-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3169569
BLAST score
                  542
E value
                  1.0e-55
Match length
                  114
% identity
NCBI Description
                  (AF062589) 3-keto-acyl-CoA thiolase 2 [Arabidopsis
                  thaliana] >gi_3220237 (AF062591) peroxisomal
                  3-keto-acyl-CoA thiolase 2 precursor [Arabidopsis thaliana]
Seq. No.
                  149277
Seq. ID
                  LIB3175-024-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  q3047101
BLAST score
                  258
E value
                  2.0e-22
Match length
                  105
% identity
NCBI Description
                  (AF058919) Similar to protein kinase; coded for by A.
                  thaliana cDNA H36947; coded for by A. thaliana cDNA H37158
```

[Arabidopsis thaliana]

```
149278
Seq. No.
                   LIB3175-024-P1-K1-F1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4757388
BLAST score
                   334
                   0.0e+00
E value
                   381
Match length
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   F15L12, complete sequence
                   149279
Seq. No.
Seq. ID
                   LIB3175-024-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q2129577
BLAST score
                   463
                   2.0e-46
E value
                   98
Match length
                   91
% identity
                   DnaJ homolog protein - Arabidopsis thaliana >gi_727357
NCBI Description
                   (U22340) DnaJ homolog [Arabidopsis thaliana]
                   149280
Seq. No.
                   LIB3175-024-P1-K1-F11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2281648
BLAST score
                   266
                   1.0e-148
E value
                   270
Match length
% identity
                   100
                   Arabidopsis thaliana AP2 domain containing protein RAP2.12
NCBI Description
                   mRNA, partial cds
Seq. No.
                   149281
Seq. ID
                   LIB3175-024-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g3281858
BLAST score
                   43
                   6.0e-54
E value
Match length
                   131
% identity
                   (AL031004) ribosomal protein S6 - like [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   149282
Seq. ID
                   LIB3175-024-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g4538963
BLAST score
                   48
E value
                   2.0e-44
Match length
                   105
% identity
                   89
                   (AL049488) chlorophyll a/b-binding protein-like
NCBI Description
                   [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1_AF134129_1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
```

```
149283
Seq. No.
                   LIB3175-024-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4538963
                   464
BLAST score
                   2.0e-46
E value
                   118
Match length
                    77
% identity
NCBI Description
                    (AL049488) chlorophyll a/b-binding protein-like
                    [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                    (AF134129) Lhcb5 protein [Arabidopsis thaliana]
                   149284
Seq. No.
                   LIB3175-024-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   a1703108
BLAST score
                   519
                    5.0e-53
E value
                   95
Match length
% identity
                   100
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
NCBI Description
                   thaliana >gi_1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   149285
Seq. No.
                   LIB3175-024-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1169476
BLAST score
                   613
                   5.0e-64
E value
                   117
Match length
                   100
% identity
                   ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                   ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                   vitronectin-like adhesion protein [Nicotiana tabacum]
                   149286
Seq. No.
                   LIB3175-024-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4038035
BLAST score
                   412
                   2.0e-40
E value
Match length
                   80
% identity
NCBI Description
                    (ACO05936) putative DNA-binding protein [Arabidopsis
                   thaliana]
                   149287
Seq. No.
Seq. ID
                   LIB3175-024-P1-K1-F7
Method
                   BLASTX
NCBI GI
                   q4580920
BLAST score
                   373
E value
                   6.0e-36
Match length
                   105
% identity
                   70
```

```
NCBI Description
                   (AF113545) vacuole-associated annexin VCaB42 [Nicotiana
                   tabacum]
                   149288
Seq. No.
                   LIB3175-024-P1-K1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3831437
BLAST score
                   298
E value
                   1.0e-167
Match length
                   331
                   97
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T3A4 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149289
Seq. ID
                   LIB3175-024-P1-K1-G1
Method
                   BLASTN
NCBI GI
                   g2088638
BLAST score
                   127
E value
                   4.0e-65
Match length
                   377
% identity
                   97
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T28M21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149290
Seq. ID
                   LIB3175-024-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g4510430
BLAST score
                   674
E value
                   4.0e-71
Match length
                   130
% identity
                   98
NCBI Description
                   (AC006929) unknown protein, 3' partial [Arabidopsis
                   thaliana]
Seq. No.
                   149291
Seq. ID
                   LIB3175-024-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   g1172872
BLAST score
                   594
E value
                   1.0e-61
Match length
                   112
% identity
                   100
                   CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718 drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
NCBI Description
                   precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                   (D13042) thiol protease [Arabidopsis thaliana]
                   >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                   cysteine proteinase RD19A precursor [Arabidopsis thaliana]
```

Seq. No. 149292

Seq. ID LIB3175-024-P1-K1-G3

Method BLASTN NCBI GI g4757401 BLAST score 52 E value 3.0e-20

```
Match length
                  68
% identity
                  94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGH6, complete sequence
                  149293
Seq. No.
                  LIB3175-024-P1-K1-G4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3983125
BLAST score
                  483
E value
                  9.0e-49
Match length
                  122
% identity
                  79
NCBI Description
                   (AF097648) phosphate/triose-phosphate translocator
                  precursor [Arabidopsis thaliana]
Seq. No.
                  149294
                  LIB3175-024-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3688182
BLAST score
                  590
E value
                  2.0e-61
Match length
                  115
% identity
                  97
NCBI Description
                  (AL031804) P-Protein - like protein [Arabidopsis thaliana]
Seq. No.
                  149295
                  LIB3175-024-P1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2564045
BLAST score
                  272
E value
                  1.0e-151
Match length
                  309
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K8K14, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149296
                  LIB3175-024-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1351221
BLAST score
                  464
E value
                  1.0e-46
Match length
                  113
% identity
                  81
NCBI Description
                  TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) >gi 945085
                   (U31096) transcription factor TFIIB [Arabidopsis thaliana]
                  >gi 2618697 (AC002510) transcription factor TFIIB
                   [Arabidopsis thaliana]
                  149297
Seq. No.
                  LIB3175-024-P1-K1-G8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g135860
BLAST score
                  557
E value
                  2.0e-57
Match length
                  112
```

```
% identity
                  TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP)
NCBI Description
                  (AQUAPORIN-TIP) >gi 99761 pir S22202 tonoplast intrinsic
                  protein gamma - Arabidopsis thaliana
                  >gi_16312_emb_CAA45115_ (X63552) tonoplast intrinsic
                  protein, gamma-TIP(Ara). [Arabidopsis thaliana] >gi_166732
                  (M84344) tonoplast intrinsic protein [Arabidopsis thaliana]
                  >gi 445129 prf__1908432B tonoplast intrinsic protein gamma
                  [Arabidopsis thaliana]
Seq. No.
                  149298
                  LIB3175-024-P1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2119846
                  530
BLAST score
                  2.0e-54
E value
Match length
                  106
                  95
% identity
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  149299
                  LIB3175-024-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  q4467099
NCBI GI
                  507
BLAST score
                  1.0e-51
E value
Match length
                  105
% identity
                  (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  149300
Seq. ID
                  LIB3175-024-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g3599491
BLAST score
                  258
E value
                  1.0e-22
Match length
                  72
                  67
% identity
                  (AF085149) putative aminotransferase [Capsicum chinense]
NCBI Description
                  149301
Seq. No.
                  LIB3175-024-P1-K1-H12
Seq. ID
Method
                  BLASTN
                  g4678266
NCBI GI
                  300
BLAST score
E value
                  1.0e-168
Match length
                  339
                  97
% identity
```

NCBI Description Arabidopsis thaliana DNA chromosome 3, BAC clone F15B8

(ESSA project)

```
149302
Seq. No.
Seq. ID
                   LIB3175-024-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   g1518540
BLAST score
                   545
                   5.0e-56
E value
Match length
                   114
% identity
NCBI Description
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
                   149303
Seq. No.
                   LIB3175-024-P1-K1-H3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q547390
BLAST score
                   390
E value
                   0.0e + 00
Match length
                   405
                   99
% identity
NCBI Description
                  Arabidopsis thaliana TRAP mRNA, partial cds
Seq. No.
                   149304
Seq. ID
                   LIB3175-024-P1-K1-H4
Method
                   BLASTN
NCBI GI
                   q2760829
BLAST score
                   183
E value
                   2.0e-98
Match length
                   223
                   98
% identity
                   Arabidopsis thaliana chromosome II BAC F18A8 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149305
Seq. ID
                   LIB3175-024-P1-K1-H5
Method
                   BLASTN
NCBI GI
                   q3985957
BLAST score
                   203
E value
                   1.0e-110
Match length
                   319
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149306
Seq. ID
                   LIB3175-024-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q3913651
BLAST score
                   238
E value
                   5.0e-20
Match length
                   120
% identity
                   FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                   (FNR) >gi 2225993 emb CAA74359 (Y14032)
                   ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.
                   149307
Seq. ID
                   LIB3175-024-P1-K1-H9
```

```
Method
                  BLASTN
NCBI GI
                  g2656026
BLAST score
                  270
                  1.0e-150
E value
Match length
                  333
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDF20
                  149308
Seq. No.
                  LIB3175-025-P1-K1-A10
Seq. ID
Method
                  BLASTN
                  q336391
NCBI GI
BLAST score
                  54
E value
                  2.0e-22
Match length
                  66
                  95
% identity
                  A.thaliana chloroplast ribosomal protein S17 (rps17) mRNA,
NCBI Description
Seq. No.
                  149309
                  LIB3175-025-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3858935
BLAST score
                  595
                  9.0e-62
E value
Match length
                  118
                  100
% identity
NCBI Description
                  (AL021636) synaptobrevin-like protein [Arabidopsis
                  thaliana] >qi 4103357 (AF025332) vesicle-associated
                  membrane protein 7C; synaptobrevin 7C [Arabidopsis
                  thaliana]
Seq. No.
                  149310
                  LIB3175-025-P1-K1-A4
Seq. ID
Method ·
                  BLASTX
NCBI GI
                  g2511594
BLAST score
                  352
E value
                  2.0e-33
Match length
                  72
% identity
                  97
                  (Y13694) multicatalytic endopeptidase complex, proteasome
NCBI Description
                  precursor, beta subunit [Arabidopsis thaliana]
                  >gi 2827525 emb CAA16533 (AL021633) multicatalytic
                  endopeptidase complex, proteasome precursor, beta subunit
                  [Arabidopsis thaliana] >gi 3421099 (AF043529) 20S
                  proteasome subunit PBA1 [Arabidopsis thaliana]
                  149311
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g3548806
BLAST score
                  644
                  1.0e-67
E value
Match length
                  137
% identity
                  (AC005313) unknown protein [Arabidopsis thaliana]
NCBI Description
```

```
149312
Seq. No.
                  LIB3175-025-P1-K1-A6
Seq. ID
Method
                   BLASTX
                   q3885342
NCBI GI
                   191
BLAST score
                   9.0e-15
E value
                   92
Match length
                   47
% identity
                   (ACO05623) putative DNA polymerase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  149313
                  LIB3175-025-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                   g119350
BLAST score
                   272
E value
                   2.0e-24
Match length
                   56
                   98
% identity
NCBI Description
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                   thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                   [Arabidopsis thaliana]
                   >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
                   (2-phospho-D-glycerate hydroylase); identical to P25696
                   [Arabidopsis thaliana]
Seq. No.
                  149314
                  LIB3175-025-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4128133
                   199
BLAST score
E value
                   2.0e-15
Match length
                  86
% identity
                   45
NCBI Description
                  (AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens]
Seq. No.
                  149315
                  LIB3175-025-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4741948
BLAST score
                   637
                   9.0e-67
E value
Match length
                  120
% identity
                  100
NCBI Description
                  (AF134124) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  149316
                  LIB3175-025-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1084415
BLAST score
                  327
E value
                  2.0e-30
Match length
                  111
% identity
NCBI Description RNA-binding protein - Wood tobacco >gi_624925_dbj_BAA05170_
```

```
(D26182) RNA-binding glycine rich protein (RGP-2)
                  [Nicotiana sylvestris]
Seq. No.
                  149317
                  LIB3175-025-P1-K1-B10
Seq. ID
Method
                  BLASTX
                  q1107501
NCBI GI
                  408
BLAST score
E value
                  6.0e-40
                  99
Match length
% identity
                  84
NCBI Description
                  (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
                  Match to gb_X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  149318
                  LIB3175-025-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4582468
BLAST score
                  632
                  3.0e-66
E value
Match length
                  134
% identity
                  (AC007071) putative 40S ribosomal protein; contains
NCBI Description
                  C-terminal domain [Arabidopsis thaliana]
Seq. No.
                  149319
                  LIB3175-025-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4545231
BLAST score
                  585
E value
                  1.0e-60
Match length
                  117
% identity
                  95
NCBI Description
                   (AF116243) RAS-related GTP-binding protein [Gossypium
                  hirsutum]
                  149320
Seq. No.
                  LIB3175-025-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4006885
BLAST score
                  116
E value
                  1.0e-58
Match length
                  223
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
                  149321
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q3183088
BLAST score
                  214
E value
                  4.0e-17
Match length
                  68
% identity
                  54
```

```
NCBI Description PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
                   (LTP) >gi_629658_pir__S47084 lipid transfer like protein -
                  cowpea >gi_499034_emb_CAA56113_ (X79604) lipid transfer
                  like protein [Vigna unguiculata]
                  149322
Seq. No.
                  LIB3175-025-P1-K1-B7
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3293583
BLAST score
                  201
                  1.0e-109
E value
Match length
                  433
% identity
                  100
NCBI Description
                  Arabidopsis thaliana BAC T27D20
                  149323
Seq. No.
                  LIB3175-025-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2583125
BLAST score
                   377
                   3.0e-36
E value
                  110
Match length
                   67
% identity
                   (AC002387) putative transketolase precursor [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                  149324
                  LIB3175-025-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4589398
BLAST score
                   394
E value
                   3.0e-38
                   86
Match length
% identity
                   81
                   (D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]
NCBI Description
                  149325
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-C1
Method
                   BLASTX
                   g2146739
NCBI GI
BLAST score
                   302
E value
                   2.0e-27
Match length
                   84
                   75
% identity
                  hexokinase (EC 2.7.1.1) 1 - Arabidopsis thaliana >gi_881521
NCBI Description
                   (U28214) hexokinase 1 [Arabidopsis thaliana]
                  149326
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-C11
Method
                  BLASTX
                   g2586127
NCBI GI
                   276
BLAST score
E value
                   2.0e-24
Match length
                  109
```

NCBI Description (U89510) b-keto acyl reductase [Hordeum vulgare]

50

% identity

```
149327
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g2117612
BLAST score
                  496
                  2.0e-50
E value
                  96
Match length
                  99
% identity
NCBI Description catalase (EC 1.11.1.6) 3 - Arabidopsis thaliana
                  149328
Seq. No.
                  LIB3175-025-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3157944
BLAST score
                  727
                  3.0e-77
E value
                  141
Match length
                  99
% identity
                   (AC002131) Very strong similarity to aminomethyltransferase
NCBI Description
                  precursor gb U79769 from Mesembryanthemum crystallinum.
                  ESTs gb T431\overline{6}7, gb T21076, gb H36999, gb T22773,
                  gb_N38038, gb_T13742, gb_Z26545, gb_T20753 and gb_W43123
                  come from this ge
                  149329
Seq. No.
                  LIB3175-025-P1-K1-C3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3451055
BLAST score
                  218
                  1.0e-119
E value
                  468
Match length
                  97
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F16G20
                  (ESSAII project)
                  149330
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-C4
Method
                  BLASTX
NÇBI GI
                  g3522945
BLAST score
                  518
E value
                  6.0e-53
                  95
Match length
                  100
% identity
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
                  149331
Seq. No.
                  LIB3175-025-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g584865
BLAST score
                  278
E value
                  1.0e-24
                  148
Match length
                  35
% identity
NCBI Description
                  CYTOCHROME P450 76A2 (CYPLXXVIA2) (P-450EG7)
                  >gi_542073_pir__S38534 cytochrome P450 76A2 - eggplant
                  >gi_415911_emb_CAA50648 (X71657) P450 hydroxylase [Solanum
                  melongena]
```

```
149332
Seq. No.
                  LIB3175-025-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3176874
BLAST score
                   177
E value
                   2.0e-13
                   47
Match length
                   74
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
                   149333
Seq. No.
                   LIB3175-025-P1-K1-C7
Seq. ID
Method
                   BLASTX
                   q3600031
NCBI GI
BLAST score
                   766
                   7.0e-82
E value
Match length
                   148
% identity
                   (AF080119) similar to 2,4-dihydroxyhept-2-ene-1,7-dioic
NCBI Description
                   acid aldolases [Arabidopsis thaliana]
                   149334
Seq. No.
Seq. ID
                   LIB3175-025-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   q1755162
BLAST score
                   635
                   1.0e-66
E value
Match length
                   126
% identity
                   (U75192) germin-like protein [Arabidopsis thaliana]
NCBI Description
                   149335
Seq. No.
                   LIB3175-025-P1-K1-C9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4415907
BLAST score
                   520
                   4.0e-53
E value
Match length
                   101
                   99
% identity
NCBI Description
                   (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]
                   >gi 4581159 gb AAD24643.1 AC006919 21 (AC006919) putative
                   60S ribosomal protein L24 [Arabidopsis thaliana]
Seq. No.
                   149336
Seq. ID
                   LIB3175-025-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   q1706772
BLAST score
                   317
                   2.0e-29
E value
Match length
                   63
% identity
NCBI Description
                   FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE
                   SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE)
                   >gi_1076324_pir__S54251 farnesyl-diphosphate
                   farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana
```

>gi\_798820\_emb\_CAA60385\_ (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi\_806325\_dbj\_BAA06103\_ (D29017) squalene synthase [Arabidopsis thaliana] >gi\_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi\_3096933\_emb\_CAA18843.1\_ (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi 4098519 (U79159) squalene synthase [Arabidopsis thaliana]

Seq. No. 149337 Seq. ID LIB3175-025-P1-K1-D12 Method BLASTN NCBI GI g2656029 BLAST score 107 4.0e-53 E value Match length 208

% identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

95

Seq. No. 149338

Seq. ID LIB3175-025-P1-K1-D2

Method BLASTN NCBI GI g4220638 BLAST score 360 0.0e + 00E value Match length 458 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MIF21, complete sequence [Arabidopsis thaliana]

Seq. No. 149339

LIB3175-025-P1-K1-D3 Seq. ID

Method BLASTX NCBI GI q131398 BLAST score 537 E value 4.0e-55 Match length 124 % identity

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR NCBI Description

>gi\_72714\_pir\_\_F2MU10 photosystem II 10K protein precursor - Arabidopsis thaliana >gi\_16447\_emb\_CAA39441\_ (X55970) photosystem II 10 kDa polypeptide [Arabidopsis thaliana] >gi\_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb\_X55970. ESTs gb\_Z17693, gb\_N37616, gb\_T41858, gb\_T88021, gb\_R37531, gb\_T04679, gb\_N37520,

gb\_N64965, gb\_Z17592 and gb\_N65338, gb\_N37466 and gb\_T45400

come from this gene. [Arabidopsis

Seq. No. 149340

Seq. ID LIB3175-025-P1-K1-D4

Method BLASTX NCBI GI q3377815 BLAST score 555 3.0e-57 E value Match length 110 96 % identity

```
(AF076275) similar to protein kinases (Pfam: pkinase.hmm,
NCBI Description
                  score: 255.71) [Arabidopsis thaliana]
                  149341
Seq. No.
                  LIB3175-025-P1-K1-D5
Seq. ID
Method
                  BLASTX
                  q2506443
NCBI GI
                  595
BLAST score
E value
                  6.0e-62
                  117
Match length
% identity
                  100
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi_2117520_pir__JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi_1402885_emb_CAA66816_ (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) [Arabidopsis thaliana]
                  149342
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  g115811
BLAST score
                  449
                  1.0e-60
E value
                  138
Match length
                  82
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I 37
NCBI Description
                  PRECURSOR (CAB-37) (LHCP) >gi_82254_pir__A24717 chlorophyll
                  a/b-binding protein precursor - petunia
                  >gi 20512 emb CAA28639 (X04966) chlorophyll a/b binding
                  protein [Petunia x hybrida]
Seq. No.
                  149343
Seq. ID
                  LIB3175-025-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q1550738
BLAST score
                  357
                  6.0e - 34
E value
Match length
                  104
                  72
% identity
                   (Y08061) endomembrane-associated protein [Arabidopsis
NCBI Description
                  thaliana] >gi 2982443 emb_CAA18251 (AL022224)
                  endomembrane-associated protein [Arabidopsis thaliana]
Seq. No.
                  149344
Seq. ID
                  LIB3175-025-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q2384673
BLAST score
                  334
                  3.0e-31
E value
Match length
                  62
% identity
                  100
NCBI Description
                   (AF012658) putative potassium transporter AtKT3p
                   [Arabidopsis thaliana]
```

```
149345
Seq. No.
                  LIB3175-025-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2262098
BLAST score
                   801
                   6.0e-86
E value
Match length
                   155
% identity
                   100
                   (AC002343) HSP90 isolog [Arabidopsis thaliana]
NCBI Description
                   149346
Seq. No.
                  LIB3175-025-P1-K1-E10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2262135
BLAST score
                   405
                   0.0e + 00
E value
Match length
                   433
                   98
% identity
NCBI Description
                  Arabidopsis thaliana BAC T10P11 from chromosome IV, near 15
                   cM, complete sequence
Seq. No.
                   149347
Seq. ID
                   LIB3175-025-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   q3550519
BLAST score
                   382
E value
                   7.0e-37
Match length
                   114
% identity
                   62
                   (AJ007630) oxygenase [Nicotiana tabacum]
NCBI Description
                   149348
Seq. No.
Seq. ID
                   LIB3175-025-P1-K1-E12
Method
                   BLASTN
NCBI GI
                   q3241920
BLAST score
                   63
E value
                   2.0e-27
Match length
                   140
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MAE1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149349
Seq. ID
                   LIB3175-025-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q3775985
BLAST score
                   579
E value
                   6.0e-60
Match length
                   118
% identity
NCBI Description
                   (AJ010456) RNA helicase [Arabidopsis thaliana]
                   149350
Seq. No.
                  LIB3175-025-P1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3643588
```

```
BLAST score
                   143
E value
                   1.0e-74
Match length
                   436
% identity
                   77
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   149351
Seq. No.
Seq. ID
                   LIB3175-025-P1-K1-E7
Method
                  BLASTN
NCBI GI
                   q4584387
BLAST score
                   432
E value
                   0.0e + 00
Match length
                   440
% identity
                   100
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7
NCBI Description
                   (ESSA project)
                   149352
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-E8
Method
                  BLASTN
NCBI GI
                   q3985931
BLAST score
                   209
E value
                   1.0e-114
Match length
                   229
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K21H1, complete sequence [Arabidopsis thaliana]
                   149353
Seq. No.
Seq. ID
                   LIB3175-025-P1-K1-E9
Method
                   BLASTN
NCBI GI
                   q4519193
BLAST score
                   163
E value
                   1.0e-86
Match length
                   375
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MDC11, complete sequence
Seq. No.
                   149354
Seq. ID
                   LIB3175-025-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g4512687
BLAST score
                   330
E value
                   3.0e-51
Match length
                   125
% identity
NCBI Description
                   (AC006931) floral homeotic protein AGL5 (Arabidopsis
                   thaliana]
                   149355
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-F10
Method
                  BLASTN
NCBI GI
                   g3264777
BLAST score
                   464
E value
                   0.0e+00
```

```
Match length
                   464
% identity
                   100
NCBI Description
                  Arabidopsis thaliana H-protein promoter binding factor-1
                   (HPPBF-1) mRNA, complete cds
                   149356
Seq. No.
                   LIB3175-025-P1-K1-F11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4220643
BLAST score
                   217
E value
                   1.0e-118
Match length
                   403
% identity
                   89
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MWD22, complete sequence [Arabidopsis thaliana]
                   149357
Seq. No.
Seq. ID
                   LIB3175-025-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q4585935
BLAST score
                   733
E value
                   3.0e-80
Match length
                   150
                   97
% identity
NCBI Description
                   (AC007211) putative chlorophyll A/B binding protein
                   [Arabidopsis thaliana] >gi 4741946 gb AAD28770.1 AF134123 1
                   (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                   149358
Seq. ID
                   LIB3175-025-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g395332
BLAST score
                   155
E value
                   3.0e-10
Match length
                   41
% identity
NCBI Description
                   (X69790) cytochrome P-450 [Catharanthus roseus]
Seq. No.
                   149359
Seq. ID
                   LIB3175-025-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   g4455321
BLAST score
                   201
E value
                   1.0e-109
Match length
                   370
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F4I10
                   (ESSAII project)
Seq. No.
                   149360
Seq. ID
                   LIB3175-025-P1-K1-F7
Method
                  BLASTN
NCBI GI
                   g3766106
BLAST score
                   87
E value
                   3.0e-41
Match length
                  237
% identity
                  89
```

Match length

% identity

130

```
NCBI Description Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
                  complete sequence [Arabidopsis thaliana]
                  149361
Seq. No.
                  LIB3175-025-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q3193316
BLAST score
                  583
E value
                  2.0e-60
Match length
                  123
% identity
                  91
NCBI Description
                  (AF069299) contains similarity to nucleotide sugar
                  epimerases [Arabidopsis thaliana]
Seq. No.
                  149362
                  LIB3175-025-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2656031
BLAST score
                  171
E value
                  3.0e-91
                  484
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXC20
Seq. No.
                  149363
Sec. ID
                  LIB3175-025-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q3913651
BLAST score
                  161
E value
                  7.0e-11
Match length
                  104
                  37
% identity
                  FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
NCBI Description
                  (FNR) >gi_2225993_emb_CAA74359_ (Y14032)
                  ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.
                  149364
Seq. ID
                  LIB3175-025-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  q100535
BLAST score
                  295
E value
                  1.0e-26
Match length
                  71
                  83
% identity
                  hypothetical protein - swollen duckweed
NCBI Description
                  >gi 1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna
                  gibba]
                  149365
Seq. No.
Seq. ID
                  LIB3175-025-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  689
E value
                  8.0e-73
```

NCBI GI

BLAST score

q2384671

614

```
NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                    (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                    chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                    thaliana]
                    149366
Seq. No.
                    LIB3175-025-P1-K1-G4
Seq. ID
Method
                    BLASTX
NCBI GI
                    q120675
                                                                                 · 20 ...
BLAST score
                    585
E value
                    1.0e-60
Match length
                    149
                    77
% identity
NCBI Description
                    GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                    >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                    >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                    alba]
Seq. No.
                    149367
                    LIB3175-025-P1-K1-G6
Seq. ID
Method
                    BLASTX
NCBI GI
                    q629541
BLAST score
                    505
E value
                    3.0e-51
Match length
                    119
                    86
% identity
NCBI Description
                    plasma membrane intrinsic protein 1c - Arabidopsis thaliana
                    >gi_472875_emb_CAA53476_ (X75882) plasma membrane intrinsic protein 1c [Arabidopsis thaliana]
Seq. No.
                    149368
Seq. ID
                    LIB3175-025-P1-K1-G7
Method
                    BLASTN
NCBI GI
                    q2264318
BLAST score
                    314
E value
                    1.0e-176
Match length
                    334
% identity
                    99
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                    MUP24, complete sequence [Arabidopsis thaliana]
Seq. No.
                    149369
                    LIB3175-025-P1-K1-G8
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4586263
BLAST score
                    64
E value
                    9.0e-27
                    77
Match length
% identity
                    (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    149370
                    LIB3175-025-P1-K1-G9
Seq. ID
Method
                    BLASTX
```

```
4.0e-64
E value
                  126
Match length
                  93
% identity
                   (AF012657) putative potassium transporter AtKT2p
NCBI Description
                   [Arabidopsis thaliana]
                  149371
Seq. No.
                  LIB3175-025-P1-K1-H1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4581146
BLAST score
                   622
E value
                  5.0e-65
Match length
                  133
% identity
                   (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                  cytoplasmic [Arabidopsis thaliana]
                  149372
Seq. No.
                  LIB3175-025-P1-K1-H10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3449313
                  36
BLAST score
                  1.0e-10
E value
                  85
Match length
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21P3, complete sequence [Arabidopsis thaliana]
                  149373
Seq. No.
                  LIB3175-025-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  574
E value
                  2.0e-59
                  134
Match length
                  81
% identity
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605_pir__S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb_CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  149374
                  LIB3175-025-P1-K1-H12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1514443
BLAST score
                  141
E value
                  3.0e-21
Match length
                  58
% identity
                  (X99061) blue light receptor [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  149375
                  LIB3175-025-P1-K1-H2
Seq. ID
Method
                  BLASTN
                  q2760165
NCBI GI
                  428
BLAST score
```

NCBI GI

BLAST score

g2500430

428

```
E value
                   0.0e + 00
Match length
                   468
% identity
                   100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
                   149376
Seq. No.
                   LIB3175-025-P1-K1-H7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3287695
BLAST score
                   672
                   6.0e-71
E value
Match length
                   127
% identity
                   100
NCBI Description
                   (ACO03979) Similar to hypothetical protein C34B7.2
                   gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis
                   thaliana]
Seq. No.
                   149377
Seq. ID
                   LIB3175-025-P1-K1-H8
                   BLASTX
Method
NCBI GI
                   g3337356
BLAST score
                   160
E value
                   1.0e-34
                  84
Match length
% identity
NCBI Description
                   (AC004481) putative protein transport protein SEC61 alpha
                   subunit [Arabidopsis thaliana]
Seq. No.
                   149378
Seq. ID
                  LIB3175-025-P1-K1-H9
Method
                  BLASTX
NCBI GI
                   g2130028
BLAST score
                   352
E value
                   2.0e-33
Match length
                  86
% identity
                   73
                  B12D protein - barley >gi_471319_emb_CAA54065.1_ (X76604)
NCBI Description
                   HvB12D [Hordeum vulgare] >gi_3445292_emb_CAA70936_ (Y09805)
                  B12Dg1 [Hordeum vulgare]
Seq. No.
                  149379
Seq. ID
                  LIB3175-026-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  q4589434
BLAST score
                  144
E value
                   4.0e-75
Match length
                  457
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNJ7, complete sequence
Seq. No.
                  149380
Seq. ID
                  LIB3175-026-P1-K1-A10
Method
                  BLASTX
```

```
E value
                  2.0e-42
Match length
                  84
                  98
% identity
                  40S RIBOSOMAL PROTEIN S16
NCBI Description
                  149381
Seq. No.
                  LIB3175-026-P1-K1-A11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q1170028
BLAST score
                   457
                   2.0e-53
E value
Match length
                  127
% identity
                  83
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA
NCBI Description
                  1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1)
                  >gi 454357 (U03773)
                   glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis
                   thaliana]
                  149382
Seq. No.
                  LIB3175-026-P1-K1-A12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q464720
BLAST score
                   251
E value
                   1.0e-21
                   50
Match length
% identity
                   100
                  40S RIBOSOMAL PROTEIN S28 >gi 409184 (L09755) ribosomal
NCBI Description
                  protein S28 [Arabidopsis thaliana]
                   149383
Seq. No.
                   LIB3175-026-P1-K1-A3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4263694
                   195
BLAST score
E value
                   1.0e-105
Match length
                   374
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   149384
Seq. No.
                   LIB3175-026-P1-K1-A4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2645971
                   724
BLAST score
E value
                   2.0e-83
Match length
                   161
                   94
% identity
                   (AF034255) reversibly glycosylated polypeptide-3
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   149385
                   LIB3175-026-P1-K1-A5
Seq. ID
Method
                   BLASTX
                   q1755162
NCBI GI
BLAST score
                   823
```

```
E value
                   2.0e-88
Match length
                   159
% identity
NCBI Description
                   (U75192) germin-like protein [Arabidopsis thaliana]
                   149386
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-A7
Method
                  BLASTX
NCBI GI
                   q4586263
BLAST score
                   323
E value
                   3.0e - 34
Match length
                   112
% identity
NCBI Description
                   (AL049640) putative protein [Arabidopsis thaliana]
Seq. No.
                  149387
                  LIB3175-026-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3273743
BLAST score
                   601
                   2.0e-62
E value
Match length
                   118
% identity
                   97
NCBI Description
                   (AF057357) lipid transfer protein 2 precursor [Arabidopsis
                   thaliana] >gi 3786019 (AC005499) unknown protein
                   [Arabidopsis thaliana]
                   149388
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-A9
Method
                  BLASTX
NCBI GI
                   g3024500
BLAST score
                   486
E value
                   4.0e-49
Match length
                   104
                   91
% identity
NCBI Description
                  RAS-RELATED PROTEIN RAB11A >gi 1370142 emb CAA98177
                   (Z73949) RAB11A [Lotus japonicus]
Seq. No.
                   149389
Seq. ID
                   LIB3175-026-P1-K1-B10
Method
                  BLASTN
NCBI GI
                   q3449313
BLAST score
                   324
E value
                   0.0e+00
Match length
                   365
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21P3, complete sequence [Arabidopsis thaliana]
                  149390
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q4335744
BLAST score
                  229
E value
                   1.0e-126
Match length
                   487
% identity
                   99
```

NCBI Description

```
NCBI Description Arabidopsis thaliana chromosome II BAC T4M8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                   149391
Seq. No.
                  LIB3175-026-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4753651
BLAST score
                   639
E value
                   5.0e-67
                  132
Match length
                   92
% identity
                   (ALO49751) ribosomal protein L13a like protein [Arabidopsis
NCBI Description
                   thaliana]
                   149392
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-B2
                  BLASTX
Method
NCBI GI
                   g4468813
BLAST score
                   686
E value
                   2.0e-72
Match length
                  137
                   97
% identity
                  (AL035601) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149393
                  LIB3175-026-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2129594
                   310
BLAST score
                   1.0e-28
E value
Match length
                   93
% identity
                   germin type 2 - Arabidopsis thaliana
NCBI Description
                   >gi_1107491_emb_CAA63023_ (X91957) germin type2
                   [Arabidopsis thaliana]
Seq. No.
                   149394
Seq. ID
                   LIB3175-026-P1-K1-B4
Method
                   BLASTN
NCBI GI
                   q3298610
BLAST score
                   57
E value
                   2.0e-23
Match length
                   141
% identity
                  Arabidopsis thaliana BAC T2H3
NCBI Description
Seq. No.
                   149395
Seq. ID
                  LIB3175-026-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q3402745
BLAST score
                   110
E value
                   5.0e-55
Match length
                   291
% identity
```

(ESSAII project)

Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5

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```
149396
Seq. No.
                  LIB3175-026-P1-K1-B6
Seq. ID
                  BLASTX
Method
                  g99735
NCBI GI
                  692
BLAST score
                  3.0e-73
E value
                  134
Match length
                  97
% identity
                  L-ascorbate peroxidase (EC 1.11.1.11) precursor -
NCBI Description
                  Arabidopsis thaliana (fragment)
                  149397
Seq. No.
                  LIB3175-026-P1-K1-B7
Seq. ID
Method
                  BLASTX
                  g3329294
NCBI GI
                  191
BLAST score
                   2.0e-14
E value
                   142
Match length
                   35
% identity
                   (AE001355) Zinc Metalloprotease (insulinase family)
NCBI Description
                   [Chlamydia trachomatis]
                   149398
Seq. No.
                  LIB3175-026-P1-K1-B8
Seq. ID
                  BLASTX
Method
NCBI GI
                   g2104536
BLAST score
                   648
                   5.0e-68
E value
                   151
Match length
% identity
                   77
                   (AF001308) predicted glycosyl transferase [Arabidopsis
NCBI Description
                   thaliana]
                   149399
Seq. No.
                  LIB3175-026-P1-K1-B9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4583542
BLAST score
                   392
                   6.0e-38
E value
                   100
Match length
                   77
% identity
                   (Y16847) 16 kDa polypeptide of oxygen-evolving complex
NCBI Description
                   [Arabidopsis thaliana]
                   149400
Seq. No.
                   LIB3175-026-P1-K1-C11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4158221
BLAST score
                   586
E value
                   1.0e-60
                   132
Match length
                   80
% identity
                   (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
NCBI Description
Seq. No.
                   149401
                   LIB3175-026-P1-K1-C12
Seq. ID
                   BLASTN
Method
```

```
g3449327
NCBI GI
BLAST score
                   122
                   6.0e-62
E value
Match length
                   453
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCA23, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149402
Seq. ID
                   LIB3175-026-P1-K1-C2
Method
                   BLASTN
NCBI GI
                   q2623294
BLAST score
                   365
E value
                   0.0e + 00
Match length
                   493
% identity
                  Arabidopsis thaliana chromosome II BAC T20B5 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149403
                   LIB3175-026-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2244911
BLAST score
                   596
E value
                   7.0e-62
Match length
                   135
% identity
                   (Z97339) similar to indole-3-acetate
NCBI Description
                  beta-glucosyltransferase [Arabidopsis thaliana]
Seq. No.
                   149404
Seq. ID
                   LIB3175-026-P1-K1-C4
Method
                   BLASTX
NCBI GI
                   q1724100
BLAST score
                   211
E value
                   5.0e-17
Match length
                   71
% identity
                  (U79765) porin [Mesembryanthemum crystallinum]
NCBI Description
Seq. No.
                   149405
Seq. ID
                   LIB3175-026-P1-K1-C5
Method
                   BLASTX
NCBI GI
                   g2341034
BLAST score
                   405
E value
                   9.0e-40
Match length
                   81
% identity
NCBI Description
                   (AC000104) F19P19.13 [Arabidopsis thaliana]
                   149406
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g81615
BLAST score
                  388
E value
                   3.0e-69
Match length
                  160
```

% identity

NCBI Description G-box-binding factor 1 - Arabidopsis thaliana

>gi\_16286\_emb\_CAA45356\_ (X63894) G-box binding factor 1

[Arabidopsis thaliana]

Seq. No. 149407

LIB3175-026-P1-K1-C8 Seq. ID

Method BLASTX NCBI GI g4056467 BLAST score 669 2.0e-70 E value 130 Match length % identity 98

NCBI Description (AC005990) Strong similarity to gb AB006693 spermidine

synthase from Arabidopsis thaliana. ESTs qb AA389822, gb\_T41794, gb\_N38455, gb\_AI100106, gb\_F14442 and gb\_F14256 come from this gene. [Arabidopsis thaliana]

Seq. No. 149408

LIB3175-026-P1-K1-C9 Seq. ID

Method BLASTX NCBI GI g1170373 BLAST score 624 E value 3.0e-65 Match length 123 % identity 97

NCBI Description HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302

> heat shock cognate protein 70-1 - Arabidopsis thaliana >gi 397482 emb CAA52684 (X74604) heat shock protein 70

cognate [Arabidopsis thaliana]

Seq. No. 149409

Seq. ID LIB3175-026-P1-K1-D10

Method BLASTX NCBI GI g3126967 BLAST score 430 E value 1.0e-42 96

Match length % identity

NCBI Description (AF061807) polyubiquitin [Elaeagnus umbellata]

Seq. No. 149410

Seq. ID LIB3175-026-P1-K1-D11

Method BLASTX NCBI GI g99696 BLAST score 691 E value 3.0e-73Match length 124 99 % identity

glutamate--ammonia ligase (EC 6.3.1.2) precursor, NCBI Description

> chloroplast (clone lambdaAtgsl1) - Arabidopsis thaliana >gi 240070 bbs 69728 (S69727) Light-regulated glutamine synthetase isoenzyme [Arabidopsis thaliana, Peptide, 430 aa] [Arabidopsis thaliana] >gi 228453 prf 1804333A Gln

synthetase [Arabidopsis thaliana]

Seq. No. 149411

```
LIB3175-026-P1-K1-D12
Seq. ID
Method
                  BLASTX
                  q464720
NCBI GI
BLAST score
                  248
                  4.0e-21
E value
                  50
Match length
% identity
                  98
                  40S RIBOSOMAL PROTEIN S28 >gi 409184 (L09755) ribosomal
NCBI Description
                  protein S28 [Arabidopsis thaliana]
                  149412
Seq. No.
                  LIB3175-026-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006834
BLAST score
                  752
E value
                  3.0e - 80
Match length
                  148
% identity
NCBI Description
                  (AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis
                  thaliana]
                  149413
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q320558
BLAST score
                  557
E value
                  3.0e-57
Match length
                  141
                  82
% identity
NCBI Description
                  DNA-binding protein - Arabidopsis thaliana >gi_601843
                  (M25268) DNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  149414
Seq. ID
                  LIB3175-026-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q119143
BLAST score
                  318
E value
                  9.0e-30
Match length
                  69
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_81606_pir_S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                  (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi 1369927 emb CAA34454 (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                  >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                  149415
Seq. ID
                  LIB3175-026-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g119350
BLAST score
                  621
E value
                  7.0e-65
```

```
Match length
                    127
% identity
                     96
NCBI Description
                    ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                    (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187 phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                    thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                     [Arabidopsis thaliana]
                    >gi_4581151_gb_AAD24635.1_AC006919 13 (AC006919) enolase
                     (2-phospho-D-glycerate hydroylase); identical to P25696
                     [Arabidopsis thaliana]
Seq. No.
                    149416
                    LIB3175-026-P1-K1-D7
Seq. ID
Method
                    BLASTN
NCBI GI
                    q4376087
BLAST score
                    316
E value
                    1.0e-178
Match length
                     423
                     93
% identity
                    Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                    fragment No
Seq. No.
                    149417
Seq. ID
                    LIB3175-026-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g132794
BLAST score
                     378
E value
                     2.0e-36
Match length
                     99
                     79
% identity
NCBI Description
                    CHLOROPLAST 50S RIBOSOMAL PROTEIN L22 >gi 71288 pir R5NT22
                    ribosomal protein L22 - common tobacco chloroplast >gi_11866_emb_CAA77382 (Z00044) ribosomal protein L22 [Nicotiana tabacum] >gi_225236_prf__1211235BU ribosomal
                    protein L22 [Nicotiana tabacum]
Seq. No.
                    149418
Seq. ID
                    LIB3175-026-P1-K1-D9
Method
                     BLASTX
NCBI GI
                     a2160133
BLAST score
                     408
E value
                     7.0e-40
Match length
                     142
% identity
                     (AC000375) Strong similarity to Arabidopsis
NCBI Description
                     gb X91953, F19K23.3, F19K23.15. ESTs
                     gb T21984, gb ATTS0219, gb ATTS0207, gb T21984 come from this
                     gene. [Arabidopsis thaliana]
Seq. No.
                    149419
Seq. ID
                    LIB3175-026-P1-K1-E10
Method
                    BLASTX
NCBI GI
                     q115783
BLAST score
                     538
E value
                     3.0e-55
Match length
                     110
% identity
                     94
```

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NCBI Description CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-140) (LHCP) >gi_16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thalianal
                  149420
Seq. No.
                  LIB3175-026-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1490552
BLAST score
                  320
                  1.0e-180
E value
Match length
                  354
% identity
                  98
NCBI Description
                  Arabidopsis thaliana S-adenosylmethionine decarboxylase
                  (SAMdc) mRNA, complete cds
                  149421
Seq. No.
                  LIB3175-026-P1-K1-E12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4455253
BLAST score
                  616
E value
                  3.0e-64
Match length
                  146
% identity
NCBI Description
                  (AL035523) superoxide dismutase (EC 1.15.1.1)
                  (Fe)(fragment) [Arabidopsis thaliana]
Seq. No.
                  149422
                  LIB3175-026-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860277
BLAST score
                  46
E value
                  5.0e-58
Match length
                  142
                  77
% identity
NCBI Description
                  (AC005824) putative ribosomal protein L10 [Arabidopsis
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
Seq. No.
                  149423
                  LIB3175-026-P1-K1-E3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3522945
BLAST score
                  543
                  5.0e-75
E value
Match length
                  152
% identity
NCBI Description
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  149424
                  LIB3175-026-P1-K1-E5
Seq. ID
Method
                  BLASTN
NCBI GI
                  a1109698
BLAST score
                  131
E value
                  1.0e-67
Match length
                  231
% identity
                  90
```

```
NCBI Description A.thaliana mRNA for gibberellin 20-oxidase (1425 bp)
                  149425
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  q3450888
                   429
BLAST score
E value
                  0.0e + 00
Match length
                   457
                   99
% identity
NCBI Description
                  Arabidopsis thaliana 19S proteosome subunit 9 mRNA,
                  complete cds
                  149426
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g1351017
BLAST score
                  267
E value
                   2.0e-23
Match length
                  76
% identity
                   67
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (S4) >gi_629697_pir__S45375
                  ribosomal protein S4 - common tobacco (fragment)
                  >gi_443960_emb_CAA78463_ (Z14085) RIBOSOMAL PROTEIN S4
                   [Nicotiana tabacum]
Seq. No.
                  149427
                  LIB3175-026-P1-K1-F10
Seq. ID
Method
                  BLASTN
                  g16557
NCBI GI
BLAST score
                  349
E value
                  0.0e+00
Match length
                   380
                   98
% identity
NCBI Description
                  A.thaliana TOP1 mRNA for topoisomerase I
Seq. No.
                  149428
                  LIB3175-026-P1-K1-F11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4468993
BLAST score
                   621
E value
                   6.0e-65
                  117
Match length
% identity
                  100
                   (AL035605) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  149429
Seq. ID
                  LIB3175-026-P1-K1-F12
Method
                  BLASTX
                  g2500082
NCBI GI
BLAST score
                  765
E value
                  1.0e-81
Match length
                  148
% identity
NCBI Description
                  PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN)
                   (PHOTOSYSTEM II PROTEIN D1) >gi 984735 emb CAA56907
                   (X80932) photosystem II Dl protein [Vigna unguiculata]
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Seq. No.
                   149430
                   LIB3175-026-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1922937
                   479
BLAST score
                   2.0e-48
E value
                   102
Match length
% identity
                   (AC000106) Similar to Glycine SRC2 (gb AB000130). ESTs
NCBI Description
                   gb_H76869,gb_T21700,gb_ATTS5089 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   149431
Seq. ID
                   LIB3175-026-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q2924779
BLAST score
                   727
                   3.0e-77
E value
Match length
                   149
% identity
NCBI Description
                   (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
                   thaliana] >gi_2981616_dbj_BAA25248_ (AB008854)
                   3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                   >gi_2981618_dbj_BAA25249_ (AB008855) 3-ketoacyl-CoA
                   thiolase [Arabidopsis thaliana]
                   149432
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-F4
Method
                   BLASTN
NCBI GI
                   q1550737
BLAST score
                   186
E value
                   1.0e-100
Match length
                   273
                   92
% identity
NCBI Description
                  A.thaliana mRNA for endomembrane-associated protein
                   149433
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-F6
Method
                  BLASTX
NCBI GI
                   g421929
BLAST score
                   501
E value
                   1.0e-57
Match length
                   139
% identity
                   13
NCBI Description
                  ubiquitin - tomato >gi 312160 emb CAA51679 (X73156)
                  ubiquitin [Lycopersicon esculentum]
Seq. No.
                   149434
                  LIB3175-026-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741944
BLAST score
                   661
E value
                   1.0e-69
Match length
                  123
% identity
NCBI Description
                   (AF134122) Lhcb2 protein [Arabidopsis thaliana]
```

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149435
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q2565275
BLAST score
                  675
                  4.0e-71
E value
                  142
Match length
                  85
% identity
                  (AF023611) Dim1p homolog [Homo sapiens]
NCBI Description
                  149436
Seq. No.
                  LIB3175-026-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4580745
BLAST score
                  291
E value
                  1.0e-163
Match length
                  337
                  96
% identity
                  Arabidopsis thaliana chromosome 1 BAC F1003 sequence,
NCBI Description
                  complete sequence
                  149437
Seq. No.
                  LIB3175-026-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1550737
                  54
BLAST score
E value
                  1.0e-21
Match length
                  194
                  82
% identity
NCBI Description A.thaliana mRNA for endomembrane-associated protein
                  149438
Seq. No.
                  LIB3175-026-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1550738
BLAST score
                  321
E value
                  8.0e-30
                  79
Match length
% identity
                  82
NCBI Description
                   (Y08061) endomembrane-associated protein [Arabidopsis
                  thaliana] >gi_2982443_emb_CAA18251_ (AL022224)
                  endomembrane-associated protein [Arabidopsis thaliana]
                  149439
Seq. No.
                  LIB3175-026-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3510256
BLAST score
                  177
E value
                  9.0e-13
                  63
Match length
% identity
                  49
                  (AC005310) unknown protein [Arabidopsis thaliana]
NCBI Description
                  149440
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-H1
Method
                  BLASTX
```

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g3150402
NCBI GI
BLAST score
                   199
                   2.0e-27
E value
Match length
                  98
% identity
                   71
                   (AC004165) putative malonyl-CoA: Acyl carrier protein
NCBI Description
                  transacylase [Arabidopsis thaliana]
                   149441
Seq. No.
                  LIB3175-026-P1-K1-H10
Seq. ID
Method
                  BLASTX
                   g4584548
NCBI GI
                   575
BLAST score
                   1.0e-59
E value
Match length
                  116
% identity
NCBI Description
                  (AL049608) putative protein [Arabidopsis thaliana]
                  149442
Seq. No.
                  LIB3175-026-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4371282
BLAST score
                   224
E value
                   4.0e-63
                   141
Match length
% identity
                   (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                   thaliana]
                   149443
Seq. No.
Seq. ID
                   LIB3175-026-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g2494130
BLAST score
                   448
                   3.0e-52
E value
Match length
                   110
% identity
                   96
                   (AC002376) Contains similarity to Glycine SRC2
NCBI Description
                   (gb AB000130). [Arabidopsis thaliana]
                   149444
Seq. No.
Seq. ID
                   LIB3175-026-P1-K1-H3
Method
                   BLASTX
NCBI GI
                   q4544399
BLAST score
                   331
                   8.0e-31
E value
Match length
                   131
% identity
NCBI Description
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
                   thalianal
                   149445
Seq. No.
Seq. ID
                  LIB3175-026-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g4185505
BLAST score
                  268
E value
                   9.0e-24
```

80 Match length % identity 68 (AF101038) nonspecific lipid-transfer protein precursor NCBI Description [Brassica napus] 149446 Seq. No. LIB3175-026-P1-K1-H8 Seq. ID BLASTX Method q2494113 NCBI GI BLAST score 714 9.0e-76E value 128 Match length 100 % identity (AC002376) Strong similarity to Musa pectate lyase NCBI Description (gb X92943). ESTs gb AA042458, gb ATTS4502, gb N38552 come from this gene. [Arabidopsis thaliana] 149447 Seq. No. LIB3175-026-P1-K1-H9 Seq. ID BLASTN Method g4519192 NCBI GI 26 BLAST score 7.0e-05 E value 273 Match length 86 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MBK21, complete sequence 149448 Seq. No. LIB3175-027-P1-K1-A10 Seq. ID Method BLASTN NCBI GI g2828183 BLAST score 258 1.0e-143 E value 437 Match length % identity Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description MPL12, complete sequence [Arabidopsis thaliana] 149449 Seq. No. LIB3175-027-P1-K1-A11 Seq. ID BLASTX Method NCBI GI q131372 BLAST score 161 3.0e-11 E value 34 Match length 100 % identity PHOTOSYSTEM II REACTION CENTRE M PROTEIN NCBI Description >gi\_72719\_pir\_\_F2RZM photosystem II protein psbM - rice chloroplast >gi\_11969\_emb\_CAA33984\_ (X15901) PSII low MW protein [Oryza sativa] >gi\_2924261\_emb\_CAA77413\_ (Z00044) PSII M-protein [Nicotiana tabacum] >gi\_226687\_prf\_\_1603356M photosystem II low MW protein [Oryza sativa]

Seq. No. 149450

Seq. ID LIB3175-027-P1-K1-A2

Method BLASTX

18978

13,10

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NCBI GI
                   g2226202
BLAST score
                   146
                   4.0e-09
E value
Match length
                   90
% identity
                   41
                   (Y14082) hypothetical protein [Bacillus subtilis]
NCBI Description
                   >gi 2633281 emb CAB12785 (Z99109) similar to amino acid
                   transporter [Bacillus subtilis]
Seq. No.
                   149451
Seq. ID
                   LIB3175-027-P1-K1-A4
                   BLASTX
Method
NCBI GI
                   g3914666
BLAST score
                   319
                   1.0e-29
E value
Match length
                   100
                   73
% identity
                   CHLOROPLAST 50S RIBOSOMAL PROTEIN L4 PRECURSOR
NCBI Description
                   >gi_2791998_emb_CAA74895_ (Y14566) ribosomal protein L4
[Arabidopsis thaliana] >gi_2792000_emb_CAA74894_ (Y14565)
                   ribosomal protein L4 [Arabidopsis thaliana]
                   149452
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-A5
Method
                   BLASTN
NCBI GI
                   g3985933
BLAST score
                   204
                   1.0e-111
E value
Match length
                   208
                   100
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K9E15, complete sequence [Arabidopsis thaliana]
                   149453
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-A6
Method
                   BLASTX
NCBI GI
                   q4335761
BLAST score
                   402
E value
                   3.0e-39
Match length
                   77
% identity
NCBI Description
                   (AC006284) unknown protein [Arabidopsis thaliana]
                   149454
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g2129538
BLAST score
                   715
E value
                   7.0e-76
Match length
                   143
                   97
% identity
NCBI Description
                   AT103 protein - Arabidopsis thaliana >gi_1033195 (U38232)
                   AT103 [Arabidopsis thaliana]
Seq. No.
                   149455
                   LIB3175-027-P1-K1-B10
Seq. ID
Method
                   BLASTN
```

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g529643
NCBI GI
BLAST score
                   34
E value
                   3.0e-10
Match length
                   62
% identity
                   89
NCBI Description
                  Pinus thunbergii chloroplast DNA, complete sequence
                   149456
Seq. No.
                   LIB3175-027-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4325282
BLAST score
                   406
                   7.0e-40
E value
                   99
Match length
                   79
% identity
NCBI Description
                   (AF123310) NAC domain protein NAM [Arabidopsis thaliana]
                   >gi_4325286_gb_AAD17314_ (AF123311) NAC domain protein NAM
                   [Arabidopsis thaliana]
                   149457
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-B3
Method
                   BLASTX
                   g1575130
NCBI GI
BLAST score
                   69
E value
                   5.0e-09
                   55
Match length
% identity
                   57
                   (U58209) lumenal binding protein cBiPe3 [Zea mays]
NCBI Description
                   149458
Seq. No.
                  LIB3175-027-P1-K1-B4
Seq. ID
Method
                   BLASTX
                   g4539327
NCBI GI
BLAST score
                   95
E value
                   7.0e-16
Match length
                   70
% identity
                   66
NCBI Description
                   (AL035679) putative proton pump [Arabidopsis thaliana]
                   149459
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-B5
Method
                   BLASTN
NCBI GI
                   g2160155
BLAST score
                   223
E value
                   1.0e-122
Match length
                   423
                   99
% identity
NCBI Description
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
                  149460
Seq. No.
                  LIB3175-027-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3337356
BLAST score
                   226
E value
                   3.0e-19
Match length
                  45
```

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% identity
                   (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                   subunit [Arabidopsis thaliana]
                   149461
Seq. No.
                   LIB3175-027-P1-K1-B7
Seq. ID
Method
                   BLASTX
                   g1703108
NCBI GI
                   442
BLAST score
                   7.0e-44
E value
Match length
                   104
                   85
% identity
                   ACTIN 2/7 >gi_2129525_pir__S71210 actin 2 - Arabidopsis thaliana >gi_2129528_pir__S68107 actin 7 - Arabidopsis
NCBI Description
                   thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
                   thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                   thaliana]
                   149462
Seq. No.
                   LIB3175-027-P1-K1-B9
Seq. ID
                   BLASTX
Method
                   g4469023
NCBI GI
BLAST score
                   436
                   4.0e-43
E value
                   133
Match length
% identity
                   66
                   (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149463
                   LIB3175-027-P1-K1-C1
Seq. ID
Method
                   BLASTN
                   q2264319
NCBI GI
                   45
BLAST score
                   4.0e-16
E value
                   97
Match length
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXA21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149464
                   LIB3175-027-P1-K1-C11
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4519192
BLAST score
                   143
                   5.0e-75
E value
Match length
                   151
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MBK21, complete sequence
                   149465
Seq. No.
                   LIB3175-027-P1-K1-C12
Seq. ID
                   BLASTN
Method
NCBI GI
                   g3449315
                   62
BLAST score
                   1.0e-26
E value
                   110
Match length
```

12. STA 3-13.

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89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K23L20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149466
                  LIB3175-027-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3242075
BLAST score
                   669
E value
                   2.0e-70
Match length,
                  139
% identity
                   93
                   (Z97059) S-adenosyl-L-homocysteine hydrolase [Arabidopsis
NCBI Description
                   thaliana]
                  149467
Seq. No.
                  LIB3175-027-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3046847
BLAST score
                   101
E value
                   2.0e-49
Match length
                   353
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
NCBI Description
                  K11J9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149468
                   LIB3175-027-P1-K1-C5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2262167
BLAST score
                   660
E value
                   2.0e-69
Match length
                   127
% identity
                   (AC002329) cytosolic ribosomal protein S4 [Arabidopsis
NCBI Description
                   thaliana]
                   149469
Seq. No.
                   LIB3175-027-P1-K1-C7
Séq. ID
Method
                  BLASTX
NCBI GI
                   q4586265
BLAST score
                   523
E value
                   2.0e-53
                   137
Match length
% identity
                   75
                   (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149470
Seq. ID
                   LIB3175-027-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g2623962
BLAST score
                   430
E value
                   2.0e-42
Match length
                   90
                   92
% identity
NCBI Description
                   (Y12540) isocitrate dehydrogenase (NADP+) [Apium
                   graveolens]
```

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149471
Seq. No.
                  LIB3175-027-P1-K1-D1
Seq. ID
Method
                  BLASTX
                  q1709002
NCBI GI
                  141
BLAST score
                   5.0e-21
E value
                   72
Match length
                   74
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE) >gi 1033190
                   (U38186) S-adenosyl methionine synthetase [Pinus banksiana]
                   149472
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-D11
                  BLASTX
Method
NCBI GI
                   q115783
                   721
BLAST score
                   1.0e-76
E value
Match length
                   140
                   99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   149473
Seq. No.
                  LIB3175-027-P1-K1-D2
Seq. ID
Method
                  BLASTN
                   q3510337
NCBI GI
BLAST score
                   301
                   1.0e-169
E value
                   454
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19E20, complete sequence [Arabidopsis thaliana]
                   149474
Seq. No.
                   LIB3175-027-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1076316
BLAST score
                   545
                   5.0e - 56
E value
Match length
                   106
                   98
% identity
                  drought-induced protein Di19 - Arabidopsis thaliana
NCBI Description
                   >gi 469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis
                   thaliana]
                   149475
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q3738335
BLAST score
                   333
                   4.0e-31
E value
Match length
                   152
                   52
% identity
```

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NCBI Description (AC005170) unknown protein [Arabidopsis thaliana]
                  149476
Seq. No.
Seq. ID
                  LIB3175-027-P1-K1-D6
Method
                  BLASTN
NCBI GI
                  g4757392
BLAST score
                  223
                  1.0e-122
E value
Match length
                  255
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
                  K14A17, complete sequence
                  149477
Seq. No.
Seq. ID
                  LIB3175-027-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2052383
BLAST score
                  654
E value
                  3.0e-69
Match length
                  140
                  93
% identity
NCBI Description
                  (U66345) calreticulin [Arabidopsis thaliana]
Seq. No.
                  149478
Seq. ID
                  LIB3175-027-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q112739
BLAST score
                  408
E value
                  6.0e-40
Match length
                  119
% identity
                  70
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  149479
Seq. ID
                  LIB3175-027-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g1911774
BLAST score
                  173
E value
                  2.0e-12
Match length
                  71
% identity
                  39
NCBI Description
                  (S83364) putative Rab5-interacting protein {clone L1-57}
                  [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]
Seq. No.
                  149480
Seq. ID
                  LIB3175-027-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  763
E value
                  1.0e-81
Match length
                  140
```

```
% identity
NCBI Description
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
                  149481
Seq. No.
                  LIB3175-027-P1-K1-E11
Seq. ID
                  BLASTX
Method
                  g3063465
NCBI GI
BLAST score
                  473
                  1.0e-47
E value
                  95
Match length
                  99
% identity
NCBI Description
                  (AC003981) F22013.27 [Arabidopsis thaliana]
                  149482
Seq. No.
                  LIB3175-027-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3319457
BLAST score
                  163
                  3.0e-11
E value
                  98
Match length
                  39
% identity
                   (AF077542) contains similarity to O-linked GlcNAc
NCBI Description
                  transferases [Caenorhabditis elegans]
Seq. No.
                  149483
Seq. ID
                  LIB3175-027-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g3355463
BLAST score
                  200
E value
                  1.0e-108
Match length
                  284
% identity
                  Arabidopsis thaliana chromosome II BAC F12L6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  149484
Seq. No.
Seq. ID
                  LIB3175-027-P1-K1-E4
Method
                  BLASTN
                  g3242700
NCBI GI
                  39
BLAST score
E value
                  1.0e-12
Match length
                  153
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC F26B6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149485
Seq. ID
                  LIB3175-027-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4406814
BLAST score
                  493
                  8.0e-50
E value
Match length
                  98
% identity
                  100
                   (AC006201) putative peptidyl-prolyl isomerase [Arabidopsis
NCBI Description
                  thaliana]
```

```
Seq. No.
                   149486
Seq. ID
                   LIB3175-027-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   g2829275
BLAST score
                   323
E value
                   4.0e-30
Match length
                   60
                   100
% identity
NCBI Description
                   (AF044265) nucleoside diphosphate kinase 3 [Arabidopsis
                   thaliana] >gi_3513740 (AF080118) contains similarity to
                   nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana] >gi_4539375_emb_CAB40069.1_
                    (AL049525) nucleoside diphosphate kinase 3 (ndpk3)
                    [Arabidopsis thaliana]
                   149487
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q1705677
BLAST score
                   674
E value
                   4.0e-76
Match length
                   148
% identity
                   66
NCBI Description
                   CELL DIVISION CYCLE PROTEIN 48 HOMOLOG
                   >gi_2118115_pir__S60112 cell division control protein CDC48
                   homolog - Arabidopsis thaliana >gi_1019904 (U37587) cell
                   division cycle protein [Arabidopsis thaliana]
Seq. No.
                   149488
Seq. ID
                   LIB3175-027-P1-K1-E9
Method
                   BLASTN
NCBI GI
                   g3668174
BLAST score
                   42
E value
                   2.0e-14
Match length
                   50
% identity
NCBI Description
                   Arabidopsis thaliana Vsp2 gene for vegetative storage
                   protein, complete cds
Seq. No.
                   149489
Seq. ID
                   LIB3175-027-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g1657855
BLAST score
                   174
E value
                   1.0e-12
Match length
                   77
% identity
NCBI Description
                   (U73216) cold acclimation protein WCOR413 [Triticum
                   aestivum]
Seq. No.
                   149490
Seq. ID
                   LIB3175-027-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q899608
BLAST score
                   641
                   3.0e-67
E value
Match length
                   130
```

```
% identity
                  (U29158) polyubiquitin [Zea mays]
NCBI Description
                  149491
Seq. No.
                  LIB3175-027-P1-K1-F11
Seq. ID
                  BLASTN
Method
                  g3643588
NCBI GI
                  283
BLAST score
                  1.0e-158
E value
Match length
                  450
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149492
                  LIB3175-027-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1644388
BLAST score
                  328
                  2.0e-30
E value
                  145
Match length
% identity
                  41
                  (U72654) flavonoid 3'5'-hydroxylase [Eustoma grandiflorum]
NCBI Description
                  149493
Seq. No.
                  LIB3175-027-P1-K1-F3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3985949
BLAST score
                  105
                  2.0e-52
E value
                  141
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOB24, complete sequence [Arabidopsis thaliana]
                  149494
Seq. No.
Seq. ID
                  LIB3175-027-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g3786017
BLAST score
                  507
                  2.0e-51
E value
                  104
Match length
% identity
                  95
                   (ACO05499) putative non-green plastid inner envelope
NCBI Description
                  membrane protein [Arabidopsis thaliana]
                  149495
Seq. No.
Seq. ID
                  LIB3175-027-P1-K1-F6
Method
                  BLASTN
NCBI GI
                  q2623294
BLAST score
                  66
E value
                  1.0e-28
                  157
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T20B5 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                   149496
Seq. ID
                   LIB3175-027-P1-K1-F7
Method
                   BLASTN
NCBI GI
                   g4757395
BLAST score
                   185
                   1.0e-99
E value
Match length
                   424
                   99
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K21L13, complete sequence
                   149497
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g135406
BLAST score
                   626
                   2.0e-65
E value
Match length
                   118
                   99
% identity
NCBI Description
                   TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
                   alpha-5 chain - Arabidopsis thaliana >g\overline{i}_16\overline{69}12 (M17189)
                   alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                   alpha-5 tubulin [Arabidopsis thaliana]
                   149498
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-G10
Method
                   BLASTN
NCBI GI
                   q2828185
BLAST score
                   324
                   0.0e+00
E value
Match length
                   324
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUD21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149499
Seq. ID
                   LIB3175-027-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   q4158221
BLAST score
                   133
E value
                   4.0e-61
Match length
                   139
% identity
NCBI Description
                   (Y18624) reversibly glycosylated polypeptide [Oryza sativa]
                   149500
Seq. No.
Seq. ID
                   LIB3175-027-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   q131398
BLAST score
                   471
E value
                   2.0e-47
Match length
                   113
% identity
                   84
NCBI Description
                   PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR
                   >gi_72714_pir__F2MU10 photosystem II 10K protein precursor
                   - Arabidopsis thaliana >gi_16447_emb_CAA39441_ (X55970)
                   photosystem II 10 kDa polypeptide [Arabidopsis thaliana]
```

```
>gi_3152571 (AC002986) Match to photosystem II 10kDa polypeptide gb_X55970. ESTs gb_Z17693, gb_N37616, gb_T41858, gb_T88021, gb_R37531, gb_T04679, gb_N37520, gb_N64965, gb_Z17592 and gb_N65338, gb_N37466 and gb_T45400 come from this gene. [Arabidopsis

149501
LIB3175-027-P1-K1-G4
BLASTN
g4469002
304
1.0e-170
```

% identity 100
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
(ESSA project)

 Seq. No.
 149502

 Seq. ID
 LIB3175-027-P1-K1-G5

 Method
 BLASTX

 NCBI GI
 g4589398

 BLAST score
 438

457

BLAST score 438
E value 2.0e-43
Match length 105
% identity 74

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score

Match length

NCBI Description (D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]

Seq. No. 149503

Seq. ID LIB3175-027-P1-K1-G6

Method BLASTX
NCBI GI g3024697
BLAST score 569
E value 9.0e-59
Match length 115
% identity 100

NCBI Description T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)

(CCT-EPSILON) >gi\_2213618 (AC000103) F21J9.12 [Arabidopsis

thaliana]

Seq. No. 149504

Seq. ID LIB3175-027-P1-K1-G7

Method BLASTX
NCBI GI g3983125
BLAST score 624
E value 3.0e-65
Match length 145
% identity 83

NCBI Description (AF097648) phosphate/triose-phosphate translocator

precursor [Arabidopsis thaliana]

Seq. No. 149505

Seq. ID LIB3175-027-P1-K1-G8

Method BLASTN
NCBI GI g2584827
BLAST score 180
E value 1.0e-96
Match length 329

```
% identity
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   149506
Seq. No.
                   LIB3175-027-P1-K1-G9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2811226
BLAST score
                   460
                   5.0e-46
E value
Match length
                   91
% identity
                   99
                   (AF042669) fimbrin 2 [Arabidopsis thaliana] >gi 2811232
NCBI Description
                   (AF042671) fimbrin 2 [Arabidopsis thaliana]
Seq. No.
                   149507
                  LIB3175-027-P1-K1-H10
Seq. ID
Method
                   BLASTX
                   g2645971
NCBI GI
BLAST score
                   470
E value
                   3.0e-47
Match length
                   100
                   84
% identity
NCBI Description
                   (AF034255) reversibly glycosylated polypeptide-3
                   [Arabidopsis thaliana]
Seq. No.
                   149508
                   LIB3175-027-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4586265
BLAST score
                   254
E value
                   2.0e-49
Match length
                   130
                   76
% identity
NCBI Description
                   (AL049640) putative protein [Arabidopsis thaliana]
Seq. No.
                   149509
                  LIB3175-027-P1-K1-H3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4220636
BLAST score
                   35
E value
                   2.0e-10
Match length
                   123
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:
NCBI Description
                  MFB16, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149510
Seq. ID
                  LIB3175-027-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g1172872
BLAST score
                   594
E value
                   1.0e-61
Match length
                   114
                   98
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >qi 541856 pir JN0718
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
```

```
(D13042) thiol protease [Arabidopsis thaliana]
                  >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                  149511
                  LIB3175-027-P1-K1-H5
Seq. ID
                  BLASTX
Method
                  g4335719
NCBI GI
BLAST score
                  638
                  5.0e-67
E value
                  118
Match length
                  100
% identity
                  (AC006248) putative RING-H2 finger protein RHG1a
NCBI Description
                  [Arabidopsis thaliana]
                  149512
Seq. No.
                  LIB3175-027-P1-K1-H7
Seq. ID
                  BLASTX
Method
                  q4741952
NCBI GI
                  700
BLAST score
                  4.0e-74
E value
                  130
Match length
                  76
% identity
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
NCBI Description
                  149513
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q421929
BLAST score
                  413
                  1.0e-40
E value
Match length
                  86
% identity
                  14
                  ubiquitin - tomato >gi_312160_emb CAA51679 (X73156)
NCBI Description
                  ubiquitin [Lycopersicon esculentum]
                  149514
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-A10
Method
                  BLASTX
                  g1531762
NCBI GI
BLAST score
                  195
                  6.0e-15
E value
                  51
Match length
                  75
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  149515
Seq. No.
                  LIB3175-028-P1-K1-A11
Seq. ID
Method
                  BLASTX
                  g417103
NCBI GI
BLAST score
                  226
                  7.0e-19
E value
```

precursor - Arabidopsis thaliana >gi\_435618\_dbj BAA02373

18991

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

68

69

Match length

% identity

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429)
histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563
(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460)
histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone
H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2
[Medicago sativa] >gi\_488577 (U09465) histone H3.2
[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone
H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)
histone H3 variant H3.3 [Lycopersicon esculentum]
>gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana
tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa]
>gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia
coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone
H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_
(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 149516 Seq. ID LIB3175-028-P1-K1-A2 Method BLASTX NCBI GI g3786005 504 BLAST score E value 3.0e-51 106 Match length % identity 93 (AC005499) putative phosphoethanolamine NCBI Description cytidylyltransferase [Arabidopsis thaliana]

 Seq. No.
 149517

 Seq. ID
 LIB3175-028-P1-K1-A3

 Method
 BLASTX

 NCBI GI
 g1209756

 BLAST score
 449

 E value
 8.0e-45

Match length 126 % identity 71

NCBI Description (U43629) integral membrane protein [Beta vulgaris]

Seq. No. 149518

Seq. ID LIB3175-028-P1-K1-A8

Method BLASTN
NCBI GI g3868723
BLAST score 271
E value 1.0e-151
Match length 330
% identity 96

NCBI Description Arabidopsis thaliana chromosome V map 60.5 cM, complete

sequence [Arabidopsis thaliana]

Seq. No. 149519

Seq. ID LIB3175-028-P1-K1-A9

Method BLASTX
NCBI GI g4741952
BLAST score 514
E value 2.0e-52

```
Match length
                  95
                   70
% identity
NCBI Description
                   (AF134126) Lhcb3 protein [Arabidopsis thaliana]
                  149520
Seq. No.
                  LIB3175-028-P1-K1-B1
Seq. ID
                  BLASTX
Method
                  q2435522
NCBI GI
BLAST score
                  503
                   4.0e-51
E value
Match length
                  126
% identity
                   (AF024504) contains similarity to other AMP-binding enzymes
NCBI Description
                   [Arabidopsis thaliana]
                  149521
Seq. No.
                  LIB3175-028-P1-K1-B10
Seq. ID
Method
                  BLASTN
                  q4309719
NCBI GI
BLAST score
                  202
                   1.0e-110
E value
                  266
Match length
                   94
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T30D6 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  149522
Seq. No.
                  LIB3175-028-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3915826
BLAST score
                  502
E value
                  5.0e-51
Match length
                  119
% identity
                  80
NCBI Description
                  60S RIBOSOMAL PROTEIN L5
Seq. No.
                  149523
                  LIB3175-028-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q231586
BLAST score
                  223
                  3.0e-18
E value
Match length
                  100
% identity
                  54
                  ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR
NCBI Description
                  >gi_82027_pir__S20504 H+-transporting ATP synthase (EC
                  3.6.1.34) beta chain, mitochondrial - Para rubber tree
                  >gi_18831_emb_CAA41401_ (X58498) mitochondrial ATP synthase
                  beta-subunit [Hevea brasiliensis]
Seq. No.
                  149524
Seq. ID
                  LIB3175-028-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q464621
BLAST score
                  217
E value
                  9.0e-18
Match length
```

```
% identity
                  60S RIBOSOMAL PROTEIN L6 (YL16-LIKE) >gi 280374 pir S28586
NCBI Description
                  ribosomal protein ML16 - common ice plant
                  >gi 19539 emb CAA49175 (X69378) ribosomal protein YL16
                   [Mesembryanthemum crystallinum]
                  149525
Seq. No.
                  LIB3175-028-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1363489
BLAST score
                  841
E value
                  1.0e-90
Match length
                  154
% identity
                  99
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
NCBI Description
                  thaliana >gi 984052 emb_CAA61592_ (X89413) thioglucoside
                  glucohydrolase [Arabidopsis thaliana]
                  149526
Seq. No.
                  LIB3175-028-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2132124
BLAST score
                  279
                  8.0e-25
E value
Match length
                  102
% identity
NCBI Description
                  hypothetical protein YOR304w - yeast (Saccharomyces
                  cerevisiae) >gi 1420671_emb_CAA99622_ (Z75212) ORF YOR304w
                   [Saccharomyces cerevisiae]
Seq. No.
                  149527
Seq. ID
                  LIB3175-028-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g1619300
BLAST score
                  309
E value
                   2.0e-28
Match length
                   66
% identity
                  85
                   (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                  149528
Seq. No.
                  LIB3175-028-P1-K1-C1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119350
BLAST score
                  579
                   5.0e-60
E value
                  112
Match length
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi_16271_emb_CAA41114 (X58107) enolase
                   [Arabidopsis thaliana]
                  >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
                   (2-phospho-D-glycerate hydroylase); identical to P25696
                   [Arabidopsis thaliana]
```

```
149529
Seq. No.
                  LIB3175-028-P1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351069
BLAST score
                  172
                  7.0e-92
E value
                  391
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSH12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149530
Seq. ID
                  LIB3175-028-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  g3643588
BLAST score
                  207
                  1.0e-113
E value
                  403
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F17H15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149531
                  LIB3175-028-P1-K1-C2
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3033384
BLAST score
                  108
                  3.0e-42
E value
                  141
Match length
% identity
                  (AC004238) putative CTP synthase [Arabidopsis thaliana]
NCBI Description
                  149532
Seq. No.
                  LIB3175-028-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1888557
BLAST score
                  331
E value
                  8.0e-31
                  81
Match length
                  74
% identity
                  (U89841) diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase
NCBI Description
                   [Lupinus angustifolius]
                  149533
Seq. No.
                  LIB3175-028-P1-K1-C5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g345829
BLAST score
                  315
E value
                  6.0e-29
Match length
                  96
                  64
% identity
NCBI Description ubiquitin carrier protein E2 - human
                  149534
Seq. No.
                  LIB3175-028-P1-K1-C6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2191132
```

```
BLAST score
                   453
E value
                   4.0e-45
                   140
Match length
                   74
% identity
                   (AF007269) contains weak similarity to nebulin [Arabidopsis
NCBI Description
                   thaliana]
                   149535
Seq. No.
                  LIB3175-028-P1-K1-C7
Seq. ID
                   BLASTX
Method
                   g3450842
NCBI GI
BLAST score
                   284
                   3.0e-27
E value
                   112
Match length
                   61
% identity
                   (AF080436) mitogen activated protein kinase kinase [Oryza
NCBI Description
                   sativa]
                   149536
Seq. No.
                   LIB3175-028-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2191184
BLAST score
                   630
                   6.0e-66
E value
                   142
Match length
                   90
% identity
NCBI Description
                   (AF007271) Similar to sodium/hydrogen exchanger; coded for
                   by A. thaliana cDNA T75860 [Arabidopsis thaliana]
                   149537
Seq. No.
                   LIB3175-028-P1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2369714
BLAST score
                   402
                   2.0e-39
E value
                   85
Match length
                   95
% identity
NCBI Description
                   (Z97178) elongation factor 2 [Beta vulgaris]
                   149538
Seq. No.
                   LIB3175-028-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2062161
BLAST score
                   64
E value
                   2.0e-55
                   126
Match length
                   60
% identity
                   (ACO01645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                   thaliana]
                   149539
Seq. No.
Seq. ID
                   LIB3175-028-P1-K1-D10
Method
                   BLASTX
                   g2244750
NCBI GI
BLAST score
                   718
                   3.0e-76
E value
                   147
Match length
```

```
% identity
                  90
NCBI Description
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
                  >gi_3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
                  149540
Seq. No.
                  LIB3175-028-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220510
                  259
BLAST score
E value
                  1.0e-144
Match length
                  415
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                  (ESSAII project)
                  149541
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-D12
Method
                  BLASTN
NCBI GI
                  g2351062
BLAST score
                  197
E value
                  1.0e-107
Match length
                  329
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAH20, complete sequence [Arabidopsis thaliana]
                  149542
Seq. No.
                  LIB3175-028-P1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2281648
BLAST score
                  234
                  1.0e-129
E value
Match length
                  238
% identity
                  100
NCBI Description
                  Arabidopsis thaliana AP2 domain containing protein RAP2.12
                  mRNA, partial cds
                  149543
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3158376
BLAST score
                  405
                  1.0e-39
E value
Match length
                  120
% identity
NCBI Description
                  (AF035385) unknown [Arabidopsis thaliana]
Seq. No.
                  149544
Seq. ID
                  LIB3175-028-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4467099
BLAST score
                  603
E value
                  7.0e-63
Match length
                  118
% identity
                  (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
```

## [Arabidopsis thaliana] 149545 LIB3175-028-P1-K1-E10

Seq. ID LIB3175-028Method BLASTX
NCBI GI g1710151
BLAST score 702
E value 2.0e-74
Match length 135
% identity 98

NCBI Description (U72711) proline iminopeptidase [Arabidopsis thaliana]

Seq. No. Seq. ID

Seq. No.

LIB3175-028-P1-K1-E12

149546

Method BLASTN
NCBI GI g2435510
BLAST score 217
E value 1.0e-118
Match length 404
% identity 98

NCBI Description Arabidopsis thaliana BAC TM017A05

Seq. No.

149547 LIB3175-028-P1-K1-E2

Seq. ID LIB3175-0
Method BLASTN
NCBI GI g3449329
BLAST score 262
E value 1.0e-145
Match length 379

% identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

MDH9, complete sequence [Arabidopsis thaliana]

Seq. No. 149548

Seq. ID LIB3175-028-P1-K1-E3

Method BLASTN
NCBI GI g3176701
BLAST score 181
E value 2.0e-97
Match length 235
% identity 94

NCBI Description Arabidopsis thaliana chromosome II BAC T20K24 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 149549

Seq. ID LIB3175-028-P1-K1-E4

Method BLASTN
NCBI GI g4741939
BLAST score 167
E value 4.0e-89
Match length 239
% identity 93

NCBI Description Arabidopsis thaliana Lhca2 protein (Lhca2) mRNA, complete

cds

Seq. No. 149550

Seq. ID LIB3175-028-P1-K1-E5

```
Method
                   BLASTX
                   g4741940
NCBI GI
BLAST score
                   593
E value
                   1.0e-61
                   108
Match length
                   67
% identity
                   (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
                   149551
Seq. No.
                   LIB3175-028-P1-K1-E6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q99698
                   667
BLAST score
E value
                   3.0e-70
Match length
                   150
% identity
                   85
                   glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone
NCBI Description
                   lambdaAtgskb6) - Arabidopsis thaliana
                   149552
Seq. No.
                   LIB3175-028-P1-K1-E7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539408
BLAST score
                   145
E value
                   1.0e-10
Match length
                   65
% identity
                   63
                   (AL049524) putative alpha NAC [Arabidopsis thaliana]
NCBI Description
                   149553
Seq. No.
Seq. ID
                   LIB3175-028-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g3024697
                   379
BLAST score
                   1.0e-36
E value
Match length
                   76
% identity
                   100
                   T-COMPLEX PROTEIN 1, EPSILON SUBUNIT (TCP-1-EPSILON)
NCBI Description
                   (CCT-EPSILON) >gi_2213618 (AC000103) F21J9.12 [Arabidopsis
                   thaliana]
Seq. No.
                   149554
                   LIB3175-028-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1518540
BLAST score
                   368
E value
                   2.0e-44
Match length
                   107
% identity
                   89
                   (U53418) UDP-glucose dehydrogenase [Glycine max]
NCBI Description
                   149555
Seq. No.
Seq. ID
                   LIB3175-028-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   g4741940
BLAST score
                   311
E value
                   7.0e-29
```

```
Match length
                   57
% identity
                   100
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
                   149556
Seq. No.
                  LIB3175-028-P1-K1-F2
Seq. ID
                   BLASTX
Method
                   g2894574
NCBI GI
                   679
BLAST score
                   9.0e-72
E value
                   127
Match length
                   100
% identity
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
NCBI Description
                   >gi 2961341 emb CAA18099.1 (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
Seq. No.
                   149557
                  LIB3175-028-P1-K1-F3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2842474
                   39
BLAST score
                   5.0e-13
E value
                   71
Match length
                   89
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                   (ESSAII project)
Seq. No.
                   149558
                   LIB3175-028-P1-K1-F4
Seq. ID
                   BLASTX
Method
                   g3929649
NCBI GI
BLAST score
                   138
                   7.0e-09
E value
                   40
Match length
                   68
% identity
                   (AJ131205) mitochondrial NAD-dependent malate dehydrogenase
NCBI Description
                   [Arabidopsis thaliana]
                   149559
Seq. No.
                   LIB3175-028-P1-K1-F6
Seq. ID
                   BLASTX
Method
                   g2317729
NCBI GI
BLAST score
                   744
E value
                   3.0e-79
Match length
                   141
% identity
NCBI Description
                   (AF013627) reversibly glycosylated polypeptide-1
                   [Arabidopsis thaliana]
Seq. No.
                   149560
                   LIB3175-028-P1-K1-F7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2317729
BLAST score
                   266
                   6.0e-42
E value
Match length
                   98
                   90
% identity
```

```
(AF013627) reversibly glycosylated polypeptide-1
NCBI Description
                  [Arabidopsis thaliana]
                  149561
Seq. No.
                  LIB3175-028-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170503
                  506
BLAST score
E value
                  1.0e-51
                  100
Match length
                  99
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-1 (EIF-4A-1)
NCBI Description
                  >gi_322503_pir__JC1452 translation initiation factor
                  eIF-4A1 - Arabidopsis thaliana >gi_16554 emb CAA46188
                   (X65052) eukaryotic translation initiation factor 4A-1
                   [Arabidopsis thaliana]
                  149562
Seq. No.
                  LIB3175-028-P1-K1-F9
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3914442
BLAST score
                  443
                  4.0e-44
E value
                  126
Match length
                  71
% identity
                  PHOTOSYSTEM I REACTION CENTRE SUBUNIT VI PRECURSOR
NCBI Description
                   (LIGHT-HARVESTING COMPLEX I 11 KD PROTEIN) (PSI-H)
                  >gi 1916350 (U92504) PSI-H subunit [Brassica rapa]
                  149563
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  q1490552
BLAST score
                  126
E value
                  1.0e-64
Match length
                  134
% identity
                  99
                  Arabidopsis thaliana S-adenosylmethionine decarboxylase
NCBI Description
                   (SAMdc) mRNA, complete cds
                  149564
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-G10
Method
                  BLASTN
NCBI GI
                  g16316
BLAST score
                  216
E value
                  1.0e-118
Match length
                  272
% identity
                  99
NCBI Description
                  A.thaliana gene for histone H1-1
                  149565
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q2960364
                  442
BLAST score
                  5.0e-44
E value
```

106

Match length

```
% identity
NCBI Description
                   (AJ224986) cinnamoyl CoA reductase [Populus balsamifera
                   subsp. trichocarpa]
                   149566
Seq. No.
                   LIB3175-028-P1-K1-G2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1209241
BLAST score
                   64
                   5.0e-28
E value
                   108
Match length
% identity
                   90
NCBI Description
                   Arabidopsis thaliana metallothionein mRNA sequence
Seq. No.
                   149567
Seq. ID
                   LIB3175-028-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   g2459406
BLAST score
                   139
E value
                   2.0e-72
Match length
                   271
% identity
                   100
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F4P9 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149568
                   LIB3175-028-P1-K1-G5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g416681
BLAST score
                   239
E value
                   5.0e-20
Match length
                   109
% identity
                   41
NCBI Description
                   ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR
                   >gi_280404_pir__S26198 H+-transporting ATP synthase (EC
                   3.6.1.34) delta chain precursor, chloroplast - common tobacco >gi_19787_emb_CAA45153_ (X63607) chloroplast ATP
                   synthase (delta subunit) [Nicotiana tabacum]
Seq. No.
                   149569
Seq. ID
                   LIB3175-028-P1-K1-G6
Method
                   BLASTX
NCBI GI
                   g1061040
BLAST score
                   569
                   7.0e-59
E value
Match length
                   108
% identity
                   98
                   (X89867) sterol-C-methyltransferase [Arabidopsis thaliana]
NCBI Description
                   >gi 1587694 prf 2207220A sterol C-methyltransferase
                   [Arabidopsis thaliana]
Seq. No.
                   149570
Seq. ID
                   LIB3175-028-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g4388726
BLAST score
                   727
E value
                   3.0e-77
```

BLAST score

339

```
Match length
                  145
% identity
                  98
                   (AC006413) putative 12-oxophytodienoate-10,11-reductase
NCBI Description
                  [Arabidopsis thaliana]
                  149571
Seq. No.
                  LIB3175-028-P1-K1-H10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g266731
BLAST score
                  157
                  5.0e-42
E value
Match length
                  130
                  74
% identity
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE 1 >gi_282927_pir__$25303
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - garden pea
                  >gi_217980_dbj_BAA00885_ (D10001) phenylalanine
                  ammonia-lyase [Pisum sativum] >gi 217982 dbj BAA00886
                  (D10002) phenylalanine ammonia-lyase [Pisum sativum]
                  149572
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-H11
                  BLASTN
Method
NCBI GI
                  g1402874
BLAST score
                  325
E value
                  0.0e + 00
                  376
Match length
% identity
                  99
NCBI Description A.thaliana 81kb genomic sequence
                  149573
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g832876
BLAST score
                  277
E value
                  6.0e-25
                  59
Match length
% identity
                  86
NCBI Description
                  (L41345) ascorbate free radical reductase [Solanum
                  lycopersicum] >gi_1097368_prf__2113407A ascorbate free
                  radical reductase [Lycopersicon esculentum]
                  149574
Seq. No.
Seq. ID
                  LIB3175-028-P1-K1-H4
Method
                  BLASTN
NCBI GI
                  g3068806
BLAST score
                  146
E value
                  8.0e-77
Match length
                  158
                  98
% identity
NCBI Description
                  Arabidopsis thaliana Skp1 homolog (SKP1a) mRNA, complete
Seq. No.
                  149575
                  LIB3175-028-P1-K1-H7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4468103
```

```
0.0e + 00
E value
Match length
                     351
% identity
NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
                     (ESSA project)
                    149576
Seq. No.
Seq. ID
                    LIB3175-028-P1-K1-H8
Method
                    BLASTN
NCBI GI
                    q3228389
BLAST score
                    189
                     1.0e-102
E value
Match length
                     460
% identity
NCBI Description
                    Genomic sequence for Arabidopsis thaliana BAC F17L21,
                    complete sequence [Arabidopsis thaliana]
Seq. No.
                    149577
                    LIB3175-028-P1-K1-H9
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2129769
BLAST score
                    182
E value
                     2.0e-13
Match length
                     98
                     52
% identity
NCBI Description
                    xyloglucan endo-transglycosylase precursor - Arabidopsis
                     thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan
                    transferase [Arabidopsis thaliana]
                    149578
Seq. No.
Seq. ID
                    LIB3175-029-P1-K1-A1
Method
                    BLASTX
NCBI GI
                     q4090884
BLAST score
                     527
E value
                     6.0e-54
Match length
                    104
% identity
                     97
NCBI Description
                     (AF025333) vesicle-associated membrane protein 7B;
                    synaptobrevin 7B [Arabidopsis thaliana]
Seq. No.
                    149579
Seq. ID
                    LIB3175-029-P1-K1-A10
Method
                    BLASTX
NCBI GI
                    q4337175
BLAST score
                    290
E value
                    2.0e-47
Match length
                    127
% identity
NCBI Description
                     (AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906,
                    gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                    149580
Seq. ID
                    LIB3175-029-P1-K1-A11
Method
                    BLASTN
NCBI GI
                    g4206766
```

```
BLAST score
                  235
                  1.0e-129
E value
Match length
                  267
% identity
NCBI Description
                  Arabidopsis thaliana glycine-rich protein 3 short isoform
                   (GRP3S) mRNA, complete cds
                  149581
Seq. No.
                  LIB3175-029-P1-K1-A2
Seq. ID
Method
                  BLASTX
                  g1669387
NCBI GI-
BLAST score
                  513
E value
                  3.0e-52
Match length
                  95
% identity
                  99
NCBI Description
                  (U41998) actin 2 [Arabidopsis thaliana]
                  149582
Seq. No.
                  LIB3175-029-P1-K1-A3
Seq. ID
Method
                  BLASTX
                  g99688
NCBI GI
BLAST score
                  666
E value
                  3.0e-70
                  130
Match length
                  99
% identity
                  translation elongation factor eEF-1 alpha chain (gene A4) -
NCBI Description
                  Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
                  149583
Seq. No.
                  LIB3175-029-P1-K1-A5
Seq. ID
Method
                  BLASTX
                  g2497753
NCBI GI
BLAST score
                  263
E value
                  7.0e-23
Match length
                  95
% identity
                  49
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                   [Prunus dulcis]
                  149584
Seq. No.
                  LIB3175-029-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2688824
BLAST score
                  283
E value
                  4.0e-25
Match length
                  130
                  52
% identity
NCBI Description
                   (U93273) putative auxin-repressed protein [Prunus
                  armeniaca]
Seq. No.
                  149585
Seq. ID
                  LIB3175-029-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  q4519183
BLAST score
                  397
```

```
E value
                  0.0e+00
                  420
Match length
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K15C23, complete sequence
                  149586
Seq. No.
                  LIB3175-029-P1-K1-A8
Seq. ID
                  BLASTX
Method
                  g1086263
NCBI GI
                  313
BLAST score
                  8.0e-29
E value
                  126
Match length
                  52
% identity
                  TMV resistance protein N - tobacco (Nicotiana glutinosa)
NCBI Description
                  >gi 558887 (U15605) N [Nicotiana glutinosa]
Seq. No.
                  149587
                  LIB3175-029-P1-K1-A9
Seq. ID
Method
                  BLASTN
                  g3766106
NCBI GI
                  156
BLAST score
                   3.0e-82
E value
                  423
Match length
                   97
% identity
                  Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  149588
                  LIB3175-029-P1-K1-B1
Seq. ID
                  BLASTN
Method
                  q3449331
NCBI GI
                   63
BLAST score
                   3.0e-27
E value
                  143
Match length
                   86
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MNC17, complete sequence [Arabidopsis thaliana]
                  149589
Seq. No.
                  LIB3175-029-P1-K1-B10
Seq. ID
                  BLASTX
Method
                  g115783
NCBI GI
                   697
BLAST score
                   9.0e-74
E value
                  138
Match length
                   97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb_CAA27543_
                                                             (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   149590
Seq. No.
                  LIB3175-029-P1-K1-B11
Seq. ID
Method
                  BLASTX
                   g2497753
NCBI GI
                   276
BLAST score
```

```
E value
                  2.0e-24
Match length
                  110
                  49
% identity
NCBI Description
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
                  >gi_1321915_emb_CAA65477_ (X96716) lipid transfer protein
                  [Prunus dulcis]
                  149591
Seq. No.
                  LIB3175-029-P1-K1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3766106
                  170
BLAST score
                  9.0e-91
E value
                  292
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome 1 BAC F9K20 sequence,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  149592
Seq. ID
                  LIB3175-029-P1-K1-B2
                  BLASTX
Method
NCBI GI
                  g119143
BLAST score
                  714
E value
                  1.0e-75
Match length
                  138
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_81606_pir__S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi_295788 emb_CAA34453_
                  (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi_1369927_emb_CAA34454_ (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                  >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                  149593
                  LIB3175-029-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1486472
BLAST score
                  578
E value
                  8.0e-60
Match length
                  128
% identity
NCBI Description
                  (X99853) oxoglutarate malate translocator [Solanum
                  tuberosum]
Seq. No.
                  149594
                  LIB3175-029-P1-K1-B4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4469002
BLAST score
                  339
E value
                  0.0e + 00
Match length
                  413
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T29A15
NCBI Description
```

Seq. No.

Seq. ID

Method

NCBI GI

E value Match length

Seq. No.

Seq. ID

NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

BLAST score

Match length

% identity

Method

BLAST score

% identity

```
(ESSA project)
                  149595
                  LIB3175-029-P1-K1-B6
                  BLASTX
                  q3122622
                  215
                  2.0e-31
                  111
                  PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP) >gi 2267237
NCBI Description
                  (U70473) PEP carboxykinase [Candida albicans]
                  149596
                  LIB3175-029-P1-K1-B7
                  BLASTX
                  q267136
                  287
                  5.0e-26
                  96
                  67
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2C (WATER-STRESS INDUCED
NCBI Description
                  TONOPLAST INTRINSIC PROTEIN) (WSI-TIP)
                  >gi_217869_dbj_BAA02520_ (D13254) transmembrane channel
                  protein [Arabidopsis thaliana] >gi_4371283_gb_AAD18141
                  (AC006260) putative plasma membrane intrinsic protein 2C
                  [Arabidopsis thaliana] >gi_384324_prf__1905411A
                  transmembrane channel [Arabidopsis thaliana]
                  149597
                  LIB3175-029-P1-K1-B8
                  BLASTN
                  q2584827
                  219
                  1.0e-120
                  238
                  99
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                  complete sequence [Arabidopsis thaliana] ...
                  149598
                  LIB3175-029-P1-K1-B9
```

NCBI Description

Seq. No.

Seq. ID

Method BLASTX NCBI GI g3482924 BLAST score 326 E value 3.0e-30 Match length 119 % identity

NCBI Description (AC003970) Highly similar to cinnamyl alcohol dehydrogenase, gi\_1143445 [Arabidopsis thaliana]

Seq. No. 149599

Seq. ID LIB3175-029-P1-K1-C1

Method BLASTN NCBI GI q4467094 BLAST score 159 E value 3.0e-84

Seq. ID

```
Match length
                  268
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
                  (ESSA project)
                  149600
Seq. No.
                  LIB3175-029-P1-K1-C10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  445
E value
                  0.0e + 00
Match length
                  449
% identity
                  100
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  149601
                  LIB3175-029-P1-K1-C11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g120667
BLAST score
                  477
E value
                  5.0e-48
Match length
                  107
% identity
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                  thaliana >gi 166706 (M64116) cystolic
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                  dehydrogenase [Arabidopsis thaliana]
                  149602
Seq. No.
                  LIB3175-029-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4507703
BLAST score
                  202
E value
                  1.0e-15
Match length
                  148
% identity
NCBI Description
                  tumor suppressing subtransferable candidate 1
                  >gi_2655037_gb_AAC51911_ (AF019952) tumor suppressing STF
                  cDNA 1 [Homo sapiens]
Seq. No.
                  149603
Seq. ID
                  LIB3175-029-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g2961390
BLAST score
                  647
E value
                  9.0e-73
Match length
                  134
% identity
NCBI Description
                  (AL022141) beta-galactosidase like protein [Arabidopsis
                  thaliana]
Seq. No.
                  149604
```

19009

LIB3175-029-P1-K1-C3

```
Method
                  BLASTN
                   q2264304
NCBI GI
BLAST score
                   217
E value
                   1.0e-118
Match length
                   421
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBG8, complete sequence [Arabidopsis thaliana]
                   149605
Seq. No.
Seq. ID
                   LIB3175-029-P1-K1-C6
Method
                   BLASTX
NCBI GI
                   a4455253
BLAST score
                   506
E value
                   2.0e-60
                   139
Match length
% identity
                   86
                   (AL035523) superoxide dismutase (EC 1.15.1.1)
NCBI Description
                   (Fe)(fragment) [Arabidopsis thaliana]
Seq. No.
                   149606
                   LIB3175-029-P1-K1-C7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1402876
                   767
BLAST score
E value
                   6.0e-82
                   159
Match length
% identity
                   (X98130) putative phosphate permease [Arabidopsis thaliana]
NCBI Description
                   >gi_1495255_emb_CAA66116_ (X97484) orf01 [Arabidopsis
                   thaliana]
                   149607
Seq. No.
                   LIB3175-029-P1-K1-C8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1170601
BLAST score
                   313
                   1.0e-28
E value
Match length
                   151
% identity
                   FRUIT PROTEIN PKIWI502 >gi 1085869 pir S48036 hypothetical
NCBI Description
                   protein - kiwi fruit >gi 450237 (L27809) pKIWI502
                   [Actinidia deliciosa]
                   149608
Seq. No.
                   LIB3175-029-P1-K1-C9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3849811
BLAST score
                   431
E value
                   0.0e + 00
Match length
                   439
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T2P11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149609
Seq. ID
                  LIB3175-029-P1-K1-D1
```

```
Method
                   BLASTX
                   g1345595
NCBI GI
BLAST score
                   653
                   1.0e-68
E value
Match length
                  135
                   98
% identity
                  14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
NCBI Description
                   >gi_1084332_pir__S53727 14-3-3-like protein (ATF1) -
                  Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like
                   protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14
                   lambda [Arabidopsis thaliana]
Seq. No.
                   149610
                  LIB3175-029-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2924512
BLAST score
                   61
                   1.0e-43
E value
Match length
                  133
                   56
% identity
NCBI Description
                   (AL022023) beta-galactosidase-like protein [Arabidopsis
                   thaliana]
                  149611
Seq. No.
Seq. ID
                  LIB3175-029-P1-K1-D11
Method
                  BLASTX
NCBI GI
                   g4567207
BLAST score
                   812
E value
                   3.0e-87
Match length
                  155
                   98
% identity
NCBI Description
                   (AC007168) unknown protein [Arabidopsis thaliana]
                  149612
Seq. No.
                  LIB3175-029-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2342727
BLAST score
                   540
E value
                   2.0e-55
Match length
                  134
                   77
% identity
NCBI Description
                   (AC002341) hypothetical protein [Arabidopsis thaliana]
                  149613
Seq. No.
                  LIB3175-029-P1-K1-D2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585882
BLAST score
                   740
E value
                   9.0e-79
Match length
                  141
% identity
                   99
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                  149614
Seq. No.
                  LIB3175-029-P1-K1-D3
Seq. ID
Method
                  BLASTX
```

```
NCBI GI
                  g132110
BLAST score
                  680
                  9.0e-72
E value
Match length
                  129
                  97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  149615
Seq. No.
Seq. ID
                  LIB3175-029-P1-K1-D4
Method
                  BLASTX
                  g2218152
NCBI GI
BLAST score
                  778
                  3.0e-83
E value
                  150
Match length
% identity
                  (AF005279) type IIIa membrane protein cp-wap13 [Vigna
NCBI Description
                  unguiculata]
Seq. No.
                  149616
                  LIB3175-029-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1203832
BLAST score
                  128
                  8.0e-15
E value
                  92
Match length
% identity
                   (U46003) beta-D-glucan exohydrolase, isoenzyme ExoII
NCBI Description
                   [Hordeum vulgare] >gi_1588407_prf__2208395A beta-D-glucan
                  exohydrolase [Hordeum vulgare]
Seq. No.
                  149617
Seq. ID
                  LIB3175-029-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q3169028
BLAST score
                  205
                  5.0e-16
E value
Match length
                  81
% identity
                  47
NCBI Description
                   (AL023702) putative cationic amino acid transporter
                  [Streptomyces coelicolor]
Seq. No.
                  149618
Seq. ID
                  LIB3175-029-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q1171993
BLAST score
                  687
E value
                  1.0e-72
Match length
                  143
% identity
NCBI Description
                  PHENYLALANINE AMMONIA-LYASE 2 >gi 1076370 pir _S52991
                  phenylalanine ammonia-lyase (EC 4.3.1.5) - Arabidopsis
                  thaliana >gi_497421 (L33678) phenylalanine ammonia lyase
```

% identity

NCBI Description

```
[Arabidopsis thaliana]
Seq. No.
                  149619
Seq. ID
                  LIB3175-029-P1-K1-D9
Method
                  BLASTX
NCBI GI
                   q4490329
BLAST score
                   441
                   8.0e-44
E value
Match length
                   106
                   80
% identity
NCBI Description
                   (AL035656) extensin-like protein [Arabidopsis thaliana]
                  149620
Seq. No.
                  LIB3175-029-P1-K1-E1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129727
BLAST score
                  167
                   1.0e-11
E value
Match length
                   72
                   56
% identity
                  RNA-binding protein 37 - Arabidopsis thaliana >gi_1174153
NCBI Description
                   (U44134) RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  149621
                  LIB3175-029-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                   a1174847
BLAST score
                   823
                   2.0e-88
E value
Match length
                   158
% identity
                   97
                  UBIQUITIN-CONJUGATING ENZYME E2-21 KD 1 (UBIQUITIN-PROTEIN
NCBI Description
                  LIGASE 4) (UBIQUITIN CARRIER PROTEIN 4) >gi 431266 (L19354)
                  ubiquitin conjugating enzyme [Arabidopsis thaliana]
Seq. No.
                  149622
Seq. ID
                  LIB3175-029-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                   470
E value
                   1.0e-74
Match length
                   149
                   96
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  149623
Seq. ID
                  LIB3175-029-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q135467
BLAST score
                  142
E value
                  7.0e-81
Match length
                  154
```

TUBULIN BETA-4 CHAIN >gi\_2129546\_pir\_\_S68122 beta-tubulin 4

- Arabidopsis thaliana >gi 166640 (M21415) beta-tubulin [Arabidopsis thaliana]

Seq. No. 149624

LIB3175-029-P1-K1-E3 Seq. ID

Method BLASTN NCBI GI q4159708 BLAST score 216 E value 1.0e-118 Match length 472 % identity 98

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MKP6, complete sequence

Seq. No. 149625

LIB3175-029-P1-K1-E4 Seq. ID

Method BLASTX NCBI GI q2129659 332 BLAST score E value 5.0e-31 121 Match length 62 % identity

oleosin, isoform 21K - Arabidopsis thaliana >gi 725260 NCBI Description

(L40954) oleosin [Arabidopsis thaliana]

149626 Seq. No.

LIB3175-029-P1-K1-E5 Seq. ID

Method BLASTX NCBI GI q4566505 BLAST score 520 E value 6.0e-53 Match length 150

% identity 65

(AF102868) beta-D-glucan exohydrolase isoenzyme ExoI NCBI Description

[Hordeum vulgare]

Seq. No. 149627

Seq. ID LIB3175-029-P1-K1-E6

Method BLASTX NCBI GI q399013 BLAST score 556 E value 3.0e-57 Match length 111 % identity

ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1) NCBI Description

(ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)

>gi\_99658\_pir\_\_S21313 ADP,ATP carrier protein - Arabidopsis

thaliana (fragment) >gi\_16175\_emb\_CAA46518\_ (X65549)

adenylate translocator [Arabidopsis thaliana] >gi 445607 prf 1909354A adenylate translocator

[Arabidopsis thaliana]

Seq. No. 149628

Seq. ID LIB3175-029-P1-K1-E8

Method BLASTX NCBI GI g625977 BLAST score 436

Method

NCBI GI

E value

BLAST score

BLASTN

374

g3212846

0.0e+00

```
E value
                   2.0e-43
Match length
                   86
% identity
                   99
NCBI Description
                   p40 protein homolog - Arabidopsis thaliana >gi 402904
                   (U01955) laminin receptor-like protein [Arabidopsis
                   thaliana]
                   149629
Seq. No.
Seq. ID
                   LIB3175-029-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   g3785981
BLAST score
                   499
E value
                   1.0e-50
Match length
                   127
% identity
                   72
NCBI Description
                   (AC005560) putative major latex protein [Arabidopsis
                   thaliana]
                   149630
Seq. No.
Seq. ID
                   LIB3175-029-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g2062161
BLAST score
                   689
E value
                   8.0e-73
                   134
Match length
% identity
NCBI Description
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
                   thaliana]
                   149631
Seq. No.
Seq. ID
                   LIB3175-029-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g4585882
BLAST score
                   531
E value
                   3.0e-54
Match length
                   125
% identity
                   84
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   149632
Seq. ID
                   LIB3175-029-P1-K1-F11
Method
                   BLASTN
NCBI GI
                   q4582428
BLAST score
                   165
E value
                   1.0e-87
Match length
                   345
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T18C20 genomic
                   sequence, complete sequence
Seq. No.
                   149633
Seq. ID
                  LIB3175-029-P1-K1-F12
```

E value

```
411
Match length
                   97
% identity
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149634
                   LIB3175-029-P1-K1-F2
Seq. ID
                   BLASTN
Method
                   g4432847
NCBI GI
BLAST score
                   41
                   1.0e-14
E value
Match length
                   73
                   89
% identity
                  Arabidopsis thaliana chromosome II BAC F13B15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149635
                   LIB3175-029-P1-K1-F3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1706551
BLAST score
                   233
E value
                   2.0e-19
                   97
Match length
                   46
% identity
NCBI Description
                   GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR
                   ((1->3)-BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE)
                   (BETA-1,3-ENDOGLUCANASE) >gi 924953 (U30323) beta
                   1,3-glucanase [Triticum aestivum]
                   149636
Seq. No.
                   LIB3175-029-P1-K1-F4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4582411
BLAST score
                   403
E value
                   0.0e+00
Match length
                   455
% identity
                   100
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC T23K8 sequence,
                   complete sequence
Seq. No.
                   149637
Seq. ID
                   LIB3175-029-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g2982262
BLAST score
                   42
E value
                   4.0e-32
Match length
                  156
% identity
NCBI Description
                   (AF051214) probable glutathione S-transferase [Picea
                  mariana]
                   149638
Seq. No.
Seq. ID
                  LIB3175-029-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g2244825
BLAST score
                   412
```

19016

.a.,

2.0e-40

```
124
Match length
                  72
% identity
                  (Z97336) light induced protein homolog [Arabidopsis
NCBI Description
                  thaliana]
                  149639
Seq. No.
                  LIB3175-029-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3212116
BLAST score
                  200
                  2.0e-15
E value
Match length
                  123
% identity
                  36
NCBI Description
                  (Y17393) prefoldin subunit 2 [Mus musculus]
                  149640
Seq. No.
                  LIB3175-029-P1-K1-F9
Seq. ID
                  BLASTX
Method
                  g2129549
NCBI GI
BLAST score
                  454
E value
                  3.0e-45
                  84
Match length
                  100
% identity
                  calcium-dependent protein kinase (EC 2.7.1.-) CDPK19 -
NCBI Description
                  Arabidopsis thaliana >gi_2129551_pir__S71778
                  calcium-dependent protein kinase 19 - Arabidopsis thaliana
                  >gi 836942 (U20624) calcium-dependent protein kinase
                  [Arabidopsis thaliana] >gi 836948 (U20627)
                  calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.
                  149641
                  LIB3175-029-P1-K1-G1
Seq. ID
Method
                  BLASTX
                  g3183568
NCBI GI
BLAST score
                  245
E value
                  1.0e-20
Match length
                  130
% identity
                  42
NCBI Description
                  HYPOTHETICAL 45.1 KD PROTEIN IN CDD-MGLC INTERGENIC REGION
                  149642
Seq. No.
Seq. ID
                  LIB3175-029-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q4503363
                  534
BLAST score
E value
                  1.0e-54
Match length
                  159
% identity
                  59
NCBI Description
                  dolichyl-phosphate mannosyltransferase polypeptide 1
                  >gi_3062806_dbj_BAA25646_ (D86198)
                  dolichol-phosphate-mannose synthase [Homo sapiens]
Seq. No.
                  149643
Seq. ID
                  LIB3175-029-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  q2369714
BLAST score
                  660
```

```
E value
                   2.0e-69
Match length
                   156
% identity
                   81
                   (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                  149644
Seq. No.
                  LIB3175-029-P1-K1-G12
Seq. ID
                   BLASTX
Method
                   g266336
NCBI GI
                   247
BLAST score
                   5.0e-21
E value
                   129
Match length
                   36
% identity
                  EUKARYOTIC INITIATION FACTOR 4A-I (EIF-4A-I)
NCBI Description
                   >gi 109295 pir S13269 initiation factor eIF-4A - rabbit
Seq. No.
                   149645
                   LIB3175-029-P1-K1-G2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3859659
                   380
BLAST score
E value
                   4.0e-37
                   131
Match length
                   72
% identity
                   (AL031394) putative potassium transporter AtKT5p (AtKT5)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   149646
                   LIB3175-029-P1-K1-G3
Seq. ID
Method
                   BLASTX
                   q529353
NCBI GI
BLAST score
                   316
                   3.0e-29
E value
                   90
Match length
                   59
% identity
                   (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
Seq. No.
                   149647
                   LIB3175-029-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115385
BLAST score
                   727
E value.
                   3.0e-77
                   139
Match length
                   100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
                   149648
Seq. No.
                   LIB3175-029-P1-K1-G7
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3861153
BLAST score
                   291
E value
                   4.0e-26
Match length
                   98
                   55
% identity
```

Seq. No.

Seq. ID

```
(AJ235272) CYANELLE 50S RIBOSOMAL PROTEIN L20 (rplT)
NCBI Description
                  [Rickettsia prowazekii]
Seq. No.
                  149649
                  LIB3175-029-P1-K1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4757415
                  426
BLAST score
                  0.0e + 00
E value
                  458
Match length
                  98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MYN21, complete sequence
Seq. No.
                  149650
Seq. ID
                  LIB3175-029-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g1170606
BLAST score
                  356
                  9.0e-34
E value
                  88
Match length
% identity
                  ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)
NCBI Description
                  >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3),
                  chloroplast - maize >gi 3114421_pdb_1ZAK_A Chain A,
                  Adenylate Kinase From Maize In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-)pentaphosphate (Ap5a)
                  >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize
                  In Complex With The Inhibitor
                  P1, P5-Bis (Adenosine-5'-)pentaphosphate (Ap5a)
Seq. No.
                  149651
                  LIB3175-029-P1-K1-H1
Seq. ID
Method
                  BLASTN
                  g3068702
NCBI GI
BLAST score
                  67
                  3.0e-29
E value
                  95
Match length
% identity
                  93
                  Arabidopsis thaliana putative transmembrane protein Glp
NCBI Description
                  (AtG1), putative nuclear DNA-binding protein G2p (AtG2),
                  Em1 protein (ATEM1), putative chlorophyll synthetase
                  (AtG4), putative transmembrane protein G5p (AtG5), put
Seq. No.
                  149652
                  LIB3175-029-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g4468802
NCBI GI
                  766
BLAST score
E value
                  8.0e-82
                  153
Match length
% identity
                  (AL035601) cytochrome p450-like protein [Arabidopsis
NCBI Description
                  thaliana]
                  149653
```

19019

LIB3175-029-P1-K1-H12

```
Method
                  BLASTX
NCBI GI
                  q2119846
                  660
BLAST score
                  2.0e-69
E value
Match length
                  127
% identity
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  149654
                  LIB3175-029-P1-K1-H2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3044218
BLAST score
                  418
                  5.0e-41
E value
                  110
Match length
% identity
                  75
                  (AF057144) signal peptidase [Arabidopsis thaliana]
NCBI Description
                  149655
Seq. No.
                  LIB3175-029-P1-K1-H3
Seq. ID
                  BLASTX
Method
                  g4218123
NCBI GI
                  176
BLAST score
                  2.0e-29
E value
                  129
Match length
% identity
                   (AL035353) photosystem I subunit PSI-E-like protein
NCBI Description
                   [Arabidopsis thaliana]
                  149656
Seq. No.
Seq. ID
                  LIB3175-029-P1-K1-H4
                  BLASTN
Method
NCBI GI
                  g3241925
BLAST score
                  199
                  1.0e-108
E value
                  478
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MOK9, complete sequence [Arabidopsis thaliana]
                  149657
Seq. No.
Seq. ID
                  LIB3175-029-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g1708313
BLAST score
                  548
                  3.0e-56
E value
Match length
                  113
% identity
                  HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs 163637
NCBI Description
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
```

thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis

Seq. ID

Method



## thaliana]

```
149658
Seq. No.
Seq. ID
                  LIB3175-029-P1-K1-H6
Method
                  BLASTN
                  q3869072
NCBI GI
                  136
BLAST score
E value
                  1.0e-70
                  196
Match length
                  93
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJB24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  LIB3175-029-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3024434
BLAST score
                  440
E value
                  1.0e-43
Match length
                  111
                  82
% identity
                  26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 1) (TBP-1) >gi 2564337 dbj BAA22951
                  (D88663) Tat binding protein 1 [Brassica rapa]
                  149660
Seq. No.
                  LIB3175-029-P1-K1-H8
Seq. ID
                  BLASTN
Method
NCBI GI
                  q16363
BLAST score
                  36
                  6.0e-11
E value
                  56
Match length
                  91
% identity
                  A.thaliana Lhb1B2 gene for photosystem II chlorophyll a/b
NCBI Description
                  binding protein
                  149661
Seq. No.
                  LIB3175-029-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1170689
BLAST score
                  318
E value
                  1.0e-32
Match length
                  82
% identity
                  SERINE/THREONINE-PROTEIN KINASE ATPK1/ATPK6
NCBI Description
                  >qi 625979 pir A54141 ribosomal protein S6 kinase (EC
                  2.7.1.-) Atpk1 - Arabidopsis thaliana
                  >gi 2129542_pir__S68462 ATPK6 protein - Arabidopsis
                  thaliana >gi 914080 bbs 160873 ATPK6=ribosomal-protein S6
                  kinase homolog [Arabidopsis thaliana, Peptide, 465 aa]
                  >gi 508308 (L29030) protein-serine kinase [Arabidopsis
                  thaliana] >gi 967997 dbj BAA07656 (D42056)
                  risosomal-protein S6 kinase homolog [Arabidopsis thaliana]
Seq. No.
                  149662
```

19021

LIB3175-030-P1-K1-A11

BLASTX

```
NCBI GI
                  g2119846
                  605
BLAST score
                  5.0e-63
E value
Match length
                  114
                  98
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  149663
Seq. No.
                  LIB3175-030-P1-K1-A12
Seq. ID
Method
                  BLASTX
                  g2497753
NCBI GI
BLAST score
                  253
                  9.0e-22
E value
                  94
Match length
                  48
% identity
                  NONSPECIFIC LIPID-TRANSFER PROTEIN 3 PRECURSOR (LTP 3)
NCBI Description
                  >gi 1321915 emb CAA65477 (X96716) lipid transfer protein
                  [Prunus dulcis]
                  149664
Seq. No.
                  LIB3175-030-P1-K1-A5
Seq. ID
Method
                  BLASTX
                  g4567304
NCBI GI
BLAST score
                  248
                  4.0e-21
E value
                  124
Match length
                  44
% identity
                  (AC005956) unknown protein [Arabidopsis thaliana]
NCBI Description
                  149665
Seq. No.
                  LIB3175-030-P1-K1-A6
Seq. ID
Method
                  BLASTN
                  g2618602
NCBI GI
BLAST score
                  213
                  1.0e-116
E value
Match length
                  323
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
                  149666
Seq. No.
Seq. ID
                  LIB3175-030-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3122572
                  408
BLAST score
E value
                  7.0e-40
                  128
Match length
                  65
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 75 KD SUBUNIT PRECURSOR
NCBI Description
                   (COMPLEX I-75KD) (CI-75KD) (76 KD MITOCHONDRIAL COMPLEX I
                  SUBUNIT) >gi 1084434 pir S52737 NADH dehydrogenase
```

Seq. No.

Seq. ID

E value

Seq. No. Seq. ID

Method

NCBI GI BLAST score

E value Match length

Seq. No. Seq. ID

BLAST score

Match length

% identity

Method NCBI GI

E value

% identity

BLAST score

Match length % identity

Method NCBI GI

```
(ubiquinone) (EC 1.6.5.3) 76K chain precursor - potato
                  >gi_758340_emb_CAA59818_ (X85808) 76 kDa mitochondrial
                  complex I subunit [Solanum tuberosum]
                  149667
                  LIB3175-030-P1-K1-A9
                  BLASTX
                  g3335340
                  659
                  3.0e-69
                  148
NCBI Description
                  (AC004512) Strong similarity to xylglucan
                  endo-transglycolsylase (TCH4) gene gb_U27609, first exon
                  contains strong similarity to meri 5 gene gb_Z17989 from A.
                  thaliana.
                            EST gb_N37583 comes from this gene. [Arabidopsis
                  thaliana]
                  149668
                  LIB3175-030-P1-K1-B1
                  BLASTX
                  g4544399
                  332
                  6.0e-31
                  127
NCBI Description
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thalianal
                  149669
                  LIB3175-030-P1-K1-B11
                  BLASTX
                  q4580390
                  637
                  9.0e-67
                  130
                  96
NCBI Description
                  (AC007171) putative disease resistance response protein
                  [Arabidopsis thaliana]
                  149670
                  LIB3175-030-P1-K1-B12
                  BLASTX
                  g2506443
                  563
                  5.0e-58
                  137
                  79
```

Seq. No. Seq. ID Method

NCBI GI BLAST score E value Match length % identity

GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, NCBI Description

CHLOROPLAST >gi\_2117520\_pir\_\_JQ1285

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -Arabidopsis thaliana >gi\_166704 (M64117) glyceraldehyde

3-phosphate dehydrogenase [Arabidopsis thaliana]

>gi 1402885\_emb\_CAA66816\_ (X98130)

glyceraldehyde-3-phosphate dehydrogenase (NADP+)

(phosphorylating) [Arabidopsis thaliana]

```
Seq. No.
                   149671
                   LIB3175-030-P1-K1-B2
Seq. ID
Method
                   BLASTX
                   q399298
NCBI GI
                   217
BLAST score
                   2.0e-17
E value
                   66
Match length
% identity
                   70
                  STRESS-INDUCED KIN2 PROTEIN (COLD-INDUCED COR6.6 PROTEIN)
NCBI Description
                   >gi_1084343_pir__S22529 cold-regulated protein kin2 -
                   Arabidopsis thaliana >gi_16230_emb_CAA38894_ (X55053) cold
                   regulated [Arabidopsis thaliana]
Seq. No.
                   149672
                   LIB3175-030-P1-K1-B4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3608261
BLAST score
                   314
E value
                   7.0e-29
                   84
Match length
% identity
NCBI Description
                   (AB017564) dof zinc finger protein [Arabidopsis thaliana]
                   149673
Seq. No.
Seq. ID
                   LIB3175-030-P1-K1-B5
Method
                   BLASTN
NCBI GI
                   a4165340
BLAST score
                   90
                   6.0e-43
E value
Match length
                   346
% identity
                  Arabidopsis thaliana chromosome I BAC F11M15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149674
Seq. ID
                   LIB3175-030-P1-K1-B6
Method
                   BLASTN
NCBI GI
                   q4585952
BLAST score
                   370
E value
                   0.0e + 00
Match length
                   412
                   97
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F26F24,
NCBI Description
                   complete sequence
Seq. No.
                   149675
Seq. ID
                  LIB3175-030-P1-K1-B7
Method
                  BLASTN
NCBI GI
                   q2880038
BLAST score
                  165
E value
                   1.0e-87
Match length
                  452
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T11J7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                   149676
Seq. ID
                   LIB3175-030-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g2244866
BLAST score
                   782
                   1.0e-83
E value
                   152
Match length
                   97
% identity
                  (297337) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   149677
Seq. No.
                   LIB3175-030-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567197
BLAST score
                   619
E value
                   1.0e-64
Match length
                   127
% identity
                   97
                   (AC007168) unknown protein [Arabidopsis thaliana]
NCBI Description
                   149678
Seq. No.
                   LIB3175-030-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3075394
BLAST score
                   665
                   5.0e-70
E value
                   135
.Match length
% identity
NCBI Description
                   (AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis
                   thaliana] >gi 3559809 emb CAA09311 (AJ010713) fiddlehead
                   protein [Arabidopsis thaliana]
                   149679
Seq. No.
                   LIB3175-030-P1-K1-C2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2262097
BLAST score
                   224
                   1.0e-123
E value
Match length
                   361
% identity
                   Arabidopsis thaliana chromosome IV BAC T19F6 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   149680
Seq. ID
                   LIB3175-030-P1-K1-C3
Method
                   BLASTX
NCBI GI
                   g4263712
BLAST score
                   506
E value
                   2.0e-51
Match length
                   121
% identity
                   83
NCBI Description
                   (AC006223) putative ribosomal protein S12 [Arabidopsis
                   thaliana]
                   149681
Seq. No.
Seq. ID
                  LIB3175-030-P1-K1-C4
Method
                  BLASTX
```

NCBI Description

```
NCBI GI
                   q3157937
BLAST score
                   635
E value
                   2.0e-66
Match length
                   128
% identity
NCBI Description
                   (AC002131) Identical to aspartic proteinase cDNA gb U51036
                   from A. thaliana. ESTs gb_N96313, gb_T21893, gb_R30158,
                  gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269,
                   gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
                  gb_AA728734, gb
                   149682
Seq. No.
Seq. ID
                  LIB3175-030-P1-K1-C7
Method
                  BLASTX
NCBI GI
                   a3377797
BLAST score
                   603
                   1.0e-62 ..
E value
Match length
                   144
% identity
                   82
NCBI Description
                   (AF075597) Similar to 60S ribosome protein L19; coded for
                  by A. thaliana cDNA T04719; coded for by A. thaliana cDNA
                  H36046; coded for by A. thaliana cDNA T44067; coded for by
                  A. thaliana cDNA T14056; coded for by A. thaliana cDNA
                  R90691 [Ara
Seq. No.
                  149683
Seq. ID
                  LIB3175-030-P1-K1-C8
Method
                  BLASTX
NCBI GI
                   q2129769
BLAST score
                   796
E value
                   2.0e-85
Match length
                   151
                   99
% identity
NCBI Description
                  xyloglucan endo-transglycosylase precursor - Arabidopsis
                   thaliana >gi_944810_dbj_BAA09783_ (D63508) endo-xyloglucan
                   transferase [Arabidopsis thaliana]
Seq. No.
                  149684
Seq. ID
                  LIB3175-030-P1-K1-C9
Method
                  BLASTN
NCBI GI
                   q4662609
BLAST score
                   401
E value
                   0.0e + 00
Match length
                   442
                   97
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
                  complete sequence
Seq. No.
                  149685
Seq. ID
                  LIB3175-030-P1-K1-D1
Method
                  BLASTN
NCBI GI
                  q1086460
BLAST score
                  365
                  0.0e + 00
E value
Match length
                  437
% identity
```

19026

Arabidopsis thaliana Columbia ecotype metallothionein

NCBI GI

```
(MT1c) gene, complete cds
Seq. No.
                  149686
Seq. ID
                  LIB3175-030-P1-K1-D10
                  BLASTN
Method
NCBI GI
                  q2618599
BLAST score
                  46
                  1.0e-16
E value
Match length
                  95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MBD2, complete sequence [Arabidopsis thaliana]
                  149687
Seq. No.
Seq. ID
                  LIB3175-030-P1-K1-D11
Method
                  BLASTX
                  q2062164
NCBI GI
                  709
BLAST score
                  4.0e-75
E value
Match length
                  140
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  149688
Seq. No.
Seq. ID
                  LIB3175-030-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q4164398
                  209
BLAST score
                  2.0e-16
E value
Match length
                  150
% identity
                  (AL035248) serine threonine-protein kinase
NCBI Description
                  [Schizosaccharomyces pombe]
Seq. No.
                  149689
Seq. ID
                  LIB3175-030-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q2506443
BLAST score
                  640
E value
                  3.0e-67
Match length
                  130
                  97
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi_2117520_pir__JQ1285
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi_1402885_emb_CAA66816_ (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                  (phosphorylating) [Arabidopsis thaliana]
Seq. No.
                  149690
Seq. ID
                  LIB3175-030-P1-K1-D4
Method
                  BLASTX
```

19027

g2501188

% identity

% identity

```
BLAST score
E value
                  4.0e-67
Match length
                  145
% identity
                  89
                  THIAZOLE BIOSYNTHETIC ENZYME >gi_2129750_pir__S71191 TH14
NCBI Description
                  protein homolog - Arabidopsis thaliana >gi 1113783 (U17589)
                  Thil protein [Arabidopsis thaliana]
Seq. No.
                  149691
Seq. ID
                  LIB3175-030-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q2851508
BLAST score
                  724
E value
                  6.0e-77
Match length
                  139
                  99
% identity
                  60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to
NCBI Description
                  ribosomal protein L21 (gb L38826). ESTs
                  gb_AA395597,gb_ATTS5197 come from this gene. [Arabidopsis
                  thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                  L21 [Arabidopsis thaliana]
Seq. No.
                  149692
Seq. ID
                  LIB3175-030-P1-K1-D6
Method
                  BLASTX
```

 Seq. No.
 149692

 Seq. ID
 LIB3175-030-P1-K1-D6

 Method
 BLASTX

 NCBI GI
 g2252841

 BLAST score
 63

 E value
 2.0e-62

 Match length
 152

NCBI Description (AF013293) No definition line found [Arabidopsis thaliana]

 Seq. No.
 149693

 Seq. ID
 LIB3175-030-P1-K1-D7

 Method
 BLASTX

 NCBI GI
 g4581146

 BLAST score
 601

 E value
 2.0e-62

 Match length
 131

NCBI Description (AC006919) putative fructose-bisphosphate aldolase,

cytoplasmic [Arabidopsis thaliana]

Seq. No. 149694

Seq. ID LIB3175-030-P1-K1-D8

Method BLASTN
NCBI GI g3176695
BLAST score 208
E value 1.0e-113
Match length 451
% identity 96

NCBI Description Arabidopsis thaliana chromosome I BAC F14J9 genomic

sequence contains phyA marker, complete sequence

[Arabidopsis thaliana]

Seq. No. 149695

Seq. ID LIB3175-030-P1-K1-D9

```
Method
                  BLASTX
NCBI GI
                  g112739
BLAST score
                  418
E value
                  4.0e-41
Match length
                  120
                  70
% identity
NCBI Description
                  2S SEED STORAGE PROTEIN 2 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi_68854_pir__NWMU2 2S albumin 2 precursor -
                  Arabidopsis thaliana >gi_166615 (M22033) albumin 2S subunit
                  2 precursor [Arabidopsis thaliana] >gi_395205_emb_CAA80871_
                  (Z24745) 2S albumin isoform 2 [Arabidopsis thaliana]
                  >gi_4490711_emb_CAB38845.1_ (AL035680) NWMU2-2S albumin 2
                  precursor [Arabidopsis thaliana]
Seq. No.
                  149696
Seq. ID
                  LIB3175-030-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q1076668
BLAST score
                  448
E value
                  1.0e-44
Match length
                  130
% identity
NCBI Description
                  NADH dehydrogenase (EC 1.6.99.3) - potato
                  >gi 639834 emb CAA58823 (X83999) NADH dehydrogenase
                  [Solanum tuberosum]
                  149697
Seq. No.
                  LIB3175-030-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3201625
BLAST score
                  272
                  6.0e-24
E value
Match length
                  67
% identity
                  78
                  (AC004669) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  149698
                  LIB3175-030-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3451065
BLAST score
                  634
E value
                  2.0e-66
Match length
                  126
% identity
                  (AL031326) water channel - like protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  149699
Seq. ID
                  LIB3175-030-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  q4512646
BLAST score
                  224
E value
                  1.0e-123
Match length
                  286
% identity
                  94
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F23N11 genomic
                  sequence, complete sequence
```

NCBI Description

```
149700
Seq. No.
Seq. ID
                  LIB3175-030-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4586265
                  533
BLAST score
E value
                  2.0e-54
                  123
Match length
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  149701
Seq. No.
Seq. ID
                  LIB3175-030-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  a2924651
                  287
BLAST score
E value
                  1.0e-160
Match length
                  410
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2A18, complete sequence [Arabidopsis thaliana]
                  149702
Seq. No.
Seq. ID
                  LIB3175-030-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4741940
BLAST score
                  624
E value
                  3.0e-65
                  139
Match length
                  60
% identity
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
                  149703
Seq. No.
                  LIB3175-030-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  54
                  2.0e-78
E value
                  150
Match length
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi 81603 pir_A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540_ (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  149704
Seq. ID
                  LIB3175-030-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  q2760164
BLAST score
                  397
E value
                  0.0e + 00
Match length
                  429
% identity
```

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

NCBI GI

g710625

```
K18P6, complete sequence [Arabidopsis thaliana]
                  149705
Seq. No.
                  LIB3175-030-P1-K1-F12
Seq. ID
                  BLASTX
Method
                  g119350
NCBI GI
                  599
BLAST score
                  2.0e-62
E value
                  116
Match length
                  100
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
                  [Arabidopsis thaliana]
                  >gi_4581151_gb_AAD24635.1 AC006919 13 (AC006919) enolase
                  (2-phospho-D-glycerate hydroylase); identical to P25696
                  [Arabidopsis thaliana]
                  149706
Seq. No.
                  LIB3175-030-P1-K1-F2
Seq. ID
Method
                  BLASTX
                  g4263519
NCBI GI
                  443
BLAST score
                  3.0e-44
E value
                  91
Match length
                  97
% identity
NCBI Description
                  (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis
                  thaliana]
                  149707
Seq. No.
                  LIB3175-030-P1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589427
                  429
BLAST score
                  0.0e + 00
E value
                  453
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFG13, complete sequence
                  149708
Seq. No.
                  LIB3175-030-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2498883
BLAST score
                  481
                  2.0e-48
E value
                  134
Match length
                  68
% identity
                  SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150)
NCBI Description
                  >gi 1173905 (U41371) spliceosome associated protein [Homo
                  sapiens]
                  149709
Seq. No.
                  LIB3175-030-P1-K1-F6
Seq. ID
Method
                  BLASTN
```

```
BLAST score
E value
                  1.0e-122
Match length
                  293
% identity
                  95
NCBI Description Arabidopsis thaliana mRNA for ERD15 protein, complete cds
                  149710
Seq. No.
                  LIB3175-030-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4558678
BLAST score
                  208
                  1.0e-16
E value
Match length
                  86
% identity
                  44
NCBI Description (AC006586) unknown protein [Arabidopsis thaliana]
                  149711
Seq. No.
                  LIB3175-030-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3608155
BLAST score
                  498
                  2.0e-50
E value
Match length
                  106
% identity
                  (ACO05314) putative RNA helicase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  149712
                  LIB3175-030-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q544425
BLAST score
                  416
                  6.0e-41
E value
Match length
                  83
% identity
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                  >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8)
                  - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                  glycine rich protein [Arabidopsis thaliana] >gi_166658
                  (L04171) ORF [Arabidopsis thaliana] >gi 166839 (L00649)
                  RNA-binding protein [Arabidopsis thaliana]
Seq. No.
                  149713
Seq. ID
                  LIB3175-030-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q730526
BLAST score
                  503
E value
                  4.0e-51
Match length
                  118
% identity
                  79
NCBI Description
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
                  >gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                  thaliana >gi_404166 emb_CAA53005_ (X75162) BBC1 protein
                  [Arabidopsis thaliana]
Seq. No.
                  149714
                  LIB3175-030-P1-K1-G10
Seq. ID
Method
                  BLASTX
```

```
NCBI GI
                   q529353
BLAST score
                   487
                   4.0e-49
E value
Match length
                   151
% identity
NCBI Description
                   (U12757) diphenol oxidase [Acer pseudoplatanus]
                   149715
Seq. No.
Seq. ID
                   LIB3175-030-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   q3702315
BLAST score
                   180
                   1.0e-96
E value
Match length
                   462
% identity
                   97
NCBI Description
                   Arabidopsis thaliana chromosome II BAC T3F17 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   149716
Seq. No.
Seq. ID
                   LIB3175-030-P1-K1-G2
Method
                   BLASTN
NCBI GI
                   q2244991
BLAST score
                   205
E value
                   1.0e-111
Match length
                   352
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   149717
Seq. No.
Seq. ID
                   LIB3175-030-P1-K1-G3
Method
                   BLASTN
NCBI GI
                   q4160401
BLAST score
                   38
E value
                   6.0e-12
Match length
                   62
% identity
                   90
NCBI Description
                  Zea mays eIF-5 gene, exons 1-2
                   149718
Seq. No.
Seq. ID
                   LIB3175-030-P1-K1-G4
Method
                   BLASTN
NCBI GI
                   g4455168
BLAST score
                   329
E value
                   0.0e + 00
Match length
                   465
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10
                   (ESSAII project)
Seq. No.
                   149719
Seq. ID
                   LIB3175-030-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   g3930517
BLAST score
                   160
E value
                   8.0e-11
Match length
                   106
```

```
% identity
                  40
                   (AF059906) ubiquitin fusion degradation protein-2
NCBI Description
                   [Schizosaccharomyces pombe]
                  149720
Seq. No.
                  LIB3175-030-P1-K1-G6
Seq. ID
                  BLASTN
Method
                  g2947056
NCBI GI
                  266
BLAST score
                  1.0e-148
E value
                  418
Match length
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC T20F6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  149721
Seq. No.
                  LIB3175-030-P1-K1-G7
Seq. ID
                  BLASTX
Method
                  g132939
NCBI GI
                  521
BLAST score
                  3.0e-53
E value
                  108
Match length
                  91
% identity
                  60S RIBOSOMAL PROTEIN L3 >gi_81657_pir__JQ0771 ribosomal
NCBI Description
                  protein L3 (ARP1) - Arabidopsis thaliana >gi_166858
                   (M32654) ribosomal protein [Arabidopsis thaliana]
                  149722
Seq. No.
Seq. ID
                  LIB3175-030-P1-K1-G9
                  BLASTX
Method
                  g1841355
NCBI GI
BLAST score
                  198
                   3.0e-15
E value
                  117
Match length
                   46
% identity
                   (D85381) cytochrome c oxidase subunit Vb precursor [Oryza
NCBI Description
                   sativa]
                   149723
Seq. No.
                   LIB3175-030-P1-K1-H1
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4539408
BLAST score
                   250
                   2.0e-21
E value
Match length
                   73
% identity
                   (AL049524) putative alpha NAC [Arabidopsis thaliana]
NCBI Description
                   149724
Seq. No.
                   LIB3175-030-P1-K1-H11
Seq. ID
                   BLASTN
Method
                   g3212846
NCBI GI
BLAST score
                   412
E value
                   0.0e + 00
Match length
                   428
% identity
                  Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
```

## sequence, complete sequence [Arabidopsis thaliana]

 Seq. No.
 149725

 Seq. ID
 LIB3175-030-P1-K1-H12

 Method
 BLASTN

 NCBI GI
 g4756963

 BLAST score
 326

 E value
 0.0e+00

 Match length
 384

 % identity
 95

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F10M23

(ESSA project)

Seq. No. 149726

Seq. ID LIB3175-030-P1-K1-H3

Method BLASTX
NCBI GI g549010
BLAST score 422
E value 1.0e-41
Match length 93
% identity 91

NCBI Description EUKARYOTIC PEPTIDE CHAIN RELEASE FACTOR SUBUNIT 1 (ERF1) (OMNIPOTENT SUPPRESSOR PROTEIN 1 HOMOLOG) (SUP1 HOMOLOG)

>gi\_322554\_pir\_\_S31328 omnipotent suppressor protein SUP1

homolog (clone G18) - Arabidopsis thaliana

>gi\_16514\_emb\_CAA49172\_ (X69375) similar to yeast

omnipotent suppressor protein SUP1 (SUP45) [Arabidopsis thaliana] >gi\_1402882\_emb\_CAA66813\_ (X98130) eukaryotic early release factor subunit 1-like protein [Arabidopsis thaliana] > in 1405040 emb\_CAA66813\_ (X07406) = DE1 3

thaliana] >gi\_1495249\_emb\_CAA66118\_ (X97486) eRF1-3

[Arabidopsis thaliana]

Seq. No. 149727

Seq. ID LIB3175-030-P1-K1-H4

Method BLASTX
NCBI GI g3169173
BLAST score 740
E value 8.0e-79
Match length 139
% identity 99

NCBI Description (AC004401) putative serine carboxypeptidase I [Arabidopsis

thaliana] >gi\_3445215 (AC004786) putative serine

carboxypeptidase I [Arabidopsis thaliana]

Seq. No. 149728

Seq. ID LIB3175-030-P1-K1-H5

Method BLASTX
NCBI GI g1076316
BLAST score 594
E value 9.0e-62
Match length 117
% identity 97

NCBI Description drought-induced protein Di19 - Arabidopsis thaliana

>gi\_469110\_emb\_CAA55321\_ (X78584) Di19 [Arabidopsis

thaliana]

Seq. No. 149729

```
Seq. ID
                   LIB3175-030-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   q4544399
BLAST score
                   318
E value
                   2.0e-29
Match length
                   123
% identity
NCBI Description
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
                   thaliana]
Seq. No.
                   149730
Seq. ID
                   LIB3175-030-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q3080442
BLAST score
                   612
                   8.0e-64
E value
Match length
                   129
% identity
                   (AL022605) putative protein [Arabidopsis thaliana]
NCBI Description
                   149731
Seq. No.
                   LIB3175-031-P1-K1-A1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2252848
BLAST score
                   45
E value
                   4.0e-16
Match length
                   231
% identity
                  Arabidopsis thaliana BAC TM018A10
NCBI Description
Seq. No.
                   149732
                   LIB3175-031-P1-K1-A11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4336756
BLAST score
                   525
E value
                   1.0e-53
Match length
                   103
% identity
                   (AF104453) catalase [Brassica juncea]
NCBI Description
                   149733
Seq. No.
Seq. ID
                   LIB3175-031-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   q4538963
BLAST score
                   518
                   8.0e-53
E value
Match length
                   130
% identity
                   (AL049488) chlorophyll a/b-binding protein-like
NCBI Description
                   [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
Seq. No.
                   149734
Seq. ID
                   LIB3175-031-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q4580389
BLAST score
                   636
```

```
1.0e-66
E value
Match length
                   134
                   58
% identity
NCBI Description
                   (AC007171) unknown protein [Arabidopsis thaliana]
                   149735
Seq. No.
                   LIB3175-031-P1-K1-A4
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2827710
BLAST score
                   771
                   2.0e-82
E value
                                      Match length
                   147
                   97
% identity
                   (AL021684) lysosomal Pro-X carboxypeptidase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   149736
Seq. No.
                   LIB3175-031-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   g1352681
NCBI GI
BLAST score
                   92
                   8.0e-56
E value
                   111
Match length
                   100
% identity
                   PROTEIN PHOSPHATASE 2C (PP2C) >gi_1076391_pir__S55457 phosphoprotein phosphatase (EC 3.1.3.16) 2C - Arabidopsis
NCBI Description
                   thaliana >gi_633028_dbj_BAA07287_ (D38109) protein
                   phosphatase 2C [Arabidopsis thaliana]
                   149737
Seq. No.
                   LIB3175-031-P1-K1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4220638
BLAST score
                   47
                   4.0e-18
E value
                   71
Match length
% identity
                   89
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MIF21, complete sequence [Arabidopsis thaliana]
                   149738
Seq. No.
Seq. ID
                   LIB3175-031-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   g1370186
BLAST score
                   586
E value
                   8.0e-61
Match length
                   114
% identity
                   98
NCBI Description
                   (Z73942) RAB7C [Lotus japonicus]
                   149739
Seq. No.
                   LIB3175-031-P1-K1-A8
Seq. ID
Method
                   BLASTX
                   g1256509
NCBI GI
                   266
BLAST score
                   3.0e-23
E value
                   90
Match length
```

```
% identity
NCBI Description
                   (X92943) pectate lyase [Musa acuminata]
Seq. No.
                   149740
Seq. ID
                   LIB3175-031-P1-K1-A9
Method
                   BLASTX
NCBI GI
                   g3927825
BLAST score
                   545
E value
                   6.0e-56
Match length
                   115
% identity
NCBI Description
                   (AC005727) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                   149741
Seq. ID
                   LIB3175-031-P1-K1-B12
Method
                   BLASTN
NCBI GI
                   q4589430
BLAST score
                   132
E value
                   5.0e-68
Match length
                   372
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MLD14, complete sequence
Seq. No.
                   149742
Seq. ID
                   LIB3175-031-P1-K1-B2
Method
                   BLASTN
NCBI GI
                   g3426033
BLAST score
                   182
E value
                   8.0e-98
Match length
                   426
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC F12C20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149743
Seq. ID
                   LIB3175-031-P1-K1-B3
Method
                   BLASTX
NCBI GI
                   q1175013
BLAST score
                   630
E value
                   6.0e-66
Match length
                   139
% identity
NCBI Description
                   PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi 629542 pir__S44084
                   plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                   >gi_472877_emb_CAA53477_ (X75883) plasma membrane intrinsic
                   protein 2a [Arabidopsis thaliana]
                   149744
Seq. No.
Seq. ID
                   LIB3175-031-P1-K1-B5
Method
                   BLASTN
NCBI GI
                   q4589438
BLAST score
                   131
E value
                   2.0e-67
Match length
                  151
% identity
                   97
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQJ2, complete sequence
                  149745
Seq. No.
                  LIB3175-031-P1-K1-B7
Seq. ID
Method
                  BLASTN
                  g3776000
NCBI GI
                  272
BLAST score
                  1.0e-151
E value
                  283
Match length
                  99
% identity
                  Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH12
NCBI Description
                  149746
Seq. No.
                  LIB3175-031-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3169173
BLAST score
                  415
                  5.0e-41
E value
                  97
Match length
                  85
% identity
                  (AC004401) putative serine carboxypeptidase I [Arabidopsis
NCBI Description
                  thaliana] >gi 3445215 (AC004786) putative serine
                  carboxypeptidase I [Arabidopsis thaliana]
Seq. No.
                  149747
Seq. ID
                  LIB3175-031-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2435515
BLAST score
                  269
                  1.0e-23
E value
                  53
Match length
                  94
% identity
                  (AF024504) No definition line found [Arabidopsis thaliana]
NCBI Description
                  149748
Seq. No.
Seq. ID
                  LIB3175-031-P1-K1-C1
Method
                  BLASTX
                  g1170040
NCBI GI
BLAST score
                  444
                  4.0e-44
E value
Match length
                  86
% identity
                  100
                  GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE)
NCBI Description
                  >gi 451198 dbj BAA03137 (D14049) glutathione reductase
                  precursor [Arabidopsis thaliana] >gi_1944448_dbj_BAA19653_
                  (D89620) glutathione reductase precursor [Arabidopsis
                  thaliana] >gi_740576_prf__2005376A glutathione reductase
                  [Arabidopsis thaliana]
                  149749
Seq. No.
Seq. ID
                  LIB3175-031-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1209655.
BLAST score
                  252
E value
                  1.0e-21
Match length
                  95
```

```
% identity
NCBI Description
                        (U37428) gl1 [Zea mays]
Seq. No.
                         149750
Seq. ID
                         LIB3175-031-P1-K1-C12
Method
                         BLASTX
NCBI GI
                         q2246621
BLAST score
                         573
E value
                         2.0e-59
Match length
                         119
% identity
                         96
                         (AF004393) salt-stress induced tonoplast intrinsic protein
NCBI Description
                         [Arabidopsis thaliana]
Seq. No.
                         149751
                         LIB3175-031-P1-K1-C2
Seq. ID
Method
                         BLASTX
NCBI GI
                         g122085
BLAST score
                         515
E value
                         2.0e-52
Match length
                         121
% identity
                        HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_(X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_(X13680) histone H3
NCBI Description
                         (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3
                         (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays]
                         >gi_168497 (M13379) h\overline{i}stone H3 [Zea mays] >gi_168506
                         (M3\overline{5}388) histone H3 [Zea mays] >gi_169655 (M7\overline{7}493) histone
                         H3 [Petroselinum crispum] >gi 169657 (M77494) histone H3
                         [Petroselinum crispum] >gi_169657 (M77494) histone H3
[Petroselinum crispum] >gi_169659 (M77495) histone H3
[Petroselinum crispum] >gi_387565 (M17130) histone H3
[Arabidopsis thaliana] >gi_387567 (M17131) histone H3
[Arabidopsis thaliana] >gi_886738 emb_CAA59111 (X84377)
                         histone 3 [Zea mays] >gi 1\overline{040764} (M35\overline{387}) histone H3
                         [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3
                         homolog [Brassica napus] >gi 1531754 emb CAA57811 (X82414)
                         Histone H3 [Asparagus officinalis] >\overline{g}i_1\overline{16}67592 (U77296)
                         histone 3 [Oryza sativa] >gi 3249101 (AC003114) Match to
                         histone H3 gene gb M17131 and gb M35387 from A. thaliana.
                         ESTs gb H76511 gb H76255, gb AA712452, gb N65260 and
                         gb T42306 come from this gene. [Arabidopsis thaliana]
                         >gi 225459_prf 1303352A histone H3 [Helicoverpa zea]
>gi 225839_prf 1314298B histone H3 [Arabidopsis thaliana]
Seq. No.
                         149752
Seq. ID
                         LIB3175-031-P1-K1-C3
Method
                         BLASTX
NCBI GI
                         g4337175
BLAST score
                         495
E value
                         4.0e-50
Match length
                         126
                         78
% identity
                         (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
NCBI Description
                         gb T04111, gb R841\overline{8}0, gb R654\overline{2}8, gb T444\overline{3}9, gb T76570,
```

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```
gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and
                  gb_AA720210 come from this gene. [Arabidopsis thaliana]
                  149753
Seq. No.
                  LIB3175-031-P1-K1-C4
Seq. ID
                  BLASTX
Method
                  g3785989
NCBI GI
BLAST score
                  517
                  6.0e-53
E value
Match length
                  99
                  100
% identity
                  (AC005560) unknown protein [Arabidopsis thaliana]
NCBI Description
                  149754
Seq. No.
                  LIB3175-031-P1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4049332
BLAST score
                  137
                  3.0e-71
E value
                  198
Match length
                  96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
NCBI Description
                  (ESSAII project)
Seq. No.
                  149755
Seq. ID
                  LIB3175-031-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g4263818
BLAST score
                  301
                  2.0e-27
E value
                  82
Match length
                  66
% identity
                  (AC006067) unknown protein [Arabidopsis thaliana]
NCBI Description
                  149756
Seq. No.
                  LIB3175-031-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2252857
BLAST score
                  272
                  5.0e-24
E value
Match length
                  113
% identity
                   (AF013294) similar to acidic ribosomal protein p1
NCBI Description
                   [Arabidopsis thaliana]
                  149757
Seq. No.
                  LIB3175-031-P1-K1-C8
Seq. ID
Method
                  BLASTX
                  g4006878
NCBI GI
BLAST score
                  327
E value
                  9.0e-31
                  77
Match length
                  82
% identity
                  (Z99707) MAP3K-like protein kinase [Arabidopsis thaliana]
NCBI Description
                  149758
Seq. No.
                  LIB3175-031-P1-K1-D1
Seq. ID
```

```
Method
                  BLASTX
NCBI GI
                   q4584255
BLAST score
                   215
E value
                   2.0e-17
Match length
                   49
% identity
                   76
NCBI Description
                   (Y18471) SINAlp [Vitis vinifera]
Seq. No.
                   149759
Seq. ID
                  LIB3175-031-P1-K1-D10
Method
                  BLASTN
NCBI GI
                  g2827513
BLAST score
                  193
E value
                   1.0e-104
Match length
                   255
                   98
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16
                   (ESSAII project)
Seq. No.
                   149760
Seq. ID
                  LIB3175-031-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  q405130
BLAST score
                   310
E value
                   1.0e-174
Match length
                   342
% identity
                   98
NCBI Description
                  Arabidopsis thaliana nuclear-encoded chloroplast stromal
                  cyclophilin (ROC4) mRNA, complete cds
Seq. No.
                   149761
                  LIB3175-031-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3122387
BLAST score
                   515
E value
                   2.0e-52
Match length
                  109
% identity
                   90
NCBI Description
                  WD-40 REPEAT PROTEIN MSI1 >gi 2394229 (AF016846) WD-40
                  repeat protein [Arabidopsis thaliana]
Seq. No.
                  149762
Seq. ID
                  LIB3175-031-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g3435279
BLAST score
                   489
E value
                  2.0e-49
Match length
                  118
% identity
NCBI Description
                   (AF082391) protein kinase homolog [Arabidopsis thaliana]
Seq. No.
                  149763
Seq. ID
                  LIB3175-031-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  g2781354
BLAST score
                  576
E value
                  8.0e-60
```

```
Match length
                  118
% identity
NCBI Description
                   (AC003113) F2401.10 [Arabidopsis thaliana]
Seq. No.
                  149764
                  LIB3175-031-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4502315
BLAST score
                  116
                  1.0e-09
E value
Match length
                  101
                   35
% identity
NCBI Description
                  ATPase, H+ transporting, lysosomal (vacuolar proton pump)
                  42kD >gi_401329_sp_P21283_VATC_HUMAN VACUOLAR ATP SYNTHASE
                  SUBUNIT C (V-ATPASE C SUBUNIT) >gi_542836_pir__JN0907
                  H+-transporting ATPase (EC 3.6.1.35) chain C, vacuolar -
                  human >gi_37643_emb_CAA48903_ (X69151) vacuolar
                  proton-ATPase [Homo sapiens]
                  149765
Seq. No.
                  LIB3175-031-P1-K1-D6
Seq. ID
Method
                  BLASTX
                  g404670
NCBI GI
BLAST score
                  539
E value
                  3.0e-55
Match length
                  121
% identity
                  88
NCBI Description
                   (L21154) phytochrome A [Arabidopsis thaliana] >gi_3482934
                   (AC003970) phytochrome A [Arabidopsis thaliana]
                  149766
Seq. No.
                  LIB3175-031-P1-K1-D8
Seq. ID
Method
                  BLASTX
                  g1669389
NCBI GI
BLAST score
                  392
E value
                  4.0e-38
Match length
                  75
% identity
NCBI Description
                  (U42007) actin 8 [Arabidopsis thaliana]
                  149767
Seq. No.
Seq. ID
                  LIB3175-031-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g1669389
BLAST score
                  167
                  9.0e-12
E value
Match length
                  67
% identity
NCBI Description
                  (U42007) actin 8 [Arabidopsis thaliana]
                  149768
Seq. No.
                  LIB3175-031-P1-K1-E1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2160155.
BLAST score
                  114
                  2.0e-57
E value
Match length
                  202
```

```
% identity
NCBI Description
                  Sequence of BAC F21M12 from Arabidopsis thaliana chromosome
                   1, complete sequence [Arabidopsis thaliana]
                   149769
Seq. No.
                  LIB3175-031-P1-K1-E10
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4582428
BLAST score
                  222
E value
                   1.0e-121
                   369
Match length
                   98
% identity
                  Arabidopsis thaliana chromosome II BAC T18C20 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   149770
                  LIB3175-031-P1-K1-E11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3063472
BLAST score
                   598
E value
                   3.0e-62
Match length
                   119
% identity
                   94
NCBI Description
                   (AC003981) F22013.34 [Arabidopsis thaliana]
Seq. No.
                  149771
                  LIB3175-031-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                   g115385
BLAST score
                   442
E value
                   4.0e-44
                   89
Match length
                   97
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                   149772
Seq. No.
Seq. ID
                  LIB3175-031-P1-K1-E2
Method
                  BLASTX
NCBI GI
                   g4490332
BLAST score
                   501
E value
                   5.0e-73
Match length
                  145
% identity
                   98
NCBI Description
                   (AL035656) putative protein [Arabidopsis thaliana]
Seq. No.
                  149773
Seq. ID
                  LIB3175-031-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score
                  326
E value
                  1.0e-30
Match length
                  66
                  100
% identity
NCBI Description
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
```

```
Seq. No.
                   149774
Seq. ID
                   LIB3175-031-P1-K1-E5
                   BLASTN
Method
NCBI GI
                   q3985957
BLAST score
                   210
E value
                   1.0e-114
Match length
                   444
                   98
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MYN8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149775
                   LIB3175-031-P1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2435510
BLAST score
                   239
E value
                   1.0e-132
Match length
                   424
                   100
% identity
NCBI Description
                 Arabidopsis thaliana BAC TM017A05
                   149776
Seq. No.
Seq. ID
                  LIB3175-031-P1-K1-E7
Method
                   BLASTX
NCBI GI
                   q2244845
BLAST score
                   593
E value
                   1.0e-61
Match length
                   144
                   85
% identity
NCBI Description
                   (Z97337) cytosolic O-acetylserine(thiol)lyase (EC 4.2.99.8)
                   [Arabidopsis thaliana]
                   149777
Seq. No.
                   LIB3175-031-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1710114
BLAST score
                   397
                   1.0e-38
E value
Match length
                   123
% identity
NCBI Description
                   (U53865) PRH26 [Arabidopsis thaliana]
                   149778
Seq. No.
Seq. ID
                  LIB3175-031-P1-K1-F1
Method
                  BLASTX
NCBI GI
                   g2739389
BLAST score
                   162
E value
                   1.0e-11
Match length
                  57
% identity
                   54
NCBI Description
                  (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
                  149779
Seq. No.
Seq. ID
                  LIB3175-031-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g2245093
BLAST score
                  94
```

```
E value
                   6.0e-45
Match length
                   122
% identity
                   84
NCBI Description
                   (Z97343) membrane channel protein [Arabidopsis thaliana]
Seq. No.
                   149780
                   LIB3175-031-P1-K1-F11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2191126
BLAST score
                   354
E value
                   0.0e + 00
Match length
                   358
% identity
                   100
NCBI Description
                  Arabidopsis thaliana BAC IG002N01
                   149781
Seq. No.
Seq. ID
                   LIB3175-031-P1-K1-F12
Method.
                   BLASTX
NCBI GI
                   q3983125
BLAST score
                   161
E value
                   6.0e-11
Match length
                   51
% identity
NCBI Description
                   (AF097648) phosphate/triose-phosphate translocator
                   precursor [Arabidopsis thaliana]
Seq. No.
                   149782
Seq. ID
                   LIB3175-031-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   g4531433
BLAST score
                   411
E value
                   0.0e+00
Match length
                   426
% identity
                   99
NCBI Description
                   Arabidopsis thaliana chromosome II P1 MFL8 genomic
                   sequence, complete sequence
Seq. No.
                   149783
Seq. ID
                   LIB3175-031-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   g1708313
BLAST score
                   552
E value
                   8.0e-57
Match length
                   117
                   97
% identity
NCBI Description
                   HEAT SHOCK PROTEIN 81-3 (HSP81-3) >gi 999396 bbs 163637
                   (S77849) heat-shock Protein=HSP81-3 [Arabidopsis
                   thaliana=thale-cress, Peptide, 699 aa] [Arabidopsis
                   thaliana]
                   149784
Seq. No.
                   LIB3175-031-P1-K1-F6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3176666
BLAST score
                   260
E value
                   1.0e-22
Match length
                   119
```

```
% identity
                  52
NCBI Description
                  (ACO04393) Contains similarity to hypothetical protein
                  gb Z97343 from A. thaliana. [Arabidopsis thaliana]
                  149785
Seq. No.
                  LIB3175-031-P1-K1-F7
Seq. ID
Method
                  BLASTX
                  g2244974
NCBI GI
BLAST score
                  583
E value
                  2.0e-60
                  138
Match length
% identity
NCBI Description
                  (Z97340) similarity to pore protein Pisum sativum
                  [Arabidopsis thaliana]
                  149786
Seq. No.
                  LIB3175-031-P1-K1-F8
Seq. ID
                  BLASTX
Method
                  g115783
NCBI GI
BLAST score
                  644
E value
                  1.0e-67
Match length
                  124
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_
                                                             (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  149787
Seq. No.
                  LIB3175-031-P1-K1-G10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1402874
BLAST score
                  166
E value
                  3.0e-88
Match length
                  347
                  98
% identity
NCBI Description A.thaliana 81kb genomic sequence
                  149788
Seg. No.
                  LIB3175-031-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4586265
BLAST score
                  498
E value
                  2.0e-50
                  124
Match length
% identity
NCBI Description
                  (AL049640) putative protein [Arabidopsis thaliana]
                  149789
Seq. No.
                  LIB3175-031-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4586265
BLAST score
                  96
                  2.0e-23
E value
Match length
                  111
% identity
                  57
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
```

```
149790
Seq. No.
                  LIB3175-031-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1155261
BLAST score
                  600
                  2.0e-62
E value
                  120
Match length
                  98
% identity
                  (U40217) eukaryotic release factor 1 homolog [Arabidopsis
NCBI Description
                  thaliana]
                  149791
Seq. No.
                  LIB3175-031-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4432856
BLAST score
                  618
                  1.0e-64
E value
                  118
Match length
                  100
% identity
                  (AC006300) putative 2A6 protein [Arabidopsis thaliana]
NCBI Description
                  149792
Seq. No.
                  LIB3175-031-P1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220643
BLAST score
                  115
E value
                  7.0e-58
                  429
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MWD22, complete sequence [Arabidopsis thaliana]
                  149793
Seq. No.
                  LIB3175-031-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  618
E value
                  1.0e-64
                  138
Match length
                  87
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi_81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  149794
                  LIB3175-031-P1-K1-G8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4580530
BLAST score
                  267
E value
                  1.0e-148
Match length
                  374
% identity
NCBI Description
                  Arabidopsis thaliana scarecrow-like 14 (SCL14) mRNA,
                  partial cds
```

Method

BLASTN

```
149795
Seq. No.
                  LIB3175-031-P1-K1-H10
Seq. ID
                  BLASTX
Method
                  g4586265
NCBI GI
BLAST score
                  409
                   4.0e-40
E value
                  115
Match length
                  71
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  149796
Seq. No.
                  LIB3175-031-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  g1402910
NCBI GI
BLAST score
                   714
                   9.0e-76
E value
                  138
Match length
                   98
% identity
                   (X98316) peroxidase [Arabidopsis thaliana]
NCBI Description
                  >gi 1429223 emb_CAA67550_ (X99096) peroxidase [Arabidopsis
                  thaliana]
                  149797
Seq. No.
                  LIB3175-031-P1-K1-H4
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3047100
BLAST score
                  81
                   6.0e-38
E value
                  93
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana BAC F6N23
                  149798
Seq. No.
                  LIB3175-031-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2341034
BLAST score
                   633
                   2.0e-66
E value
Match length
                  126
                   100
% identity
                  (ACO00104) F19P19.13 [Arabidopsis thaliana]
NCBI Description
                  149799
Seq. No.
                  LIB3175-031-P1-K1-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4468976
BLAST score
                  265
                   1.0e-147
E value
Match length
                   377
                   97
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18
NCBI Description
                   (ESSA project)
                  149800
Seq. No.
                  LIB3175-031-P1-K1-H9
Seq. ID
```

```
NCBI GI
                   q4106339
BLAST score
                   344
                   0.0e + 00
E value
Match length
                   368
                   98
% identity
NCBI Description
                   Arabidopsis thaliana protein phosphatase 2A regulatory
                   subunit isoform B' delta mRNA, complete cds
Seq. No.
                   149801
Seq. ID
                   LIB3175-032-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q4581146
BLAST score
                   413
                   4.0e-51
E value
Match length
                   110
                   100
% identity
                   (AC006919) putative fructose-bisphosphate aldolase,
NCBI Description
                   cytoplasmic [Arabidopsis thaliana]
Seq. No.
                   149802
                   LIB3175-032-P1-K1-A12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4586265
BLAST score
                   526
E value
                   9.0e-54
Match length
                   137
% identity
                   (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   149803
Seq. ID
                   LIB3175-032-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   q120667
BLAST score
                   539
E value
                   3.0e-55
Match length
                   118
% identity
                   89
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
thaliana >gi_166706 (M64116) cystolic
                   glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                   thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                   dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   149804
Seq. ID
                   LIB3175-032-P1-K1-A3
Method
                   BLASTX
NCBI GI
                   q2811278
BLAST score
                   271
E value
                   7.0e-24
Match length
                   92
% identity
NCBI Description
                   (AF043284) expansin [Gossypium hirsutum]
Seq. No.
                   149805
Seq. ID
                   LIB3175-032-P1-K1-A4
```

```
Method
                   BLASTX
                   q730544
NCBI GI
                   325
BLAST score
E value
                   3.0e-30
                   122
Match length
                   78
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L24
                   149806
Seq. No.
                   LIB3175-032-P1-K1-A5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2182289
                   419
BLAST score
                   0.0e + 00
E value
Match length
                   419
                   100
% identity
                   Arabidopsis thaliana chromosome I BAC F11P17 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149807
                   LIB3175-032-P1-K1-A6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3688799
BLAST score
                   618
                   1.0e-64
E value
Match length
                   124
% identity
                   (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   149808
                   LIB3175-032-P1-K1-A7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4314378
BLAST score
                   405
E value
                   1.0e-39
Match length
                   113
% identity
NCBI Description
                  (AC006232) putative lipase [Arabidopsis thaliana]
                   149809
Seq. No.
                   LIB3175-032-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417103
BLAST score
                   645
E value
                   1.0e-67
Match length
                   129
% identity
                   HISTONE H3.2, MINOR >qi 282871 pir S24346 histone
NCBI Description
                   H3.3-like protein - Arabidopsis thaliana
                   >gi_16324_emb_CAA42957 (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958 (X60429)
                   histone H3.3 like protein [Arabidopsis thaliana] >gi 488563
                   (U09458) histone H3.2 [Medicago sativa] >gi 488567 (Ū09460)
                   histone H3.2 [Medicago sativa] >gi_488569 (\overline{U}09461) histone
                   H3.2 [Medicago sativa] >gi 488575 (U09464) histone H3.2
```

[Medicago sativa] >gi 488577 (U09465) histone H3.2

```
[Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone
H3 [Lolium temulentum] >gi 1435157 emb_CAA58445_ (X83422)
histone H3 variant H3.3 [Lycopersicon esculentum]
>gi 2558944 (AF024716) histone 3 [Gossypium hirsutum]
>gi 3273350 dbj_BAA31218 (AB015760) histone H3 [Nicotiana
tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa]
>gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia
```

coarctata] >gi\_4490754\_emb\_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_ (AL035708) Histon H3 [Arabidopsis thaliana]

```
Seq. No.
                   149810
                   LIB3175-032-P1-K1-A9
Seq. ID
Method
                   BLASTN
                   g4510323
NCBI GI
BLAST score
                   343
                   0.0e + 00
E value
Match length
                   347
```

100

% identity NCBI Description Arabidopsis thaliana BAC T7B11 from chromosome IV near 10

cM, complete sequence

```
149811
Seq. No.
Seq. ID
                   LIB3175-032-P1-K1-B10
Method
                   BLASTN
NCBI GI
                   q3046851
BLAST score
                   416
E value
                   0.0e + 00
```

Match length 416 100 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:

MIJ24, complete sequence [Arabidopsis thaliana]

```
149812
Seq. No.
                   LIB3175-032-P1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4314386
BLAST score
                   408
E value
                   6.0e - 40
```

Match length 110 % identity 75

NCBI Description (AC006232) putative rac GTPase activating protein [Arabidopsis thaliana]

Seq. No. 149813 Seq. ID LIB3175-032-P1-K1-B12 Method BLASTN NCBI GI q4755185 BLAST score 247 E value 1.0e-136

Match length 402 % identity

NCBI Description Arabidopsis thaliana chromosome II BAC F5G3 genomic sequence, complete sequence

Seq. No. 149814 Seq. ID LIB3175-032-P1-K1-B3

```
Method
                  BLASTX
NCBI GI
                  q4185505
                  467
BLAST score
                  8.0e-47
E value
Match length
                  115
                  77
% identity
                   (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                   [Brassica napus]
                  149815
Seq. No.
                  LIB3175-032-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3006148
BLAST score
                  162
                  4.0e-11
E value
Match length
                  42
                  76
% identity
                  (AL022299) rps9-b, 40s ribosomal protein s9
NCBI Description
                   [Schizosaccharomyces pombe]
Seq. No.
                  149816
                  LIB3175-032-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2252848
BLAST score
                  45
                  4.0e-16
E value
Match length
                  231
% identity
                  84
NCBI Description Arabidopsis thaliana BAC TM018A10
                  149817
Seq. No.
                  LIB3175-032-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2894574
BLAST score
                  640
E value
                  4.0e-67
Match length
                  122
% identity
                  100
                   (AL021890) peroxidase prxrl [Arabidopsis thaliana]
NCBI Description
                  >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                   [Arabidopsis thaliana]
Seq. No.
                  149818
                  LIB3175-032-P1-K1-B9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  273
E value
                  1.0e-152
Match length
                  418
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
Seq. No.
                  149819
                  LIB3175-032-P1-K1-C1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3873174
```

```
BLAST score
                   387
                   0.0e + 00
E value
Match length
                   399
                   99
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F14N23,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
                   149820
Seq. No.
                   LIB3175-032-P1-K1-C11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2656029
BLAST score
                   411
                   0.0e+00
E value
                   411
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   149821
Seq. No.
                   LIB3175-032-P1-K1-C12
Seq. ID
Method
                   BLASTX
                   g2494119
NCBI GI
BLAST score
                   719
                   2.0e-76
E value
Match length
                   138
                   100
% identity
                   (AC002376) EST gb_T04104 comes from this gene. [Arabidopsis
NCBI Description
                   thaliana]
                   149822
Seq. No.
                   LIB3175-032-P1-K1-C5
Seq. ID
Method
                   BLASTX
                   g4206197
NCBI GI
BLAST score
                   714
                   8.0e-76
E value
Match length
                   139
% identity
                   17
NCBI Description
                   (AF071527) putative pre-mRNA splicing factor [Arabidopsis
                   thaliana]
                   149823
Seq. No.
Seq. ID
                   LIB3175-032-P1-K1-C6
Method
                   BLASTX
                   g2623962
NCBI GI
                   598
BLAST score
                   3.0e-62
E value
Match length
                   138
% identity
                   (Y12540) isocitrate dehydrogenase (NADP+) [Apium
NCBI Description
                   graveolens]
                   149824
Seq. No.
Seq. ID
                   LIB3175-032-P1-K1-C7
Method
                   BLASTX
NCBI GI
                   g2129636
BLAST score
                   635
E value
                   1.0e-66
```

```
Match length
                   122
% identity
                   100
                  lipase - Arabidopsis thaliana >gi 1145627 (U38916) lipase
NCBI Description
                   [Arabidopsis thaliana]
                   149825
Seq. No.
                   LIB3175-032-P1-K1-C8
Seq. ID
                   BLASTN
Method
                   g3763915
NCBI GI
BLAST score
                   52
                   3.0e-20
E value
                   355
Match length
                   31
% identity
                  Arabidopsis thaliana chromosome II BAC F14B2 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149826
                   LIB3175-032-P1-K1-C9
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4519188
BLAST score
                   149
                   3.0e-78
E value
                   323
Match length
                  96
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K21L19, complete sequence
                   149827
Seq. No.
                  LIB3175-032-P1-K1-D1
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4689466
BLAST score
                   256
E value
                   1.0e-142
                   401
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T23015 genomic
NCBI Description
                   sequence, complete sequence
                   149828
Seq. No.
                   LIB3175-032-P1-K1-D10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4510323
BLAST score
                   392
E value
                   0.0e+00
Match length
                   396
                   100
% identity
                  Arabidopsis thaliana BAC T7B11 from chromosome IV near 10
NCBI Description
                   cM, complete sequence
Seq. No.
                   149829
Seq. ID
                  LIB3175-032-P1-K1-D11
Method
                  BLASTN
NCBI GI
                   q4589437
BLAST score
                   245
E value
                   1.0e-135
Match length
                   294
                   95
% identity
```

•



NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MPN9, complete sequence

Seq. No. 149830

Seq. ID LIB3175-032-P1-K1-D12

Method BLASTX
NCBI GI 94678328
BLAST score 410
E value 3.0e-40
Match length 85
% identity 95

NCBI Description (AL049658) aldehyde dehydrogenase (NAD+)-like protein

[Arabidopsis thaliana]

Seq. No.

Seq. ID LIB3175-032-P1-K1-D3

149831

Method BLASTN
NCBI GI g3860243
BLAST score 414
E value 0.0e+00
Match length 414
% identity 100

NCBI Description Arabidopsis thaliana chromosome II BAC F15K20 genomic

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 149832

Seq. ID LIB3175-032-P1-K1-D4

Method BLASTX
NCBI GI g1710581
BLAST score 625
E value 2.0e-65
Match length 127
% identity 96

NCBI Description 60S RIBOSOMAL PROTEIN L9 >gi\_2129720\_pir\_\_S71255 ribosomal

protein L9 - Arabidopsis thaliana  $>g_1^2$ 11 $\overline{07489}$ \_emb\_CAA63024\_ (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana]

Seq. No. 149833

Seq. ID LIB3175-032-P1-K1-D5

Method BLASTX
NCBI GI g2119846
BLAST score 678
E value 1.0e-71
Match length 129
% identity 98

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi\_16364\_emb\_CAA45790\_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi\_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi\_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 149834

Seq. ID LIB3175-032-P1-K1-D6

Method BLASTN NCBI GI g2252848

```
BLAST score
E value
                   4.0e-16
Match length
                   231
% identity
                   84
NCBI Description Arabidopsis thaliana BAC TM018A10
                   149835
Seq. No.
Seq. ID
                   LIB3175-032-P1-K1-D7
Method
                   BLASTN
NCBI GI
                   g1490552
BLAST score
                   262
E value
                   1.0e-145
Match length
                   358
% identity
                   94
NCBI Description
                   Arabidopsis thaliana S-adenosylmethionine decarboxylase
                   (SAMdc) mRNA, complete cds
Seq. No.
                   149836
Seq. ID
                   LIB3175-032-P1-K1-D8
Method
                   BLASTN
NCBI GI
                   g3860243
BLAST score
                   356
E value
                   0.0e + 00
Match length
                   417
% identity
                   95
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F15K20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149837
Seq. ID
                   LIB3175-032-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g2129752
BLAST score
                   661
E value
                   1.0e-69
Match length
                   130
% identity
                   100
                   thioredoxin - Arabidopsis thaliana >qi 992964 emb CAA84612
NCBI Description
                   (Z35475) thioredoxin [Arabidopsis thaliana]
Seq. No.
                   149838
Seq. ID
                   LIB3175-032-P1-K1-E1
Method
                   BLASTX
NCBI GI
                   g1169278
BLAST score
                   299
E value
                   4.0e-27
Match length
                   137
% identity
                   51
                  DEHYDRIN ERD14 >gi 556474 dbj BAA04569 (D17715) ERD14
NCBI Description
                   protein [Arabidopsis thaliana]
                   149839
Seq. No.
Seq. ID
                   LIB3175-032-P1-K1-E10
Method
                   BLASTX
NCBI GI
                   g1352463
BLAST score
                   544
E value
                   7.0e-56
Match length
                   120
```

```
MYO-INOSITOL-1-PHOSPHATE SYNTHASE (IPS) >gi 1161312
NCBI Description
                  (U04876) myo-inositol-1-phosphate synthase [Arabidopsis
                 149840
```

Seq. No.

% identity

LIB3175-032-P1-K1-E11 Seq. ID

Method BLASTX NCBI GI g3873710 BLAST score 351 E value 3.0e-33 Match length 101 % identity

NCBI Description (Z73102) predicted using Genefinder; similar to Zinc

finger, C2H2 type; cDNA EST EMBL: M89161 comes from this gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409

Seq. No. 149841

Seq. ID LIB3175-032-P1-K1-E12

Method BLASTX NCBI GI q1755162 BLAST score 704 E value 1.0e-74 Match length 138 99 % identity

NCBI Description (U75192) germin-like protein [Arabidopsis thaliana]

149842 Seq. No.

Seq. ID LIB3175-032-P1-K1-E2

Method BLASTN NCBI GI g2924651 BLAST score 326 E value 0.0e+00Match length 347

Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K2A18, complete sequence [Arabidopsis thaliana]

Seq. No. 149843

% identity

LIB3175-032-P1-K1-E3 Seq. ID

98

Method BLASTX NCBI GI q119143 BLAST score 481 E value 3.0e-68 Match length 133 % identity 100

NCBI Description ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)

> >gi\_81606\_pir\_\_S06724 translation elongation factor eEF-1 alpha chain - Arabidopsis thaliana >gi 295788 emb CAA34453 (X16430) elongation factor 1-alpha [Arabidopsis thaliana] >gi\_1369927\_emb\_CAA34454 (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi\_1369928\_emb\_CAA34455 (X16431) elongation factor 1-alpha [Arabidopsis thaliana] >gi 1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana] >gi 1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

BLAST score

Match length

% identity

Seq. No.

Seq. ID

Method NCBI GI

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

```
>gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
                  149844
                  LIB3175-032-P1-K1-E4
                  BLASTN
                  g3600029
                  64
                  1.0e-27
                  210
                  89
                  Arabidopsis thaliana BAC T12H2O
NCBI Description
                  149845
                  LIB3175-032-P1-K1-E5
                  BLASTX
                  g1175010
                  589
                  4.0e-61
                  125
                  92
                  PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__$44082
NCBI Description
                  plasma membrane intrinsic protein la - Arabidopsis thaliana
                  >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic
                  protein la [Arabidopsis thaliana]
                  149846
                  LIB3175-032-P1-K1-E6
                  BLASTX
                  g3785977
                  264
                  8.0e-46
                  108
                  88
                  (AC005560) putative growth regulator protein [Arabidopsis
NCBI Description
                  thaliana]
                  149847
                  LIB3175-032-P1-K1-E7
                  BLASTX
                  g112681
                  571
                  5.0e-59
                  132
```

Seq. No. Seq. ID

Method

NCBI GI BLAST score E value Match length % identity

12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509 NCBI Description

cruciferin precursor (CRA1) - Arabidopsis thaliana

>gi\_166676 (M37247) 12S storage protein CRA1 [Arabidopsis

thaliana] >gi\_808936\_emb\_CAA32493\_ (X14312) 12S seed

storage protein [Arabidopsis thaliana]

149848 Seq. No.

LIB3175-032-P1-K1-E9 Seq. ID

Method BLASTN NCBI GI q4757409 135 BLAST score 8.0e-70 E value Match length 413

```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MVC8, complete sequence
Seq. No.
                   149849
                   LIB3175-032-P1-K1-F1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2129622
BLAST score
                   722
E value
                   9.0e-77
Match length
                   138
% identity
                   100
NCBI Description
                   immunophilin FKBP15-1 - Arabidopsis thaliana >gi 1272406
                   (U52046) immunophilin [Arabidopsis thaliana]
                   149850
Seq. No.
Seq. ID
                   LIB3175-032-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q4309758
BLAST score
                   307
E value
                   4.0e-28
Match length
                   64
% identity
                   100
NCBI Description
                   (AC006217) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   149851
                   LIB3175-032-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g832876
BLAST score
                   531
E value
                   2.0e-54
Match length
                   123
% identity
                   83
NCBI Description
                   (L41345) ascorbate free radical reductase [Solanum
                   lycopersicum] >gi_1097368_prf__2113407A ascorbate free
                   radical reductase [Lycopersicon esculentum]
Seq. No.
                   149852
Seq. ID
                  LIB3175-032-P1-K1-F12
Method
                  BLASTN
NCBI GI
                   g4757678
BLAST score
                   42
E value
                   3.0e-14
                   154
Match length
                   82
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F9H16 genomic
                  sequence, complete sequence
                  149853
Seq. No.
Seq. ID
                  LIB3175-032-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g1336084
BLAST score
                  251
                   4.0e-36
E value
Match length
                  81
% identity
NCBI Description
                   (U56635) Arabidopsis thaliana glutamate dehydrogenase 2
```

```
(GDH2) mRNA, complete cds. [Arabidopsis thaliana]
                  149854
Seq. No.
                  LIB3175-032-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2677828
BLAST score
                  383
                  5.0e-37
E value
                  100
Match length
                  72
% identity
                  (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
                  149855
Seq. No.
                  LIB3175-032-P1-K1-F5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2317902
BLAST score
                  749
                  6.0e-80
E value
                  139
Match length
                  100
% identity
                  (U89959) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  149856
Seq. No.
                  LIB3175-032-P1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3941542
BLAST score
                  418
E value
                  0.0e + 00
                  418
Match length
                  100
% identity
                  Arabidopsis thaliana pelota (PEL1) mRNA, complete cds
NCBI Description
Seq. No.
                  149857
                  LIB3175-032-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
BLAST score
                  726
E value
                  3.0e-77
                  138
Match length
                  98
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir _S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
```

Seq. No. 149858

Seq. ID LIB3175-032-P1-K1-F8

Method BLASTX
NCBI GI g3413714
BLAST score 405
E value 1.0e-39
Match length 122
% identity 22

NCBI Description (AC004747) putative myrosinase-binding protein [Arabidopsis

thaliana]

```
Seq. No.
                  149859
Seq. ID
                  LIB3175-032-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g114339
BLAST score
                  581
                   3.0e-60
E value
                  138
Match length
                  86
% identity
NCBI Description
                  PLASMA MEMBRANE ATPASE 3 (PROTON PUMP)
                  >gi_67974_pir__PXMUP3 H+-transporting ATPase (EC 3.6.1.35)
                  type 3, plasma membrane - Arabidopsis thaliana >gi 166625
                   (J04737) ATPase [Arabidopsis thaliana]
Seq. No.
                  149860
                  LIB3175-032-P1-K1-G1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4587685
BLAST score
                  424
E value
                  2.0e-54
Match length
                  118
                  93
% identity
NCBI Description
                   (AC007197) putative methylmalonate semi-aldehyde
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  149861
                  LIB3175-032-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2764941
BLAST score
                  600
E value
                   2.0e-62
Match length
                  105
% identity
                   100
                   (X98255) transcriptionally stimulated by gibberellins;
NCBI Description
                   expressed in meristematic region, and style [Arabidopsis
                  thaliana]
                   149862
Seq. No.
                  LIB3175-032-P1-K1-G12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3927822
BLAST score
                  324
                  0.0e + 00
E value
Match length
                  418
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149863
                  LIB3175-032-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2586127
BLAST score
                  205
E value
                   6.0e-18
Match length
                  125
                   45
% identity
                  (U89510) b-keto acyl reductase [Hordeum vulgare]
NCBI Description
```

```
Seq. No.
                   149864
Seq. ID
                   LIB3175-032-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g2832617
BLAST score
                   423
E value
                   1.0e-41
                   99
Match length
                   79
% identity
NCBI Description
                  (AL021711) putative protein [Arabidopsis thaliana]
                   149865
Seq. No.
                  LIB3175-032-P1-K1-G4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4567276
BLAST score
                   255
                   5.0e-22
E value
                   84
Match length
% identity
                   61
NCBI Description
                  (AC006841) hypothetical protein [Arabidopsis thaliana]
                   149866
Seq. No.
                   LIB3175-032-P1-K1-G5
Seq. ID
Method
                   BLASTX
                   g2505876
NCBI GI
BLAST score
                   318
E value
                   2.0e-29
Match length
                   70
% identity
NCBI Description
                   (Y12776) MYB-related protein [Arabidopsis thaliana]
Seq. No.
                   149867
                   LIB3175-032-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4586265
BLAST score
                   534
E value
                   1.0e-54
Match length
                   139
% identity
NCBI Description
                   (AL049640) putative protein [Arabidopsis thaliana]
                   149868
Seq. No.
Seq. ID
                   LIB3175-032-P1-K1-G7
Method
                   BLASTN
NCBI GI
                   g2618605
BLAST score
                   143
E value
                   1.0e-74
Match length
                   423
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUK11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149869
Seq. ID
                  LIB3175-032-P1-K1-G8
Method
                  BLASTX
NCBI GI
                   g3763925
BLAST score
                  549
E value
                   2.0e-56
```

```
Match length
                   105
                   100
% identity
                   (AC004450) putative Af10-protein [Arabidopsis thaliana]
NCBI Description
                   149870
Seq. No.
                   LIB3175-032-P1-K1-G9
Seq. ID
Method
                   BLASTN
                   g4376087
NCBI GI
                   237
BLAST score
                   1.0e-131
E value
                   312
Match length
                   93
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                   fragment No
Seq. No.
                   149871
                   LIB3175-032-P1-K1-H1
Seq. ID
Method
                   BLASTX
                   q2500082
NCBI GI
                   369
BLAST score
                   2.0e-35
E value
                   93
Match length
% identity
                   86
                   PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN)
NCBI Description
                   (PHOTOSYSTEM II PROTEIN D1) >gi_984735_emb_CAA56907
                   (X80932) photosystem II D1 protein [Vigna unguiculata]
Seq. No.
                   149872
                   LIB3175-032-P1-K1-H10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4539378
BLAST score
                   189
                   1.0e-102
E value
Match length
                   374
                   89
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F28A21
NCBI Description
                   (ESSA project)
Seq. No.
                   149873
                   LIB3175-032-P1-K1-H11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g131150
BLAST score
                   703
                   2.0e-74
E value
                   138
Match length
                   97
% identity
                   PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2
NCBI Description
                   >gi_81515_pir__S00445 photosystem I protein A2 - spinach
                   chloroplast >gi 12271 emb CAA27745 (X04131) psaB gene product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia
                   oleracea] >gi 225422 prf 1303218B gene psaB [Spinacia
                   oleracea]
                   149874
Seq. No.
                   LIB3175-032-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2851508
```

```
BLAST score
                   659
E value
                   2.0e-69
                   130
Match length
                   97
% identity
NCBI Description
                   60S RIBOSOMAL PROTEIN L21 >gi 2160162 (AC000132) Similar to
                   ribosomal protein L21 (gb_L38826). ESTs
                   gb AA395597,gb_ATTS5197 come from this gene. [Arabidopsis
                   thaliana] >gi_3482935 (AC003970) Putative ribosomal protein
                   L21 [Arabidopsis thaliana]
                   149875
Seq. No.
                   LIB3175-032-P1-K1-H2
Seq. ID
Method
                   BLASTX
                   q2317911
NCBI GI
BLAST score
                   518
E value
                   8.0e-53
                   121
Match length
                   87
% identity
                   (U89959) similar to GTP-binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   149876
Seq. No.
                   LIB3175-032-P1-K1-H4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3510345
BLAST score
                   284
E value
                   1.0e-158
                   408
Match length
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MNJ8, complete sequence [Arabidopsis thaliana]
                   149877
Seq. No.
                   LIB3175-032-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g132074
BLAST score
                   682
E value
                   5.0e-72
Match length
                   124
                   100
% identity
                   RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1.39}) small chain
                   Al precursor - Arabidopsis thaliana
Seq. No.
                   149878
Seq. ID
                   LIB3175-032-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   q2677828
BLAST score
                   438
E value
                   2.0e-43
Match length
                   117
% identity
                   (U93166) cysteine protease [Prunus armeniaca]
NCBI Description
Seq. No.
                   149879
                   LIB3175-032-P1-K1-H7
Seq. ID
```

```
Method
                   BLASTX
NCBI GI
                   a1161926
BLAST score
                   548
E value
                   2.0e-56
Match length
                   138
% identity
                   (U34392) alpha-carboxyltransferase aCT-1 precursor [Glycine
NCBI Description
                   149880
Seq. No.
Seq. ID
                   LIB3175-032-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   q4567261
BLAST score
                   425
E value
                   3.0e-46
                   125
Match length
% identity
                   (AC006841) putative NADPH dependent mannose 6-phosphate
NCBI Description
                   reductase [Arabidopsis thaliana]
                   >gi 4582439 gb AAD24824.1_AC007142_2 (AC007142) putative
                   NADPH-dependent mannose-6-phosphate reductase [Arabidopsis
                   thaliana
Seq. No.
                   149881
                   LIB3175-032-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   a1175012
BLAST score
                   691
                   4.0e-73
E value
                   133
Match length
% identity
                   100
                   PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
NCBI Description
                   B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane
                   protein TMP-B [Arabidopsis thaliana]
Seq. No.
                   149882
Seq. ID
                   LIB3175-033-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g2673904
BLAST score
                   250
                   1.0e-21
E value
Match length
                   109
% identity
                   61
NCBI Description
                   (AC002561) hypothetical protein [Arabidopsis thaliana]
                   149883
Seq. No.
Seq. ID
                   LIB3175-033-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q728868
BLAST score
                   200
E value
                   1.0e-15
Match length
                   66
% identity
NCBI Description
                   ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX)
                   >gi_99824_pir__S16748 proline-rich protein - rape
(fragment) >gi_22597_emb_CAA42924_ (X60376) proline-rich
                   protein [Brassica napus]
```

Seq. No.

```
Seq. No.
                   149884
Seq. ID
                   LIB3175-033-P1-K1-A11
-Method
                   BLASTX
NCBI GI
                   q1706772
BLAST score
                   344
                   2.0e-32
E value
                   65
Match length
 % identity
                   100
                   FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE
NCBI Description
                   SYNTHETASE) (SQS) (SS) (FPP:FPP FARNESYLTRANSFERASE)
                   >gi_1076324_pir__S54251 farnesyl-diphosphate
                   farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana
                   >gi 798820 emb CAA60385 (X86692) farnesyl-diphosphate
                   farnesyltransferase [Arabidopsis thaliana]
                   >gi_806325_dbj_BAA06103_ (D29017) squalene synthase
                   [Arabidopsis thaliana] >gi_2232212 (AF004560) squalene
                   synthase 1 [Arabidopsis thaliana]
                   >gi 3096933 emb CAA18843.1_ (AL023094) farnesyl-diphosphate
                   farnesyltransferase [Arabidopsis thaliana] >gi 4098519
                   (U79159) squalene synthase [Arabidopsis thaliana]
Seq. No.
                   149885
Seq. ID
                   LIB3175-033-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   q1053047
BLAST score
                   491
                   1.0e-49
E value
                   99
Match length
% identity
                   100
NCBI Description
                   (U38425) histone H3 [Glycine max] >gi_1053049 (U38426)
                   histone H3 [Glycine max] >gi_1053051 (U38427) histone H3
                   [Glycine max]
                   149886
Seq. No.
Seq. ID
                   LIB3175-033-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   a4678705
BLAST score
                   368
                   0.0e + 00
E value
Match length
                   384
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                   (ESSA project)
Seq. No.
                   149887
Seq. ID
                   LIB3175-033-P1-K1-A4
Method
                   BLASTN
NCBI GI
                   g4220468
BLAST score
                   52
E value
                   1.0e-20
Match length
                   156
% identity
                   Arabidopsis thaliana chromosome II BAC T8011 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
```

```
LIB3175-033-P1-K1-A5
Seq. ID
Method
                  BLASTX
                  a3319350
NCBI GI
BLAST score
                  680
                  8.0e-72
E value
                  135
Match length
                  99
% identity
                   (AF077407) No definition line found [Arabidopsis thaliana]
NCBI Description
                  149889
Seq. No.
Seq. ID
                  LIB3175-033-P1-K1-A6
Method
                  BLASTX
                  q3043415
NCBI GI
BLAST score
                  506
E value
                  2.0e-51
                  108
Match length
                  91
% identity
                  (Y17053) At-hsc70-3 [Arabidopsis thaliana]
NCBI Description
                  149890
Seq. No.
                  LIB3175-033-P1-K1-A8
Seq. ID
Method
                  BLASTX
                  g3152606
NCBI GI
BLAST score
                  665
E value
                   4.0e-70
Match length
                  133
% identity
                   (AC004482) putative ring zinc finger protein [Arabidopsis
NCBI Description
                  thaliana]
                  149891
Seq. No.
                  LIB3175-033-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1619300
                   390
BLAST score
E value
                   8.0e-38
Match length
                  81
% identity
                   (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   149892
Seq. No.
Seq. ID
                  LIB3175-033-P1-K1-B1
Method
                  BLASTX
NCBI GI
                   q1170168
                   618
BLAST score
                   1.0e-64
E value
Match length
                   120
% identity
NCBI Description
                  HOMEOBOX-LEUCINE ZIPPER PROTEIN HAT1 (HD-ZIP PROTEIN 1)
                   >gi_549883 (U09332) homeobox protein [Arabidopsis thaliana]
                  >gi_549884 (U09333) homeobox protein [Arabidopsis thaliana]
                   >gi_2245105_emb_CAB10527_ (Z97343) unnamed protein product
                   [Arabidopsis thaliana]
                   149893
Seq. No.
                   LIB3175-033-P1-K1-B10
Seq. ID
Method
                  BLASTX
```

Seq. No.

149898

```
g2739376
NCBI GI
BLAST score
                  350
                  4.0e-33
E value
                  85
Match length
% identity
                  80
                  (AC002505) putative permease [Arabidopsis thaliana]
NCBI Description
                  149894
Seq. No.
                  LIB3175-033-P1-K1-B11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2213595
BLAST score
                  518
E value
                  8.0e-53
                  127
Match length
                  80
% identity
NCBI Description
                  (AC000348) T7N9.15 [Arabidopsis thaliana]
                  149895
Seq. No.
                  LIB3175-033-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337356
BLAST score
                  203
                  2.0e-29
E value
                  79
Match length
% identity
                  90
                  (AC004481) putative protein transport protein SEC61 alpha
NCBI Description
                  subunit [Arabidopsis thaliana]
                  149896
Seq. No.
Seq. ID
                  LIB3175-033-P1-K1-B2
Method
                  BLASTX
                  g1172872
NCBI GI
BLAST score
                  259
E value
                  8.0e-23
Match length
                  54
                  93
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                  (D13042) thiol protease [Arabidopsis thaliana]
                  >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                  149897
                  LIB3175-033-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g132074
BLAST score
                  604
E value
                  6.0e-63
Match length
                  110
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi_68063_pir__RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
```

BLAST score

40

```
Seq. ID
                  LIB3175-033-P1-K1-B5
Method
                   BLASTX
NCBI GI
                   g3688799
BLAST score
                   402
                   2.0e-39
E value
                   87
Match length
% identity
                   92
                   (AF057137) gamma tonoplast intrinsic protein 2 [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   149899
                   LIB3175-033-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4586263
BLAST score
                   406
E value
                   1.0e-39
Match length
                   118
% identity
                   68
NCBI Description
                   (AL049640) putative protein [Arabidopsis thaliana]
Seq. No.
                  149900
                  LIB3175-033-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924651
BLAST score
                  136
E value
                   2.0e-70
                   315
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A18, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149901
                  LIB3175-033-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4314374
BLAST score
                  311
E value
                   1.0e-175
Match length
                  318
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F10A12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149902
Seq. ID
                  LIB3175-033-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2244814
BLAST score
                  69
E value
                  4.0e-32
Match length
                  94
% identity
NCBI Description (Z97336) protein.kinase [Arabidopsis thaliana]
Seq. No.
                  149903
Seq. ID
                  LIB3175-033-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  g4469002
```

```
E value
                   3.0e-13
Match length
                   72
                   89
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone
NCBI Description
                   (ESSA project)
                   149904
Seq. No.
                  LIB3175-033-P1-K1-C12
Seq. ID
Method
                  BLASTN
                   g2252823
NCBI GI
BLAST score
                   74
                   2.0e-33
E value
                   172
Match length
                   94
% identity
NCBI Description
                  Arabidopsis thaliana BAC IG005I10
                   149905
Seq. No.
                  LIB3175-033-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4163997
BLAST score
                   462
E value
                   3.0e-46
Match length
                   88
                   100
% identity
NCBI Description
                   (AF087483) alpha-xylosidase precursor [Arabidopsis
                   thaliana]
                   149906
Seq. No.
                  LIB3175-033-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3163946
BLAST score
                   404
E value
                   1.0e-39
Match length
                   81
                   94
% identity
NCBI Description
                   (AJ005599) alpha-tubulin 1 [Eleusine indica]
                  149907
Seq. No.
                  LIB3175-033-P1-K1-C5
Seq. ID
Method
                  BLASTX
                   g297381
NCBI GI
BLAST score
                   377
E value
                   3.0e-36
Match length
                   115
% identity
                   72
                   (X67421) extA [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  149908
Seq. ID
                  LIB3175-033-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  a3158372
BLAST score
                   280
E value
                   6.0e-25
Match length
                  95
% identity
NCBI Description (AF035383) polyubiquitin [Arabidopsis thaliana]
```

```
Seq. No.
                  149909
Seq. ID
                  LIB3175-033-P1-K1-C9
Method
                  BLASTN
NCBI GI
                  g4049332
BLAST score
                  76
E value
                  8.0e-35
Match length
                  131
% identity
                  89
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
                   (ESSAII project)
                  149910
Seq. No.
                  LIB3175-033-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q687834
BLAST score
                  153
E value
                   5.0e-10
Match length
                  87
% identity
NCBI Description
                   (U21319) similar to alcohol dehydrogenase, highest
                  similarity to B. japonicum FIXR protein (SP:FIXR BRAJA,
                  P05406) [Caenorhabditis elegans]
Seq. No.
                  149911
Seq. ID
                  LIB3175-033-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q132102
BLAST score
                  520
E value
                   4.0e-53
Match length
                  113
% identity
                   88
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 2B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 2B) >gi_68061_pir__RKMUB2
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B2 precursor - Arabidopsis thaliana >qi 16194 emb CAA32701
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
Seq. No.
                  149912
Seq. ID
                  LIB3175-033-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  g3914467
BLAST score
                  288
                  7.0e-26
E value
                  107
Match length
% identity
                  57
NCBI Description
                  26S PROTEASOME REGULATORY SUBUNIT S3 (NUCLEAR ANTIGEN 21D7)
                  >gi_1864003 dbj_BAA19252_ (AB001422) 21D7 [Nicotiana
                  tabacum]
Seq. No.
                  149913
Seq. ID
                  LIB3175-033-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g3510343
BLAST score
                  378
E value
                  0.0e+00
Match length
                  409
```

```
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJC20, complete sequence [Arabidopsis thaliana]
                  149914
Seq. No.
                  LIB3175-033-P1-K1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4220510
BLAST score
                  387
                  0.0e + 00
E value
Match length
                  407
% identity
                  99
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                  (ESSAII project)
                  149915
Seq. No.
                  LIB3175-033-P1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4220510
BLAST score
                  156
                  3.0e-82
E value
Match length
                  270
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                  (ESSAII project)
Seq. No.
                  149916
Seq. ID
                  LIB3175-033-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g2853071
BLAST score
                  77
                  1.0e-35
E value
Match length
                  157
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7
                  (ESSA project)
                  149917
Seq. No.
Seq. ID
                  LIB3175-033-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q1864017
BLAST score
                  461
E value
                  3.0e-46
Match length
                  99
                  90
% identity
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
Seq. No.
                  149918
Seq. ID
                  LIB3175-033-P1-K1-D9
Method
                  BLASTN
NCBI GI
                  q3080352
BLAST score
                  240
E value
                  1.0e-132
Match length
                  363
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18
                  (ESSAII project)
```

E value

Match length

2.0e-26

86

149919 Seq. No. LIB3175-033-P1-K1-E1 Seq. ID Method BLASTN NCBI GI g368768**7** BLAST score 78 4.0e-36 E value Match length 118 % identity 92 NCBI Description Brassica napus response regulator protein mRNA, complete 149920 Seq. No. LIB3175-033-P1-K1-E10 Seq. ID Method BLASTX NCBI GI g1750376 BLAST score 666 E value 3.0e-70 Match length 127 % identity NCBI Description (U80808) ubiquitin activating enzyme [Arabidopsis thaliana] >gi 3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana] 149921 Seq. No. LIB3175-033-P1-K1-E11 Seq. ID Method BLASTX NCBI GI q1245182 BLAST score 719 E value 2.0e-76 Match length 136 99 % identity NCBI Description (U49398) sterol delta-7 reductase [Arabidopsis thaliana] 149922 Seq. No. Seq. ID LIB3175-033-P1-K1-E12 Method BLASTX NCBI GI q2119846 BLAST score 43 E value 5.0e-66 Match length 127 % identity NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -Arabidopsis thaliana >gi\_16364\_emb\_CAA45790\_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi\_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi\_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] Seq. No. 149923 Seq. ID LIB3175-033-P1-K1-E2 Method BLASTX NCBI GI g1408460 292 BLAST score

```
% identity
                  (U40161) type 2A protein serine/threonine phosphatase 55
NCBI Description
                  kDa B regulatory subunit [Arabidopsis thaliana]
                  149924
Seq. No.
                  LIB3175-033-P1-K1-E3
Seq. ID
                  BLASTN
Method
                  q4662609
NCBI GI
                  312
BLAST score
                  1.0e-175
E value
                  415
Match length
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F10A5,
                  complete sequence
                  149925
Seq. No.
                  LIB3175-033-P1-K1-E4
Seq. ID
                  BLASTX
Method
                  g1172872
NCBI GI
                  86
BLAST score
                  2.0e-45
E value
                  118
Match length
                  86
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                   (D13042) thiol protease [Arabidopsis thaliana]
                  >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
                  149926
Seq. No.
Seq. ID
                  LIB3175-033-P1-K1-E6
Method
                  BLASTN
                  g2924651
NCBI GI
BLAST score
                  69
                  2.0e-30
E value
Match length
                  175
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K2A18, complete sequence [Arabidopsis thaliana]
                  149927
Seq. No.
                  LIB3175-033-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3894172
BLAST score
                   510
E value
                   7.0e-52
Match length
                  97
% identity
                  100
                   (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   149928
                  LIB3175-033-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4314386
BLAST score
                  196
```

```
5.0e-25
E value
Match length
                  126
                  59
% identity
                  (AC006232) putative rac GTPase activating protein
NCBI Description
                  [Arabidopsis thaliana]
                  149929
Seq. No.
                  LIB3175-033-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q135406
BLAST score
                  560
E value
                  9.0e-58
Match length
                  105
                  100
% identity
                  TUBULIN ALPHA-3/ALPHA-5 CHAIN >gi_99768_pir__A32712 tubulin
NCBI Description
                  alpha-5 chain - Arabidopsis thaliana >gi_166912 (M17189)
                  alpha-tubulin [Arabidopsis thaliana] >gi_166918 (M84698)
                  alpha-5 tubulin [Arabidopsis thaliana]
                  149930
Seq. No.
Seq. ID
                  LIB3175-033-P1-K1-F11
                  BLASTX
Method
NCBI GI
                  g280386
BLAST score
                  615
E value
                  3.0e-64
                  128
Match length
% identity
                  95
                  ubiquitin / ribosomal protein CEP52 - Arabidopsis thaliana
NCBI Description
                  >gi 166930 (J05507) ubiquitin extension protein (UBQ1)
                  [Arabidopsis thaliana] >gi_166932 (J05508) ubiquitin
                  extension protein (UBQ2) [Arabidopsis thaliana]
                  >gi 4678227 gb AAD26972.1 AC007135_8 (AC007135)
                  ubiquitin/ribosomal protein CEP52 [Arabidopsis thaliana]
                  149931
Seq. No.
Seq. ID
                  LIB3175-033-P1-K1-F12
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  578
E value
                  6.0e-60
Match length
                  117
                  93
% identity
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  149932
                  LIB3175-033-P1-K1-F2
```

Seq. ID Method BLASTN NCBI GI q2477521 BLAST score 271 1.0e-151

407 Match length

E value



% identity 25

NCBI Description Arabidopsis thaliana chromosome I BAC F22K20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 149933

Seq. ID LIB3175-033-P1-K1-F3

Method BLASTN
NCBI GI g4581161
BLAST score 156
E value 2.0e-82
Match length 334
% identity 73

NCBI Description Arabidopsis thaliana chromosome II BAC T20G20 genomic

sequence, complete sequence

Seq. No. 149934

Seq. ID LIB3175-033-P1-K1-F4

Method BLASTX
NCBI GI g1628583
BLAST score 625
E value 2.0e-65
Match length 120
% identity 100

NCBI Description (U66916) 12S cruciferin seed storage protein [Arabidopsis

thaliana] >gi\_2842495\_emb\_CAA16892\_ (AL021749) 12S

cruciferin seed storage protein [Arabidopsis thaliana]

Seq. No. 149935

Seq. ID LIB3175-033-P1-K1-F5

Method BLASTN
NCBI GI g2244901
BLAST score 198
E value 1.0e-107

E value 1.0e-10
Match length 258
% identity 94

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 149936

Seq. ID LIB3175-033-P1-K1-F6

Method BLASTX
NCBI GI g2119846
BLAST score 647
E value 6.0e-68
Match length 126
% identity 97

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -

Arabidopsis thaliana >gi\_16364\_emb\_CAA45790\_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi\_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi\_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. 149937

Seq. ID LIB3175-033-P1-K1-F7

Method BLASTX

BLAST score

542

```
q4263525
NCBI GI
BLAST score
                   535
E value
                   8.0e-55
Match length
                   126
                   83
% identity
NCBI Description
                   (AC004044) putative photosystem I reaction center subunit
                   II precursor [Arabidopsis thaliana]
Seq. No.
                   149938
Seq. ID
                  LIB3175-033-P1-K1-F8
Method
                  BLASTN
NCBI GI
                   q4220510
BLAST score
                   58
E value
                   7.0e-24
Match length
                   228
                   86
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
                   (ESSAII project)
Seq. No.
                  149939
Seq. ID
                  LIB3175-033-P1-K1-F9
Method
                  BLASTN
NCBI GI
                  q1871173
BLAST score
                   91
E value
                   1.0e-43
Match length
                   170
                   94
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T06D20 genomic
                  sequence, complete sequence
Seq. No.
                  149940
Seq. ID
                  LIB3175-033-P1-K1-G12
Method
                  BLASTN
NCBI GI
                   q4678291
BLAST score
                  101
E value
                   1.0e-49
Match length
                  213
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 3, BAC clone F28P10
                   (ESSA project)
Seq. No.
                  149941
Seq. ID
                  LIB3175-033-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  g3849811
BLAST score
                  150
E value
                  9.0e-79
Match length
                  415
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T2P11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149942
Seq. ID
                  LIB3175-033-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g4589965
```

```
E value
                  1.0e-55
Match length
                  108
                  100
% identity
NCBI Description
                  (AC007169) putative glyoxalase II [Arabidopsis thaliana]
                  149943
Seq. No.
                  LIB3175-033-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1246019
BLAST score
                  635
                  1.0e-66
E value
Match length
                  122
% identity
                  99
                  (S80554) chalcone synthase, CHS [Arabidopsis, Landsberg
NCBI Description
                  erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]
                  149944
Seq. No.
                  LIB3175-033-P1-K1-G6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757678
                  41
BLAST score
                  1.0e-13
E value
                  267
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome I BAC F9H16 genomic
NCBI Description
                  sequence, complete sequence
                  149945
Seq. No.
                  LIB3175-033-P1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4741960
BLAST score
                  372
                  8.0e-36
E value
                  92
Match length
                  79
% identity
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
NCBI Description
                  149946
Seq. No.
                  LIB3175-033-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2369714
BLAST score
                  548
E value
                  2.0e-56
Match length
                  122
                  90
% identity
NCBI Description (297178) elongation factor 2 [Beta vulgaris]
                  149947
Seq. No.
                  LIB3175-033-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076303
                  57
BLAST score
E value
                  3.0e-54
Match length
                  114
                  57
% identity
                  RNA-binding protein cp29 precursor - Arabidopsis thaliana
NCBI Description
                  >gi_681902_dbj BAA06518 (D31710) cp29 [Arabidopsis
```

```
thaliana]
                   149948
Seq. No.
Seq. ID
                   LIB3175-033-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   q2911057
                   566
BLAST score
                   2.0e-58
E value
Match length
                   127
% identity
NCBI Description
                   (AL021961) caffeoyl-CoA O-methyltransferase - like protein
                   [Arabidopsis thaliana]
                   149949
Seq. No.
Seq. ID
                   LIB3175-033-P1-K1-H12
Method
                   BLASTX
NCBI GI
                   g2911057
BLAST score
                   131
E value
                   5.0e-19
Match length
                   95
% identity
                   52
                   (AL021961) caffeoyl-CoA O-methyltransferase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   149950
Seq. No.
Seq. ID
                   LIB3175-033-P1-K1-H2
Method
                   BLASTX
NCBI GI
                   q2369714
BLAST score
                   425
                   6.0e-42
E value
Match length
                   107
% identity
                  (Z97178) elongation factor 2 [Beta vulgaris]
NCBI Description
                   149951
Seq. No.
Seq. ID
                   LIB3175-033-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q4263777
BLAST score
                   522
E value
                   3.0e-53
Match length
                   139
% identity
                   (AC006068) putative serine carboxypeptidase II [Arabidopsis
NCBI Description
                   thaliana] >gi_4510391_gb_AAD21479.1_ (AC007017) putative
                   serine carboxypeptidase II [Arabidopsis thaliana]
Seq. No.
                   149952
Seq. ID
                   LIB3175-033-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   q4538963
BLAST score
                   229
E value
                   4.0e-19
Match length
                   84
% identity
NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi_4741958_gb_AAD28776.1_AF134129_1
```

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

```
Seq. No.
                   149953
                   LIB3175-033-P1-K1-H8
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   q115783
 BLAST score
                   595
                   7.0e-62
 E value
                   116
Match length
 % identity
                   97
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                    (CAB-140) (LHCP) >gi_16376_emb_CAA27543_
                                                              (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
 Seq. No.
                   149954
                   LIB3175-034-P1-K1-A10
 Seq. ID
Method
                   BLASTX
NCBI GI
                   g1172873
                   617
 BLAST score
 E value
                   2.0e-64
                   124
Match length
                   98
 % identity
                   CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
NCBI Description
                   drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                   precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                    (D13043) thiol protease [Arabidopsis thaliana]
                   149955
Seq. No.
                   LIB3175-034-P1-K1-A12
 Seq. ID
Method
                   BLASTX
 NCBI GI
                   q3128185
BLAST score
                   462
E value
                   6.0e-50
Match length
                   123
 % identity
                   85
NCBI Description
                   (AC004521) unknown protein [Arabidopsis thaliana]
                   149956
 Seq. No.
                   LIB3175-034-P1-K1-A2
 Seq. ID
Method
                   BLASTX
NCBI GI
                   q2208903
BLAST score
                   477
 E value
                   4.0e-48
Match length
                   94
 % identity
NCBI Description
                   (AB004798) ascorbate oxidase [Arabidopsis thaliana]
Seq. No.
                   149957
Seq. ID
                   LIB3175-034-P1-K1-A3
Method
                   BLASTN
NCBI GI
                   q3250737
BLAST score
                   133
E value`
                   1.0e-68
Match length
                   301
 % identity
                   90
NCBI Description Arabidopsis thaliana ASKbeta gene, complete CDS
```

```
Seq. No.
                  149958
                  LIB3175-034-P1-K1-A5
Seq. ID
Method
                  BLASTN
                  g4757388
NCBI GI
                  437
BLAST score
                  0.0e+00
E value
Match length
                  449
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F15L12, complete sequence
                  149959
Seq. No.
                  LIB3175-034-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220474
BLAST score
                  196
                  5.0e-15
E value
Match length
                  60
% identity
                  72
                  (AC006069) putative myosin heavy chain [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  149960
                  LIB3175-034-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q119350
BLAST score
                  569
E value
                  6.0e-59
Match length
                  115
% identity
                  99
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi 16271 emb CAA41114 (X58107) enolase
                   [Arabidopsis thaliana]
                  >gi 4581151 gb AAD24635.1_AC006919_13 (AC006919) enolase
                   (2-phospho-D-gTycerate hydroylase); identical to P25696
                   [Arabidopsis thaliana]
Seq. No.
                  149961
Seq. ID
                  LIB3175-034-P1-K1-A8
Method
                  BLASTX
                  q3183088
NCBI GI
BLAST score
                  214
E value
                  4.0e-17
Match length
                  68
                  54
% identity
                  PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN AKCS9 PRECURSOR
NCBI Description
                  (LTP) >gi 629658 pir S47084 lipid transfer like protein -
                  cowpea >gi 499034 emb CAA56113 (X79604) lipid transfer
                  like protein [Vigna unguiculata]
Seq. No.
                  149962
                  LIB3175-034-P1-K1-A9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2656028
                  221
BLAST score
```

E value 1.0e-121 Match length 326 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

149963 Seq. No.

LIB3175-034-P1-K1-B10 Seq. ID

Method BLASTN NCBI GI q4220633 BLAST score 442 0.0e + 00E value Match length 452 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K7J8, complete sequence [Arabidopsis thaliana]

149964 Seq. No.

LIB3175-034-P1-K1-B11 Seq. ID

Method BLASTX g417103 NCBI GI BLAST score 612 E value 8.0e-64 Match length 122 % identity 100

NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone

H3.3-like protein - Arabidopsis thaliana

>gi\_16324\_emb\_CAA42957 (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958 (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa]  $>gi_488575$  (U09464) histone H3.2

[Medicago sativa]  $>gi_488577$  (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422)

histone H3 variant H3.3 [Lycopersicon esculentum]

>gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi 3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1 (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_

(AL035708) Histon H3 [Arabidopsis thaliana]

Seq. No. 149965

Seq. ID LIB3175-034-P1-K1-B12

Method BLASTN NCBI GI q3688169 BLAST score 33 E value 5.0e-09

Match length 97 % identity

Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 NCBI Description

(ESSAII project)

Seq. No. 149966

```
Seq. ID
                  LIB3175-034-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  q2828186
BLAST score
                  163
                  1.0e-86
E value
                  336
Match length
                  98
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K18I23, complete sequence [Arabidopsis thaliana]
                  149967
Seq. No.
                  LIB3175-034-P1-K1-B5
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2245020
BLAST score
                  449
                  1.0e-44
E value
                  90
Match length
% identity
                  100
NCBI Description (297341) growth regulator homolog [Arabidopsis thaliana]
Seq. No.
                  149968
Seq. ID
                  LIB3175-034-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  g1402904
BLAST score
                  642
E value
                  2.0e-67
                  125
Match length
                  99
% identity
NCBI Description (X98313) peroxidase [Arabidopsis thaliana]
                  149969
Seq. No.
                  LIB3175-034-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  558
E value
                  1.0e-57
Match length
                  112
                  96
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >qi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  149970
Seq. No.
Seq. ID
                  LIB3175-034-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q112682
BLAST score
                  639
E value
                  6.0e-67
Match length
                  147
% identity
                  82
NCBI Description
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi_166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >gi_808937_emb_CAA32494_ (X14313) 12S seed
```

storage protein [Arabidopsis thaliana]

```
Seq. No.
                   149971
Seq. ID
                   LIB3175-034-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   g480450
BLAST score
                   609
                   1.0e-63
E value
Match length
                   119
                   99
% identity
NCBI Description
                   ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis
                   thaliana >gi 402552 emb CAA49506 (X69880) ketol-acid
                   reductoisomerase [Arabidopsis thaliana]
                   149972
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-C1
Method
                   BLASTN
NCBI GI
                   g2351063
BLAST score
                   131
                   8.0e-68
E value
Match length
                   159
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MCL19, complete sequence [Arabidopsis thaliana]
Seq. No.
                   149973
                   LIB3175-034-P1-K1-C10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3128135
BLAST score
                   250
                   1.0e-138
E value
Match length
                   433
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K19E1, complete sequence [Arabidopsis thaliana]
                   149974
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   g3212846
BLAST score
                   33
                   7.0e-09
E value
Match length
                   401
% identity
                   Arabidopsis thaliana chromosome II BAC F6E13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   149975
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-C12
Method
                   BLASTX
NCBI GI
                   q4262180
BLAST score
                   714
E value
                   9.0e-76
Match length
                   134
% identity
                   99
NCBI Description
                   (AC005508) 29621 [Arabidopsis thaliana]
                   149976
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-C2
```

```
Method
                  BLASTX
NCBI GI
                  q127041
BLAST score
                  513
E value
                  3.0e-52
Match length
                  98
                  100
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)
                  >gi_81647_pir__JN0131 methionine adenosyltransferase (EC
                  2.5.1.6) - Arabidopsis thaliana >gi_166872 (M55077)
                  S-adenosylmethionine synthetase [Arabidopsis thaliana]
                  149977
Seq. No.
Seq. ID
                  LIB3175-034-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3273751
BLAST score
                  633
E value
                  3.0e-66
                  144
Match length
% identity
                  (AF061518) manganese superoxide dismutase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  149978
                  LIB3175-034-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3299824
BLAST score
                  182
                  4.0e-98
E value
Match length
                  212
% identity
                  95
                  Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm,
NCBI Description
                  near 17 cM, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149979
Seq. ID
                  LIB3175-034-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4006893
BLAST score
                  569
E value
                  8.0e-59
Match length
                  111
% identity
                  97
NCBI Description
                  (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
Seq. No.
                  149980
Seq. ID
                  LIB3175-034-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  q4567236
BLAST score
                  226
E value
                  6.0e-19
Match length
                  44
% identity
NCBI Description
                  (AC007119) glycine-rich RNA binding protein Ccr2
                  [Arabidopsis thaliana]
Seq. No.
                  149981
Seq. ID
                  LIB3175-034-P1-K1-C7
```

```
Method
                   BLASTX
NCBI GI
                   q4689386
BLAST score
                   166
E value
                   1.0e-11
Match length
                   59
% identity
NCBI Description
                   (AF139468) photosystem I reaction center subunit III [Vigna
                   149982
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-D10
Method
                   BLASTX
NCBI GI
                   q3236246
BLAST score
                   517
E value
                   7.0e-53
Match length
                   101
% identity
NCBI Description
                   (AC004684) putative expansin protein [Arabidopsis thaliana]
                   149983
Seq. No.
                   LIB3175-034-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4455338
BLAST score
                   573
E value
                   2.0e-59
Match length
                   117
                   97
% identity
                   (AL035525) putative protein [Arabidopsis thaliana]
NCBI Description
                   149984
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q421836
BLAST score
                   459
E value
                   6.0e-46
Match length
                   93
% identity
                   100
                   G-box-binding factor GF14 - Arabidopsis thaliana >gi_553040
NCBI Description
                   (M96855) GF14 [Arabidopsis thaliana]
                   149985
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q3367521
BLAST score
                   194
                   6.0e-15
E value
Match length
                   117
% identity
NCBI Description
                   (AC004392) Similar to gb_U08285 membrane-associated
                   salt-inducible protein from Nicotiana tabacum. ESTs
                   gb_T44131 and gb_T04378 come from this gene. [Arabidopsis
                   thaliana]
                   149986
Seq. No.
                   LIB3175-034-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2160133
```

```
BLAST score
                  416
                  5.0e-41
E value
                  96
Match length
% identity
                  89
                  (AC000375) Strong similarity to Arabidopsis
NCBI Description
                  gb X91953, F19K23.3, F19K23.15. ESTs
                  gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this
                  gene. [Arabidopsis thaliana]
                  149987
Seq. No.
Seq. ID
                  LIB3175-034-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  a2828183
BLAST score
                  188
E value
                  1.0e-101
Match length
                  381
                  92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPL12, complete sequence [Arabidopsis thaliana]
Seq. No.
                  149988
                  LIB3175-034-P1-K1-D9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2541876
BLAST score
                  300
E value
                  3.0e-27
Match length
                  120
                  42
% identity
NCBI Description
                   (D26015) CND41, chloroplast nucleoid DNA binding protein
                   [Nicotiana tabacum]
Seq. No.
                  149989
Seq. ID
                  LIB3175-034-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  q2506443
BLAST score
                  624
E value
                  2.0e-65
Match length
                  127
% identity
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR,
NCBI Description
                  CHLOROPLAST >gi_2117520_pir__JQ1285
                  glyceraldehyde-\overline{3}-phosphate dehydrogenase (NADP+)
                   (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast -
                  Arabidopsis thaliana >gi_166704 (M64117) glyceraldehyde
                  3-phosphate dehydrogenase [Arabidopsis thaliana]
                  >gi_1402885_emb_CAA66816_ (X98130)
                  glyceraldehyde-3-phosphate dehydrogenase (NADP+)
                   (phosphorylating) [Arabidopsis thaliana]
Seq. No.
                  149990
                  LIB3175-034-P1-K1-E12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1246019
BLAST score
                  551
                  9.0e-57
E value
                  105
Match length
                  100
% identity
```

NCBI Description

```
(S80554) chalcone synthase, CHS [Arabidopsis, Landsberg
NCBI Description
                  erecta, tt4, Peptide Mutant, 395 aa] [Arabidopsis]
                  149991
Seq. No.
Seq. ID
                  LIB3175-034-P1-K1-E2
Method
                  BLASTX
                   g1236190
NCBI GI
                   272
BLAST score
                   6.0e-30
E value
                  73
Match length
                   95
% identity
                   (U18365) cyclin dependent protein kinase homolog; similar
NCBI Description
                   to moth bean p34cdc2 protein, PIR Accession Number JQ2243
                   [Brassica napus]
                   149992
Seq. No.
                  LIB3175-034-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1363526
                   58
BLAST score
                   4.0e-38
E value
Match length
                   82
                   99
% identity
                  plastoquinol--plastocyanin reductase (EC 1.10.99.1)
NCBI Description
                   cytochrome b6 - maize chloroplast >gi 902251 emb CAA60315
                   (X86563) cytochrome B6 [Zea mays]
Seq. No.
                   149993
                  LIB3175-034-P1-K1-E6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g972924
                   197
BLAST score
E value
                   1.0e-107
                   277
Match length
                   93
% identity
                  Arabidopsis thaliana IAA11 (IAA11) gene, complete cds
NCBI Description
                  149994
Seq. No.
                  LIB3175-034-P1-K1-E8
Seq. ID
                  BLASTX
Method
                   g3478700
NCBI GI
BLAST score
                   529
                   4.0e-54
E value
                   118
Match length
                   87
% identity
                   (AF034387) AFT protein [Arabidopsis thaliana]
NCBI Description
                  149995
Seq. No.
                  LIB3175-034-P1-K1-E9
Seq. ID
                  BLASTX
Method
                   g3478700
NCBI GI
BLAST score
                   532
E value
                   2.0e-54
Match length
                  119
                   87
% identity
```

(AF034387) AFT protein [Arabidopsis thaliana]

```
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g4589398
BLAST score
                   333
E value
                   3.0e-31
                   74
Match length
% identity
NCBI Description
                   (D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]
Seq. No.
                   149997
Seq. ID
                   LIB3175-034-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q3687238
BLAST score
                   470
E value
                   2.0e-47
Match length
                   109
                   78
% identity
                   (AC005169) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   149998
Seq. No.
                   LIB3175-034-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3080402
BLAST score
                   628
E value
                   1.0e-65
Match length
                   124
% identity
                   (AL022603) putative NADPH quinone oxidoreductase
NCBI Description
                   [Arabidopsis thaliana] >gi_4455266_emb_CAB36802.1_
                   (AL035527) putative NADPH quinone oxidoreductase
                   [Arabidopsis thaliana]
Seq. No.
                   149999
Seq. ID
                   LIB3175-034-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q2130521
BLAST score
                   513
E value
                   2.0e-52
                   99
Match length
% identity
NCBI Description
                   (U31565) reversibly glycosylatable polypeptide [Pisum
                   sativum]
Seq. No.
                   150000
Seq. ID
                   LIB3175-034-P1-K1-F5
Method
                   BLASTX
NCBI GI
                  q3661595
BLAST score
                   640
E value
                   4.0e-67
Match length
                  126
% identity
                   (AF091844) aminoalcoholphosphotransferase [Arabidopsis
NCBI Description
                  thaliana]
                  150001
Seq. No.
Seq. ID
                  LIB3175-034-P1-K1-F6
```

```
Method
                   BLASTX
NCBI GI
                   g2642432
BLAST score
                   519
E value
                   6.0e-53
Match length
                   138
                   80
% identity
                   (AC002391) putative elicitor response element binding
NCBI Description
                   protein (WRKY3) [Arabidopsis thaliana]
                   150002
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-F7
                   BLASTX
Method
NCBI GI
                   q2351374
BLAST score
                   557
E value
                   2.0e-57
                   111
Match length
                   97
% identity
                   (U54560) putative 26S proteasome subunit athMOV34
NCBI Description
                   [Arabidopsis thaliana]
                   150003
Seq. No.
                   LIB3175-034-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3941543
BLAST score
                   342
E value
                   4.0e-32
                   83
Match length
                   83
% identity
                   (AF069497) pelota [Arabidopsis thaliana]
NCBI Description
                   >gi_4469016_emb_CAB38277_ (AL035602) pelota (PEL1)
                   [Arabidopsis thaliana]
                   150004
Seq. No.
                   LIB3175-034-P1-K1-G1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1619300
BLAST score
                   390
E value
                   8.0e-38
                   81
Match length
% identity
                   88
                   (X95269) LRR protein [Lycopersicon esculentum]
NCBI Description
                   150005
Seq. No.
                   LIB3175-034-P1-K1-G10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3798730
BLAST score
                   42
E value
                   2.0e-14
Match length
                   42
% identity
                   100
                   Arabidopsis thaliana transgenic line C DNA
NCBI Description
                   150006
Seq. No.
                   LIB3175-034-P1-K1-G11
Seq. ID
Method
                   BLASTN
                   q2351069
NCBI GI
BLAST score
                   201
```

Seq. ID

```
1.0e-109
E value
                  334
Match length
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSH12, complete sequence [Arabidopsis thaliana]
                  150007
Seq. No.
                  LIB3175-034-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3121825
BLAST score
                  549
E value
                  1.0e-56
Match length
                  111
                  95
% identity
                  2-CYS PEROXIREDOXIN BAS1 PRECURSOR (THIOL-SPECIFIC
NCBI Description
                  ANTIOXIDANT PROTEIN) >gi_1498247_emb_CAA63910_ (X94219)
                  bas1 protein [Spinacia oleracea]
                  150008
Seq. No.
                  LIB3175-034-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g481827
BLAST score
                  541
E value
                  2.0e-55
Match length
                  125
                  79
% identity
NCBI Description
                  thioglucosidase (EC 3.2.3.1) - rape
                  >gi_414103_emb_CAA79990_ (Z21978) myrosinase, thioglucoside
                  glucohydrolase [Brassica napus]
                  150009
Seq. No.
Seq. ID
                  LIB3175-034-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3915085
BLAST score
                  546
E value
                  3.0e-56
Match length
                  107
% identity
                  99
NCBI Description
                  TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID
                  4-HYDROXYLASE) (CA4H) (P450C4H) (CYTOCHROME P450 73)
                  >gi_1773289 (U71081) cinnamate-4-hydroxylase [Arabidopsis
                  thaliana] >gi_1946370 (U93215) cinnamate-4-hydroxylase
                  [Arabidopsis thaliana]
Seq. No.
                  150010
                  LIB3175-034-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4582443
BLAST score
                  430
E value
                  1.0e-42
Match length
                  88
% identity
NCBI Description
                  (AC007142) putative auxin-induced protein [Arabidopsis
                  thaliana]
                  150011
Seq. No.
```

LIB3175-034-P1-K1-G6

```
Method
                   BLASTX
NCBI GI
                   q1769905
BLAST score
                   370
E value
                   1.0e-35
Match length
                  102
                   71
% identity
NCBI Description
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
                   [Arabidopsis thaliana]
Seq. No.
                   150012
                  LIB3175-034-P1-K1-G7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129774
BLAST score
                  528
E value
                   6.0e-54
Match length
                  115
% identity
NCBI Description
                  xyloglucan endotransglycosylase-related protein XTR4 -
                  Arabidopsis thaliana (fragment) >gi_1244754 (U43486)
                  xyloglucan endotransglycosylase-related protein
                   [Arabidopsis thaliana]
Seq. No.
                   150013
Seq. ID
                  LIB3175-034-P1-K1-G8
Method
                  BLASTX
NCBI GI
                  q4218127
BLAST score
                  606
E value
                   3.0e-63
Match length
                  127
% identity
NCBI Description
                   (AL035353) myosin heavy chain-like protein (fragment)
                   [Arabidopsis thaliana]
Seq. No.
                   150014
Seq. ID
                  LIB3175-034-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q4539335
BLAST score
                  270
E value
                   8.0e-24
                  75
Match length
% identity
NCBI Description
                  (AL035539) putative protein [Arabidopsis thaliana]
                   150015
Seq. No.
Seq. ID
                  LIB3175-034-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g126985
BLAST score
                  619
E value
                   1.0e-64
Match length
                  120
% identity
NCBI Description
                  MERI-5 PROTEIN >gi 166778 (M63166) meri-5 [Arabidopsis
                  thalianal
                  150016
Seq. No.
Seq. ID
                  LIB3175-034-P1-K1-H10
Method
                  BLASTX
```

```
g2642450
NCBI GI
BLAST score
                   439
E value
                   1.0e-43
Match length
                   81
% identity
NCBI Description
                   (AC002391) putative metal ion transporter (Nramp)
                   [Arabidopsis thaliana] >gi_3169188 (AC004401) putative
                   metal ion transporter (Nramp) [Arabidopsis thaliana]
Seq. No.
                   150017
Seq. ID
                   LIB3175-034-P1-K1-H2
Method
                   BLASTX
                   g3600058
NCBI GI
BLAST score
                   579
E value
                   5.0e-60
Match length
                   119
                   100
% identity
NCBI Description
                   (AF080120) similar to vacuolar ATPases [Arabidopsis
                   thaliana]
Seq. No.
                   150018
                   LIB3175-034-P1-K1-H3
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4567260
                   574
BLAST score
E value
                   2.0e-59
Match length
                   131
% identity
NCBI Description
                   (AC006841) putative NADPH dependent mannose 6-phosphate
                   reductase [Arabidopsis thaliana]
                   >gi 4582440 gb AAD24825.1 AC007142 3 (AC007142) putative
                   NADPH-dependent mannose-6-phosphate reductase [Arabidopsis
                   thaliana]
                   150019
Seq. No.
Seq. ID
                   LIB3175-034-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   q2388574
BLAST score
                   595
                   6.0e-62
E value
Match length
                   118
% identity
NCBI Description
                   (AC000098) Strong similarity to Phalaenopsis homeobox
                  protein (gb_U34743). [Arabidopsis thaliana]
Seq. No.
                   150020
Seq. ID
                   LIB3175-034-P1-K1-H5
Method
                   BLASTX
NCBI GI
                   g3080400
BLAST score
                   183
                   7.0e-33
E value
Match length
                  81
% identity
                   (AL022603) putative protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4455264_emb_CAB36800.1_ (AL035527) putative protein
                   [Arabidopsis thaliana]
```

```
150021
Seq. No.
                  LIB3175-034-P1-K1-H6
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2914688
                   90
BLAST score
                   5.0e-43
E value
                   352
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F24L7 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   150022
Seq. No.
                   LIB3175-034-P1-K1-H7
Seq. ID
                   BLASTX
Method
NCBI GI
                   a3367568
                   190
BLAST score
                   2.0e-14
E value
                   62
Match length
                   58
% identity
NCBI Description
                   (AL031135) protein kinase - like protein [Arabidopsis
                   thaliana]
                   150023
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   q4490332
                   634
BLAST score
                   2.0e-66
E value
                   126
Match length
                   98
% identity
                   (AL035656) putative protein [Arabidopsis thaliana]
NCBI Description
                   150024
Seq. No.
                   LIB3175-035-P1-K1-A10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3367568
BLAST score
                   533
E value
                   2.0e-54
Match length
                   117
% identity
NCBI Description
                   (ALO31135) protein kinase - like protein [Arabidopsis
                   thaliana]
                   150025
Seq. No.
                   LIB3175-035-P1-K1-A12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2160132
BLAST score
                   41
E value
                   1.0e-13
Match length
                   103
                   48
% identity
                  Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
                   150026
Seq. No.
                  LIB3175-035-P1-K1-A2
Seq. ID
Method
                  BLASTN
```

```
g3298532
NCBI GI
BLAST score
                  73
                  6.0e-33
E value
Match length
                  77
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T26B15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150027
                  LIB3175-035-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2507092
BLAST score
                  213
                  3.0e-17
E value
Match length
                  47
% identity
                  PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR)
NCBI Description
                   (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi 968977
                   (U29785) NADPH:protochlorophyllide oxidoreductase B
                   [Arabidopsis thaliana] >gi_1583456_prf__2120441B
                  protochlorophyllide oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  150028
Seq. ID
                  LIB3175-035-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  q2696018
BLAST score
                  151
                  3.0e-79
E value
                  448
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150029
                  LIB3175-035-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3522929
BLAST score
                  111
                  8.0e-76
E value
Match length
                  148
% identity
NCBI Description
                   (AC002535) putative dTDP-glucose 4-6-dehydratase
                   [Arabidopsis thaliana] >gi_3738279 (AC005309) putative
                  dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.
                  150030
Seq. ID
                  LIB3175-035-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  q1628583
BLAST score
                  596
E value
                  6.0e-62
Match length
                  152
% identity
                  79
NCBI Description
                   (U66916) 12S cruciferin seed storage protein [Arabidopsis
                  thaliana] >gi 2842495 emb CAA16892 (AL021749) 12S
```

cruciferin seed storage protein [Arabidopsis thaliana]

```
150031
Seq. No.
                  LIB3175-035-P1-K1-A7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3298532
BLAST score
                  248
                  1.0e-137
E value
                  418
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC T26B15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  150032
Seq. No.
Seq. ID
                  LIB3175-035-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g3355483
BLAST score
                  314
                  6.0e-29
E value
                  89
Match length
                  64
% identity
                  (AC004218) gibberellin-regulated protein (GASA5)-like
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  150033
                  LIB3175-035-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2507092
BLAST score
                  271
                  6.0e-24
E value
                  58
Match length
                  97
% identity
                  PROTOCHLOROPHYLLIDE REDUCTASE PRECURSOR (PCR)
NCBI Description
                  (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE) >gi 968977
                  (U29785) NADPH:protochlorophyllide oxidoreductase B
                  [Arabidopsis thaliana] >gi_1583456_prf__2120441B
                  protochlorophyllide oxidoreductase [Arabidopsis thaliana]
Seq. No.
                  150034
Seq. ID
                  LIB3175-035-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g119143
BLAST score
                  205
                  1.0e-16
E value
Match length
                  50
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA)
NCBI Description
                  >gi_81606_pir_ S06724 translation elongation factor eEF-1
                  alpha chain - Arabidopsis thaliana >gi_295788_emb_CAA34453_
                  (X16430) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi_1369927_emb_CAA34454_ (X16431) elongation factor
                  1-alpha [Arabidopsis thaliana] >gi_1369928_emb_CAA34455
                  (X16431) elongation factor 1-alpha [Arabidopsis thaliana]
                  >gi_1532172 (U63815) EF-lalpha-A1 [Arabidopsis thaliana]
                  >gi_1532173 (U63815) EF-lalpha-A2 [Arabidopsis thaliana]
                  >gi 1532174 (U63815) EF-lalpha-A3 [Arabidopsis thaliana]
Seq. No.
                  150035
                  LIB3175-035-P1-K1-B10
Seq. ID
```

```
Method
                   BLASTN
NCBI GI
                  g3985954
BLAST score
                   243
E value
                   1.0e-134
                   450
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRG21, complete sequence [Arabidopsis thaliana]
                   150036
Seq. No.
                  LIB3175-035-P1-K1-B11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3128135
BLAST score
                   443
                   0.0e+00
E value
                   447
Match length
                   100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K19E1, complete sequence [Arabidopsis thaliana]
                   150037
Seq. No.
                  LIB3175-035-P1-K1-B12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g1419473
BLAST score
                   355
                   0.0e + 00
E value
                   454
Match length
% identity
                   93
NCBI Description A.thaliana chloroplast ndhA gene
Seq. No.
                   150038
                   LIB3175-035-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3062791
BLAST score
                   168
E value
                   1.0e-11
Match length
                   64
% identity
                  (AB010433) Lipid transfer protein [Brassica rapa]
NCBI Description
Seq. No.
                   150039
                   LIB3175-035-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4586264
BLAST score
                  101
E value
                   7.0e-04
Match length
                  125
% identity
                   (AL049640) blue copper-binding protein, 15K (lamin)
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   150040
Seq. ID
                  LIB3175-035-P1-K1-B5
Method
                  BLASTN
NCBI GI
                   g431257
BLAST score
                   381
E value
                   0.0e + 00
```

```
449
Match length
                   97
% identity
NCBI Description Arabidopsis thaliana lipoxygenase (Lox2) mRNA, complete cds
Seq. No.
                   150041
                   LIB3175-035-P1-K1-B6
Seq. ID
Method
                   BLASTX
                   g3367592
NCBI GI
BLAST score
                   376
E value
                   4.0e-36
Match length
                   121
% identity
                   70
NCBI Description
                   (AL031135) putative protein [Arabidopsis thaliana]
                   150042
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-B8
Method
                   BLASTN
                   g4757405
NCBI GI
BLAST score
                   183
E value
                   2.0e-98
                   344
Match length
                   88
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MOJ10, complete sequence
                   150043
Seq. No.
                   LIB3175-035-P1-K1-B9
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3123188
BLAST score
                   676
E value
                   3.0e-71
Match length
                   138
                   95
% identity
                  CATALASE 3 >gi_2347178 (U43147) catalase 3 [Arabidopsis
NCBI Description
                   thaliana] >gi_\overline{2}511726 (AF021937) catalase 3 [Arabidopsis
                   thaliana]
                   150044
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   g1619602
BLAST score
                   211
E value
                   9.0e-17
Match length
                   116
% identity
                   38
NCBI Description
                  (Y08726) MtN3 [Medicago truncatula]
Seq. No.
                   150045
Seq. ID
                  LIB3175-035-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  q4056476
BLAST score
                  52
E value
                   3.0e-20
                  96
Match length
                  89
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3G5 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

```
150046
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-C12
Method
                   BLASTN
NCBI GI
                   g2281081
                   224
BLAST score
                   1.0e-123
E value
Match length
                   415
                   97
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F18019 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   150047
Seq. No.
                   LIB3175-035-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g115385
BLAST score
                   313
                   6.0e-29
E value
Match length
                   84
% identity
                   76
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   150048
                   LIB3175-035-P1-K1-C4
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3659908
BLAST score
                   227
E value
                   1.0e-125
                   239
Match length
% identity
                   99
NCBI Description
                   Arabidopsis thaliana histidyl-tRNA synthetase mRNA,
                   complete cds
Seq. No.
                   150049
Seq. ID
                   LIB3175-035-P1-K1-C5
Method
                   BLASTN
NCBI GI
                   q4325340
BLAST score
                   247
E value
                   1.0e-136
Match length
                   444
% identity
                   100
NCBI Description Arabidopsis thaliana BAC T1J1
Seq. No.
                   150050
Seq. ID
                   LIB3175-035-P1-K1-C7
Method
                   BLASTN
NCBI GI
                   g4467094
BLAST score
                   401
E value
                   0.0e + 00
Match length
                   454
                   97
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
NCBI Description
                   (ESSA project)
Seq. No.
                   150051
```

```
Seq. ID
                  LIB3175-035-P1-K1-D1
Method
                  BLASTN
NCBI GI
                   q3776000
BLAST score
                   312
                   1.0e-175
E value
Match length
                   374
                   99
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for DEAD box RNA helicase, RH12
Seq. No.
Seq. ID
                  LIB3175-035-P1-K1-D10
Method
                  BLASTX
NCBI GI
                   q1175395
BLAST score
                   153
E value
                   5.0e-10
Match length
                   105
                   31
% identity
                  HYPOTHETICAL 14.1 KD PROTEIN C31A2.02 IN CHROMOSOME I
NCBI Description
                  >gi_2130413_pir__S58099 hypothetical protein SPAC31A2.02 -
                   fission yeast (Schizosaccharomyces pombe)
                   >gi_914880_emb_CAA90460_ (Z50113) unknown
                   [Schizosaccharomyces pombe]
Seq. No.
                   150053
                  LIB3175-035-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2911057
BLAST score
                   631
                   5.0e-66
E value
                   123
Match length
% identity
                   100
                   (ALO21961) caffeoyl-CoA O-methyltransferase - like protein
NCBI Description
                   [Arabidopsis thaliana]
                   150054
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   g4371293
BLAST score
                   67
E value
                   6.5e+00
Match length
                   139
% identity
                   (AC006260) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   150055
Seq. No.
                  LIB3175-035-P1-K1-D3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2564049
BLAST score
                   141
E value
                   2.0e-73
Match length
                   253
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  LIB3175-035-P1-K1-D4
Seq. ID
```

```
Method
                   BLASTX
NCBI GI
                   q4210449
BLAST score
                   693
E value
                   3.0e-73
Match length
                   151
                   91
% identity
NCBI Description
                  (AB016471) ARR1 protein [Arabidopsis thaliana]
Seq. No.
                   150057
Seq. ID
                   LIB3175-035-P1-K1-D5
Method
                  BLASTN
NCBI GI
                   q4733952
BLAST score
                   433
E value
                   0.0e + 00
Match length
                   458
% identity
                  Arabidopsis thaliana chromosome I BAC F23H11 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   150058
                   LIB3175-035-P1-K1-D7
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4049335
BLAST score
                   389
                   9.0e-38
E value
Match length
                  88
% identity
                   (AL034567) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150059
Seq. ID
                   LIB3175-035-P1-K1-D8
Method
                  BLASTN
NCBI GI
                   g4337026
BLAST score
                   48
                   7.0e-18
E value
Match length
                   132
% identity
NCBI Description
                  Arabidopsis thaliana MFP2 mRNA, complete cds
                   150060
Seq. No.
Seq. ID
                  LIB3175-035-P1-K1-D9
Method
                  BLASTN
NCBI GI
                   q3367500
BLAST score
                   397
                   0.0e+00
E value
Match length
                   442
% identity
                   55
NCBI Description
                  REVERSE-COMPLEMENT OF: F23J3.GCG.SEQ CHECK: 2754 FROM: 1
                  TO: 93489, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150061
Seq. ID
                  LIB3175-035-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q4587615
BLAST score
                  479
E value
                   3.0e-48
Match length
                  150
```

```
% identity
NCBI Description
                   (AC006951) putative acyl-CoA synthetase [Arabidopsis
                   thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213)
                   putative acyl-CoA synthetase [Arabidopsis thaliana]
                   150062
Seq. No.
                   LIB3175-035-P1-K1-E11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3600055
BLAST score
                   714
E value
                   9.0e-76
Match length
                   134
                   100
% identity
                   (AF080120) contains similarity to Pisum sativum disease
NCBI Description
                   resistance response protein 206-d (GB:U11716) [Arabidopsis
                   thaliana]
                   150063
Seq. No.
                   LIB3175-035-P1-K1-E12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2864614
BLAST score
                   238
E value
                   6.0e-20
Match length
                   137
% identity
                   42
NCBI Description
                   (AL021811) putative protein [Arabidopsis thaliana]
Seq. No.
                   150064
                   LIB3175-035-P1-K1-E2
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4585981
BLAST score
                   52
E value
                   4.0e-29
                   134
Match length
                   75
% identity
NCBI Description
                   (AC005287) similar to Na+/H+-exchanging proteins
                   [Arabidopsis thaliana]
                   150065
Seq. No.
                   LIB3175-035-P1-K1-E3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3894172
BLAST score
                   569
                   9.0e-59
E value
Match length
                   109
% identity
NCBI Description
                   (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis
                   thaliana]
                   150066
Seq. No.
                   LIB3175-035-P1-K1-E5
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4455199
BLAST score
                   334
E value
                   3.0e - 31
Match length
                   78
                   85
% identity
```

```
NCBI Description (AL035440) putative protein [Arabidopsis thaliana]
Seq. No.
                  150067
Seq. ID
                  LIB3175-035-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g1076402
                  629
BLAST score
E value
                  7.0e-66
Match length
                  125
% identity
                  90
NCBI Description S-like ribonuclease RNS2 - Arabidopsis thaliana
Seq. No.
                  150068
Seq. ID
                  LIB3175-035-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  q3869069
                  77
BLAST score
E value
                  3.0e - 35
Match length
                  263
% identity
                  89
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MEB5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150069
Seq. ID
                  LIB3175-035-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  q4531444
                  773
BLAST score
E value
                  1.0e-82
Match length
                  149
% identity
                  99
NCBI Description
                  (AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  150070
Seq. ID
                  LIB3175-035-P1-K1-E9
Method
                  BLASTX
NCBI GI
                  g1418990
BLAST score
                  391
E value
                  7.0e-38
Match length
                  108
% identity
                  69
NCBI Description
                  (Z75524) unknown [Lycopersicon esculentum]
Seq. No.
                  150071
                  LIB3175-035-P1-K1-F10
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4699904
BLAST score
                  259
E value
                  1.0e-144
Match length
                  294
% identity
                  98
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F1E22,
                  complete sequence
                  150072
Seq. No.
                  LIB3175-035-P1-K1-F11
Seq. ID
Method
                  BLASTN
```

```
NCBI GI
                   q4589411
BLAST score
                   35
E value
                   3.0e-10
Match length
                   83
% identity
                   86
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   F5H8, complete sequence
Seq. No.
                   150073
Seq. ID
                   LIB3175-035-P1-K1-F12
Method
                   BLASTX
NCBI GI
                   q4469003
BLAST score
                   625
E value
                   3.0e-65
Match length
                   118
                   99
% identity
NCBI Description (AL035602) putative protein [Arabidopsis thaliana]
                   150074
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q2244977
BLAST score
                   580
E value
                   4.0e-60
Match length
                   129
% identity
NCBI Description (297340) cysteine proteinase [Arabidopsis thaliana]
Seq. No.
                   150075
Seq. ID
                   LIB3175-035-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q3493611
BLAST score
                   374
E value
                   7.0e-36
Match length
                   118
% identity
NCBI Description
                   (AF068318) regulatory subunit of protein kinase CK2; CK2
                   beta-subunit [Arabidopsis thaliana]
Seq. No.
                   150076
Seq. ID
                   LIB3175-035-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q1708924
BLAST score
                   310
E value
                   2.0e-28
Match length
                   81
% identity
                   68
NCBI Description
                  MALATE OXIDOREDUCTASE (MALIC ENZYME) (ME) (NADP-DEPENDENT
                   MALIC ENZYME) (NADP-ME) >gi_515759 (L34836) malate
                   dehydrogenase (NADP+) [Vitis vinifera]
Seq. No.
                   150077
Seq. ID
                   LIB3175-035-P1-K1-F6
Method
                  BLASTN
NCBI GI
                   g3063690
BLAST score
                   418
E value
                   0.0e + 00
```

```
Match length
                  454
% identity
                  98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11
                   (ESSAII project)
                  150078
Seq. No.
                  LIB3175-035-P1-K1-F7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2351064
BLAST score
                  374
                  0.0e + 00
E value
Match length
                  386
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MDJ22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150079
                  LIB3175-035-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3687301
BLAST score
                  152
E value
                  6.0e-10
Match length
                  92
% identity
NCBI Description
                   (AJ006376) subtilisin-like protease [Lycopersicon
                  esculentum] >gi_3687309_emb_CAA07001_ (AJ006380)
                  subtilisin-like protease [Lycopersicon esculentum]
Seq. No.
                  150080
Seq. ID
                  LIB3175-035-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g1169476
BLAST score
                  613
E value
                  6.0e-64
Match length
                  120
% identity
                  98
NCBI Description
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
Seq. No.
                  150081
                  LIB3175-035-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4589969
BLAST score
                  170
E value
                  1.0e-90
Match length
                  291
% identity
                  Arabidopsis thaliana chromosome II BAC F1P15 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  150082
                  LIB3175-035-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2252844
BLAST score
                  716
E value
                  5.0e-76
```

```
Match length
                   128
% identity
                   100
NCBI Description
                   (AF013293) belongs to the cytochrome p450 family
                   [Arabidopsis thaliana]
                   150083
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   g3241922
BLAST score
                   276
E value
                   1.0e-154
Match length
                   395
                   100
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MLM24, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150084
Seq. ID
                   LIB3175-035-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g1076393 ..
BLAST score
                   607
E value
                   3.0e-63
Match length
                   125
% identity
                   98
NCBI Description
                   RCI14A protein - Arabidopsis thaliana
                   >gi 540559 emb CAA52237 (X74140) RCI14A [Arabidopsis
                   thaliana]
Seq. No.
                   150085
Seq. ID
                   LIB3175-035-P1-K1-G2
Method
                   BLASTN
NCBI GI
                   g4159703
BLAST score
                   162
                   7.0e-86
E value
Match length
                   427
% identity
                   90
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K5F14, complete sequence
Seq. No.
                   150086
Seq. ID
                   LIB3175-035-P1-K1-G3
Method
                   BLASTX
NCBI GI
                   g4539389
BLAST score
                   373
E value
                   9.0e-36
Match length
                   76
% identity
                   100
NCBI Description
                  (AL035526) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                   150087
Seq. ID
                   LIB3175-035-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   q4455354
BLAST score
                   264
E value
                   5.0e-23
Match length
                   117
% identity
                   53
```



```
NCBI Description (AL035524) putative protein [Arabidopsis thaliana]
                   150088
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   q4376815
BLAST score
                   166
                   2.0e-11
E value
Match length
                   118
% identity
NCBI Description
                   (AE001637) GutQ/KpsF Family Sugar-P Isomerase [Chlamydia
                   pneumoniae]
                   150089
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   q120667
BLAST score
                   453
                   3.0e-45
E value
Match length
                   89
                   98
% identity
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
NCBI Description
                   >gi_81622_pir__JQ1287 glyceraldehyde-3-phosphate
                   dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
thaliana >gi_166706 (M64116) cystolic
                   glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                   thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                   dehydrogenase [Arabidopsis thaliana]
                   150090
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-H1
Method
                   BLASTX
NCBI GI
                   q939726
BLAST score
                   507
E value
                   1.0e-51
Match length
                   113
% identity
NCBI Description
                   (U31370) cyclophilin [Arabidopsis thaliana]
                   150091
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   g1170606
BLAST score
                   427
E value
                   4.0e-42
Match length
                   148
```

% identity

NCBI Description ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE)

>gi\_629863\_pir\_\_S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi\_3114421\_pdb\_1ZAK\_A Chain A,

Adenylate Kinase From Maize In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-)pentaphosphate (Ap5a)

>gi\_3114422 pdb\_1ZAK\_B Chain B, Adenylate Kinase From Maize

In Complex With The Inhibitor

P1, P5-Bis (Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No. 150092

```
LIB3175-035-P1-K1-H11
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3449333
BLAST score
                   236
                   1.0e-130
E value
                   414
Match length
                   46
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXF12, complete sequence [Arabidopsis thaliana]
                   150093
Seq. No.
                   LIB3175-035-P1-K1-H12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4581114
BLAST score
                   268
E value
                   2.0e-23
Match length
                   98
                   58
% identity
                   (AC005825) putative HesB-like protein; required for
NCBI Description
                   efficient nitrogen fixation in Cyanobacteria [Arabidopsis
                   thaliana]
                   150094
Seq. No.
                   LIB3175-035-P1-K1-H2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3286693
BLAST score
                   597
                   4.0e-62
E value
Match length
                   124
                   96
% identity
                   (Y15433) 33 kDa polypeptide of oxygen-evolving complex
NCBI Description
                   (OEC) in photosystem II [Arabidopsis thaliana]
                   150095
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-H4
Method
                   BLASTX
NCBI GI
                   g2160133
BLAST score
                   409
E value
                   6.0e-40
                   141
Match length
                   62
% identity
                   (AC000375) Strong similarity to Arabidopsis
NCBI Description
                   gb X91953, F19K23.3, F19K23.15. ESTs
                   gb T21984, gb ATTS0219, gb ATTS0207, gb T21984 come from this
                   gene. [Arabidopsis thaliana]
                   150096
Seq. No.
Seq. ID
                  LIB3175-035-P1-K1-H5
Method
                   BLASTN
                   g3449325
NCBI GI
BLAST score
                   370
                   0.0e + 00
E value
                   420
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K16H17, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                   150097
Seq. ID
                   LIB3175-035-P1-K1-H6
Method
                   BLASTX
NCBI GI
                   g4417280
BLAST score
                   746
E value
                   2.0e-79
Match length
                   152
% identity
                    99
NCBI Description
                    (AC007019) putative ATP synthase [Arabidopsis thaliana]
                   150098
Seq. No.
Seq. ID
                   LIB3175-035-P1-K1-H7
Method
                   BLASTN
NCBI GI
                   q2656025
BLAST score
                   409
                   0.0e+00
E value
Match length
                   453
                   97
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCD7
Seq. No.
                   150099
Seq. ID
                   LIB3175-035-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q120675
BLAST score
                   547
E value
                   4.0e-56
Match length
                   129
% identity
                   81
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66011_pir__DEIS3C glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12), cytosolic - white mustard
                   >gi_21143_emb_CAA27844_ (X04301) GAPDH (aa 1-338) [Sinapis
                   alba]
Seq. No.
                   150100
Seq. ID
                   LIB3175-036-P1-K1-A1
Method
                   BLASTX
NCBI GI
                   g3318611
BLAST score
                   210
E value
                   1.0e-16
                   52
Match length
% identity
NCBI Description
                    (AB016063) mitochondrial phosphate transporter [Glycine
Seq. No.
                   150101
Seq. ID
                   LIB3175-036-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g2864617
BLAST score
                   290
E value
                   2.0e-45
Match length
                   127
% identity
NCBI Description
                   (ALO21811) H+-transporting ATP synthase chain9 - like
                   protein [Arabidopsis thaliana]
```

```
Seq. No.
                  150102
Seq. ID
                  LIB3175-036-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2829870
BLAST score
                   684
                   3.0e-72
E value
                  156
Match length
% identity
                   86
NCBI Description
                  (AC002396) Hypothetical protein [Arabidopsis thaliana]
                  150103
Seq. No.
Seq. ID
                  LIB3175-036-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g1169201
BLAST score
                  522
E value
                  3.0e-53
Match length
                  135
% identity
                  80
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                  thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  150104
Seq. ID
                  LIB3175-036-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g1169201
                  270
BLAST score
                  7.0e-24
E value
Match length
                  86
% identity
                   66
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                  >gi 421830 pir S33707 DRT112 protein - Arabidopsis
                  thaliana >gi 166696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                  150105
Seq. ID
                  LIB3175-036-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q3107903
BLAST score
                  257
E value
                  3.0e-22
                  84
Match length
% identity
NCBI Description
                  (D83719) polycomb-like protein [Daucus carota]
                  150106
Seq. No.
Seq. ID
                  LIB3175-036-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  q1170767
BLAST score
                  264
E value
                  4.0e-23
Match length
                  112
% identity
                  53
                  26S PROTEASE REGULATORY SUBUNIT 8 HOMOLOG (LET1 PROTEIN)
NCBI Description
                  >gi_626074 pir S45176 transcription factor SUG1 homolog -
                  fission yeast (Schizosaccharomyces pombe) >gi 406051
                  (U02280) Let1 [Schizosaccharomyces pombe]
                  >gi_4106689 emb CAA22628 (AL035065) 26s protease
```



## regulatory subunit 8 homolog [Schizosaccharomyces pombe]

Seq. No. 150107 Seq. ID LIB3175-036-P1-K1-B12 Method BLASTX NCBI GI g3157931

BLAST score 550 1.0e-56 E value Match length 125 90 % identity

(AC002131) Similar to pyrophosphate-dependent NCBI Description

phosphofuctokinase beta subunit gb Z32850 from Ricinus communis. ESTs gb N65773, gb N64925 and gb F15232 come

from this gene. [Arabidopsis thaliana]

Seq. No. 150108

Seq. ID LIB3175-036-P1-K1-B2

Method BLASTX NCBI GI g130708 BLAST score 274 E value 5.0e-24 55 Match length 89 % identity

NCBI Description SERINE/THREONINE PROTEIN PHOSPHATASE PP1

>gi\_81693\_pir\_\_S12985 phosphoprotein phosphatase (EC
3.1.3.16) 1 catalytic chain - rape (fragment)

>gi 17846 emb CAA40686 (X57438) phosphatase 1 catalytic

subunit [Brassica napus]

Seq. No. 150109

Seq. ID LIB3175-036-P1-K1-B3

Method BLASTX NCBI GI g3164140 BLAST score 385 E value 7.0e-42 Match length 152 % identity 59

NCBI Description (D78605) cytochrome P450 monooxygenase [Arabidopsis

thaliana]

Seq. No. 150110

Seq. ID LIB3175-036-P1-K1-B4

Method BLASTN NCBI GI q4220640 BLAST score 282 E value 1.0e-157 Match length 418 % identity

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: NCBI Description

MPE11, complete sequence [Arabidopsis thaliana]

Seq. No. 150111

Seq. ID LIB3175-036-P1-K1-B6

Method BLASTX NCBI GI g1402908 BLAST score 536 E value 6.0e-55

```
Match length
                    127
% identity
                    83
                    (X98315) peroxidase [Arabidopsis thaliana]
NCBI Description
                    >gi_1429221_emb_CAA67313_ (X98777) peroxidase ATP16a
[Arabidopsis thaliana] >gi_4455802_emb_CAB37193_ (AJ133036)
                    peroxidase [Arabidopsis thaliana]
                    150112
Seq. No.
                    LIB3175-036-P1-K1-B7
Seq. ID
                    BLASTX
Method
                    g2246621
NCBI GI
BLAST score
                    246
E value
                    2.0e-60
                    130
Match length
                    96
% identity
                    (AF004393) salt-stress induced tonoplast intrinsic protein
NCBI Description
                    [Arabidopsis thaliana]
                                                       4.7
Seq. No.
                    150113
Seq. ID
                    LIB3175-036-P1-K1-C1
Method
                    BLASTX
NCBI GI
                    q2842490
BLAST score
                    448
                    1.0e-44
E value
Match length
                    87
                    97
% identity
                    (ALO21749) heat-shock protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    150114
Seq. ID
                    LIB3175-036-P1-K1-C10
Method
                    BLASTN
NCBI GI
                    g3860243
BLAST score
                    37
                    3.0e-11
E value
Match length
                    117
% identity
                    83
                    Arabidopsis thaliana chromosome II BAC F15K20 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                    150115
Seq. ID
                    LIB3175-036-P1-K1-C11
Method
                    BLASTX
NCBI GI
                    g4455329
BLAST score
                    693
E value
                    2.0e-73
Match length
                    142
% identity
                    99
                    (AL035525) lysine-ketoglutarate reductase/saccharopine
NCBI Description
                    [Arabidopsis thaliana]
Seq. No.
                    150116
                    LIB3175-036-P1-K1-C12
Seq. ID
Method
                    BLASTN
NCBI GI
                    g4455262
BLAST score
                    229
                    1.0e-126
E value
Match length
                    395
```

```
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                   (ESSAII project)
                   150117
Seq. No.
                  LIB3175-036-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1353352
BLAST score
                   342
                   4.0e-32
E value
Match length
                   100
% identity
                   (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                   reinhardtiil
                  150118
Seq. No.
                  LIB3175-036-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1169201
BLAST score
                   385
                   3.0e-37
E value
Match length
                   112
                   73
% identity
NCBI Description
                  DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT112 PRECURSOR
                   >gi_421830_pir__S33707 DRT112 protein - Arabidopsis
                  thaliana >gi 1\overline{66}696 (M98456) DRT112 [Arabidopsis thaliana]
Seq. No.
                   150119
                  LIB3175-036-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q3461848
BLAST score
                   163
E value
                   3.0e-11
Match length
                   62
% identity
                   65
NCBI Description
                   (AC005315) putative ATPase [Arabidopsis thaliana]
Seq. No.
                  150120
                  LIB3175-036-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4586047
BLAST score
                   334
                   4.0e-31
E value
Match length
                   146
                   53
% identity
NCBI Description
                   (AC007020) putative ferritin protein [Arabidopsis thaliana]
                  >gi_4588004_gb_AAD25945.1_AF085279_18 (AF085279)
                  hypothetical ferritin subunit [Arabidopsis thaliana]
Seq. No.
                  150121
                  LIB3175-036-P1-K1-C8
Seq. ID
Method
                  BLASTN
NCBI GI
                  a3337347
BLAST score
                  146
E value
                  2.0e-76
Match length
                  434
                   99
% identity
```

```
Arabidopsis thaliana chromosome II BAC F13P17 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   LIB3175-036-P1-K1-D1
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1084335
BLAST score
                   318
E value
                   2.0e-48
Match length
                   102
% identity
                   96
NCBI Description
                   calcium-dependent protein kinase (EC 2.7.1.-) 2 -
                   Arabidopsis thaliana >gi_604881_dbj_BAA04830_ (D21806)
                   calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.
                   150123
Seq. ID
                   LIB3175-036-P1-K1-D11
Method
                   BLASTX
NCBI GI
                   g2829891
BLAST score
                   550
E value
                   1.0e-56
Match length
                   118
% identity
                   91
NCBI Description
                   (AC002311) Unknown protein [Arabidopsis thaliana]
Seq. No.
                   150124
Seq. ID
                   LIB3175-036-P1-K1-D12
Method
                   BLASTN
NCBI GI
                   g3860243
BLAST score
                   184
E value
                   5.0e-99
Match length
                   394
% identity
                   97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150125
Seq. ID
                   LIB3175-036-P1-K1-D5
Method
                   BLASTN
NCBI GI
                   q166695
BLAST score
                   92
E value
                   2.0e-44
Match length
                   252
% identity
NCBI Description
                  Arabidopsis thaliana recombination and DNA-damage
                   resistance protein (DRT112) mRNA, complete cds
Seq. No.
                   150126
Seq. ID
                  LIB3175-036-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  q3461848
BLAST score
                  200
E value
                   2.0e-15
Match length
                  89
% identity
                  56
NCBI Description (AC005315) putative ATPase [Arabidopsis thaliana]
```

```
150127
Seq. No.
Seq. ID
                  LIB3175-036-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g1402877
                  502
BLAST score
                  3.0e-56
E value
                  154
Match length
% identity
                  79
NCBI Description
                  (X98130) unknown [Arabidopsis thaliana]
                  >gi 1495257 emb CAA66117 (X97485) orf03 [Arabidopsis
                  thaliana]
                  150128
Seq. No.
                  LIB3175-036-P1-K1-E10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g132074
                  497
BLAST score
E value
                  2.0e-50
Match length
                  97
% identity
                  96
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  150129
Seq. ID
                  LIB3175-036-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g2645198
BLAST score
                  103
E value
                  9.0e-51
Match length
                  367
                  83
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T26J12 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150130
                  LIB3175-036-P1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2335089
BLAST score
                  107
E value
                  4.0e-53
Match length
                  379
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T11A7 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150131
Seq. ID
                  LIB3175-036-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  q4006890
BLAST score
                  368
E value
                  2.0e-40
Match length
                  91
% identity
                  97
NCBI Description
                  (Z99708) ubiquitin--protein ligase-like protein
                  [Arabidopsis thaliana]
```

Seq. No. 150132 Seq. ID LIB3175-036-P1-K1-E3 Method BLASTX NCBI GI g417103 BLAST score 417 2.0e-58 E value Match length 131 % identity 96 NCBI Description HISTONE H3.2, MINOR >gi 282871 pir S24346 histone H3.3-like protein - Arabidopsis thaliana >gi\_16324\_emb\_CAA42957\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_404825\_emb\_CAA42958\_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi\_488563 (U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2 [Medicago sativa] >gi\_510911 emb\_CAA56153 (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445 (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_ (AL035708) Histon H3 [Arabidopsis thaliana] Seq. No. 150133 Seq. ID LIB3175-036-P1-K1-E4 Method **BLASTX** NCBI GI g2911057 BLAST score 469 E value 5.0e-47 Match length 115 % identity NCBI Description (AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana] Seq. No. 150134 Seq. ID LIB3175-036-P1-K1-E5 Method BLASTX NCBI GI g2911057 BLAST score 51 E value 4.0e-13 Match length 75 % identity NCBI Description (AL021961) caffeoyl-CoA O-methyltransferase - like protein [Arabidopsis thaliana] Seq. No. 150135 Seq. ID LIB3175-036-P1-K1-E6 Method BLASTX NCBI GI g1755162 BLAST score 683 E value 3.0e-80

```
156
Match length
% identity
                 (U75192) germin-like protein [Arabidopsis thaliana]
NCBI Description
                  150136
Seq. No.
                  LIB3175-036-P1-K1-E7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1363488
BLAST score
                  369
E value
                  3.0e-43
                  102
Match length
                  94
% identity
                  IAA8 protein - Arabidopsis thaliana >gi_972919 (U18410)
NCBI Description
                  IAA8 [Arabidopsis thaliana] >gi_4314364_gb_AAD15575_
                  (AC006340) auxin-induced IAA8 protein [Arabidopsis
                  thaliana]
                  150137
Seq. No.
                  LIB3175-036-P1-K1-E9
Seq. ID
                  BLASTX
Method
                  g114335
NCBI GI
                  729
BLAST score
                  2.0e-77
E value
                  148
Match length
                  97
% identity
                  PLASMA MEMBRANE ATPASE 2 (PROTON PUMP)
NCBI Description
                  >gi_67973_pir__PXMUP2 H+-transporting ATPase (EC 3.6.1.35)
                  type 2, plasma membrane - Arabidopsis thaliana >gi 166629
                  (J05570) H+-ATPase [Arabidopsis thaliana]
                  150138
Seq. No.
                  LIB3175-036-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112681
                  587
BLAST score
                  9.0e-65
E value
                  135
Match length
                  93
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi_808936_emb_CAA32493_ (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  150139
Seq. No.
                  LIB3175-036-P1-K1-F10
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3927822
BLAST score
                  46
                  9.0e-17
E value
                  70
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC F8N16 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  150140
Seq. No.
                  LIB3175-036-P1-K1-F12
Seq. ID
```

```
Method
                   BLASTN
NCBI GI
                   q4455262
BLAST score
                   82
E value
                   3.0e-38
Match length
                   214
                   85
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
NCBI Description
                   (ESSAII project)
Seq. No.
                   150141
Seq. ID
                   LIB3175-036-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   q1362007
BLAST score
                   743
E value
                   3.0e-79
Match length
                   140
                   99
% identity
                   thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana
NCBI Description
                   >gi_871992_emb_CAA55787_ (X79195) thioglucosidase
                   [Arabidopsis thaliana]
                   150142
Seq. No.
Seq. ID
                   LIB3175-036-P1-K1-F4
Method
                   BLASTX
                   g4741948
NCBI GI
BLAST score
                   614
E value
                   4.0e-64
Match length
                   116
                   99
% identity
                   (AF134124) Lhcb2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150143
                  LIB3175-036-P1-K1-F7
Seq. ID
Method
                  BLASTX
                   g3158376
NCBI GI
BLAST score
                   75
E value
                   2.0e-61
Match length
                   127
                   94
% identity
                  (AF035385) unknown [Arabidopsis thaliana]
NCBI Description
                  150144
Seq. No.
Seq. ID
                  LIB3175-036-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g4191771
BLAST score
                  184
                   5.0e-99
E value
Match length
                   463
                   95
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3P11 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                  150145
Seq. No.
Seq. ID
                  LIB3175-036-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  q2829892
BLAST score
                  829
```

```
E value
                  3.0e-89
Match length
                  157
                  99
% identity
                  (AC002311) putative pectinesterase [Arabidopsis thaliana]
NCBI Description
                  150146
Seq. No.
Seq. ID
                  LIB3175-036-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g1429209
BLAST score
                  617
                  2.0e-64
E value
Match length
                  121
                  99
% identity
NCBI Description
                  (X99111) beta-fructosidase [Arabidopsis thaliana]
Seq. No.
                  150147
Seq. ID
                  LIB3175-036-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g131770
BLAST score
                  355
E value
                  6.0e-37
Match length
                  119
% identity
                  58
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (40S RIBOSOMAL PROTEIN 1024)
                   (VEGETATIVE SPECIFIC PROTEIN V12) >gi_70880_pir__R3D024
                  ribosomal protein S9.e - slime mold (Dictyostelium
                  discoideum) >gi_7353_emb_CAA29844_ (X06636) rp1024 protein
                  [Dictyostelium discoideum]
Seq. No.
                  150148
Seq. ID
                  LIB3175-036-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q4262156
BLAST score
                  360
E value
                  1.0e-48
Match length
                  126
% identity
                  88
NCBI Description
                   (AC005275) putative component of cytochrome B6-F complex
                   [Arabidopsis thaliana]
Seq. No.
                 150149
Seq. ID
                  LIB3175-036-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  q3341671
BLAST score
                  215
E value
                  1.0e-117
Match length
                  271
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F16B22 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  150150
Seq. No.
Seq. ID
                  LIB3175-036-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2464913
BLAST score
                  591
E value
                  3.0e-61
```

```
Match length
                   120
% identity
                   99
                  (Z99708) sugar transporter like protein [Arabidopsis
NCBI Description
                   thaliana]
                   150151
Seq. No.
                   LIB3175-036-P1-K1-H12
Seq. ID
                   BLASTN
Method
                   g4455262
NCBI GI
BLAST score
                   46
                   8.0e-17
E value
Match length
                   288
                   92
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22
                   (ESSAII project)
Seq. No.
                   150152
                   LIB3175-036-P1-K1-H2
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4406767
BLAST score
                   224
E value
                   3.0e-60
                   121
Match length
                   98
% identity
                  (AC006836) putative flavonol sulfotransferase [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   150153
                  LIB3175-036-P1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1707013
BLAST score
                   216
E value
                   2.0e-17
                  100
Match length
                   44
% identity
                  (U78721) Brassica napus hypothetical protein 2 isolog
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   150154
                  LIB3175-036-P1-K1-H5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4567283
BLAST score
                   452
E value
                   4.0e-45
Match length
                  112
                   82
% identity
                  (AC006841) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150155
                  LIB3175-036-P1-K1-H6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3157937
BLAST score
                   333
E value
                  2.0e-31
                  75
Match length
                  87
% identity
                  (AC002131) Identical to aspartic proteinase cDNA gb_U51036
NCBI Description
```

19121

.

```
from A. thaliana. ESTs qb N96313, qb T21893, qb R30158,
                   gb_T21482, gb_T43650, gb_R64749, gb_R65157, gb_T88269,
                   gb_T44552, gb_T22542, gb_T76533, gb_T44350, gb_Z34591,
                   gb_AA728734, gb
                   150156
Seq. No.
                   LIB3175-036-P1-K1-H7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2618602
BLAST score
                   152
E value
                   6.0e-80
Match length
                   391
                   95
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MSJ1, complete sequence [Arabidopsis thaliana]
                   150157
Seq. No.
Seq. ID
                   LIB3175-036-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q4337175
BLAST score
                   672
E value
                   4.0e-72
Match length
                   140
% identity
NCBI Description
                   (AC006416) ESTs gb T20589, gb T04648, gb AA597906,
                   gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570,
                   gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]
Seq. No.
                   150158
Seq. ID
                   LIB3175-037-P1-K1-A10
Method
                   BLASTX
NCBI GI
                   q4510345
BLAST score
                   436
E value
                   5.0e-43
Match length
                   90
% identity
NCBI Description
                   (AC006921) unknown protein [Arabidopsis thaliana]
                   150159
Seq. No.
Seq. ID
                   LIB3175-037-P1-K1-A11
Method
                   BLASTN
NCBI GI
                   g2924257
BLAST score
                   329
E value
                   0.0e+00
Match length
                   398
% identity
                   48
NCBI Description
                   Tobacco chloroplast genome DNA
                   150160
Seq. No.
Seq. ID
                   LIB3175-037-P1-K1-A12
Method
                   BLASTX
NCBI GI
                   q4249382
BLAST score
                   268
E value
                   1.0e-23
Match length
                   73
% identity
                   67
```

```
(AC005966) Strong similarity to gi_3337350 F13P17.3
NCBI Description
                  putative permease from Arabidopsis thaliana BAC
                  gb AC004481. [Arabidopsis thaliana]
Seq. No.
                  150161
                  LIB3175-037-P1-K1-A4
Seq. ID
                  BLASTX
Method
                  q3004557
NCBI GI
BLAST score
                  113
                   3.0e-15
E value
Match length
                  64
% identity
                  86
                   (AC003673) plasma membrane proton pump H+ ATPase, PMA1
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  150162
                  LIB3175-037-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2338712
BLAST score
                  262
E value
                  8.0e-23
                  69
Match length
                   74
% identity
NCBI Description
                   (AF013959) metallothionein-like protein [Arabidopsis
                  thaliana]
                  150163
LIB3175-037-P1-K1-A9
Seq. No.
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2618602
BLAST score
                  235
                   1.0e-129
E value
                   383
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MSJ1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150164
                  LIB3175-037-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1657616
BLAST score
                  99
E value
                   2.0e-48
Match length
                  245
% identity
                  Arabidopsis thaliana putative nuclear DNA-binding protein
NCBI Description
                  G2p (AtG2) mRNA, complete cds
Seq. No.
                   150165
                  LIB3175-037-P1-K1-B11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4512690
BLAST score
                  198
E value
                   1.0e-107
Match length
                  403
                   98
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F11A3 genomic
```



## sequence, complete sequence

```
Seq. No.
                   150166
                   LIB3175-037-P1-K1-B12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3236238
BLAST score
                   632
E value
                   3.0e-66
Match length
                   122
% identity
                   98
NCBI Description
                   (ACO04684) putative ARF1 GTPase activating protein
                   [Arabidopsis thaliana] >gi_4519792_dbj_BAA75744.1_
                   (AB017876) Aspl [Arabidopsis thaliana]
Seq. No.
                   150167
Seq. ID
                   LIB3175-037-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g4559332
BLAST score
                   322
E value
                   7.0e-30
Match length
                   66
% identity
NCBI Description
                   (AC007087) putative phosphoenolpyruvate carboxylase
                   [Arabidopsis thaliana]
Seq. No.
                   150168
Seq. ID
                   LIB3175-037-P1-K1-C11
Method
                   BLASTN
NCBI GI
                   g405130
BLAST score
                   234
E value
                   1.0e-129
Match length
                   314
% identity
                   94
NCBI Description
                   Arabidopsis thaliana nuclear-encoded chloroplast stromal
                   cyclophilin (ROC4) mRNA, complete cds
Seq. No.
                   150169
                   LIB3175-037-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1755162
BLAST score
                   565
E value
                   2.0e-58
Match length
                   112
% identity
                   96
NCBI Description
                   (U75192) germin-like protein [Arabidopsis thaliana]
Seq. No.
                   150170
                   LIB3175-037-P1-K1-C3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3482931
BLAST score
                   539
E value
                   2.0e-55
Match length
                   115
% identity
                   (AC003970) germin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150171
```

```
Seq. ID
                  LIB3175-037-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1170939
BLAST score
                  353
                  1.0e-33
E value
Match length
                  70
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                  >gi 1084408 pir S46540 methionine adenosyltransferase (EC
                  2.5.1.6) - tomato >gi 429108 emb CAA80867 (Z24743)
                  S-adenosyl-L-methionine synthetase [Lycopersicon
                  esculentum]
                  150172
Seq. No.
Seq. ID
                  LIB3175-037-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g548653
BLAST score
                  425
E value
                  5.0e-42
Match length
                  104
                  85
% identity
                  50S RIBOSOMAL PROTEIN L12-A, CHLOROPLAST PRECURSOR (CL12-A)
NCBI Description
                  >gi 541895 pir A53394 ribosomal protein L12.A, chloroplast
                  - Arabidopsis thaliana >gi 468771 emb CAA48181 (X68046)
                  ribosomal protein L12 [Arabidopsis thaliana]
Seq. No.
                  150173
Seq. ID
                  LIB3175-037-P1-K1-C8
                  BLASTX
Method
NCBI GI
                  g1705998
BLAST score
                  345
E value
                  2.0e-32
Match length
                  120
% identity
                  60
                  COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-COP)
NCBI Description
                  >gi 1082254 pir A55136 beta-coat protein - human
                  (fragment) >gi 620110 emb CAA57622 (X82103) beta-Coat
                  protein [Homo sapiens]
Seq. No.
                  150174
Seq. ID
                  LIB3175-037-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g3851636
BLAST score
                  397
E value
                  1.0e-38
                  103
Match length
                  71
% identity
NCBI Description
                  (AF098519) unknown [Avicennia marina] >gi 4128206
                  (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                  150175
Seq. ID
                  LIB3175-037-P1-K1-D1
                  BLASTX
Method
NCBI GI
                  g1086252
BLAST score
                  173
E value
                  2.0e-12
```

```
Match length
                  63
% identity
                  sucrose cleavage protein - Potato >gi_707001_bbs_157931
NCBI Description
                   (S74161) sucrolytic enzyme/ferredoxin homolog [Solanum
                  tuberosum=potatoes, cv. Cara, leaf, Peptide, 322 aa]
                  [Solanum tuberosum]
                  150176
Seq. No.
Seq. ID
                  LIB3175-037-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q4006881
BLAST score
                  43
                  6.0e-51
E value
                  116
Match length
                  67
% identity
                  (299707) putative protein [Arabidopsis thaliana]
NCBI Description
                  150177
Seq. No.
                  LIB3175-037-P1-K1-D11
Seq. ID
Method
                  BLASTN
                  q3650026
NCBI GI
                  277
BLAST score
E value
                  1.0e-154
Match length
                  380
                  93
% identity
                  Arabidopsis thaliana chromosome II BAC T26I20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  150178
Seq. No.
                  LIB3175-037-P1-K1-D12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2909783
BLAST score
                  584
                   1.0e-60
E value
Match length
                   125
% identity
NCBI Description
                   (AF020289) MgATP-energized glutathione S-conjugate pump
                   [Arabidopsis thaliana]
                  150179
Seq. No.
Seq. ID
                  LIB3175-037-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g4581138
BLAST score
                  322
E value
                  0.0e + 00
Match length
                  342
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F1011 genomic
                  sequence, complete sequence
Seq. No.
                  150180
Seq. ID
                  LIB3175-037-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  g3985950
BLAST score
                  261
E value
                  1.0e-145
Match length
                  362
```

```
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MPI10, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150181
                   LIB3175-037-P1-K1-D4
Seq. ID
                   BLASTX
Method
                   q1170089
NCBI GI
BLAST score
                   609
                   5.0e-64
E value
Match length
                   132
% identity
                   GLUTATHIONE S-TRANSFERASE ERD13 (CLASS PHI)
NCBI Description
                   >gi_481822_pir__S39542 probable glutathione transferase (EC
                   2.5.1.18) (clone ERD13) - Arabidopsis thaliana >gi_497789 dbj_BAA04554_ (D17673) glutathione S-transferase
                   [Arabidopsis thaliana] >gi_3201614 (AC004669) glutathione
                   S-transferase [Arabidopsis thaliana]
Seq. No.
                   150182
                   LIB3175-037-P1-K1-D5
Seq. ID
Method
                   BLASTX
                   g3914917
NCBI GI
BLAST score
                   333
E value
                   3.0e - 31
Match length
                   64
                   100
% identity
                   40S RIBOSOMAL PROTEIN S3A
NCBI Description
                   150183
Seq. No.
Seq. ID
                   LIB3175-037-P1-K1-D6
Method
                   BLASTN
NCBI GI
                   q3242970
BLAST score
                   198
                   1.0e-107
E value
Match length
                   368
% identity
                   98
                   Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   150184
Seq. ID
                   LIB3175-037-P1-K1-D7
Method
                   BLASTN
NCBI GI
                   q2244788
BLAST score
                   75
E value
                   5.0e-34
Match length
                   236
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   150185
Seq. No.
Seq. ID
                   LIB3175-037-P1-K1-E1
Method
                   BLASTN
NCBI GI
                   g4589419
BLAST score
                   174
E value
                   5.0e-93
```

```
433
Match length
% identity
                   53
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2I5, complete sequence
Seq. No.
                  150186
                  LIB3175-037-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3169172
BLAST score
                   452
E value
                   4.0e-45
Match length
                   122
% identity
                   70
NCBI Description
                   (AC004401) putative serine carboxypeptidase I [Arabidopsis
                   thaliana] >gi 3445214 (AC004786) putative serine
                   carboxypeptidase I [Arabidopsis thaliana]
Seq. No.
                   150187
Seq. ID
                   LIB3175-037-P1-K1-E12
Method
                  BLASTX
NCBI GI
                   g3885343
BLAST score
                   249
E value
                   3.0e-21
Match length
                   119
% identity
                   39
NCBI Description
                   (AC005623) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   150188
                  LIB3175-037-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2664210
BLAST score
                   121
E value
                   3.0e-70
Match length
                   138
% identity
                   93
NCBI Description
                   (AJ222644) asparaginyl-tRNA synthetase [Arabidopsis
                   thaliana]
Seq. No.
                   150189
Seq. ID
                  LIB3175-037-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                   527
E value
                   5.0e-54
                  104
Match length
% identity
                   96
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543
                                                              (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  150190
Seq. ID
                  LIB3175-037-P1-K1-E6
Method
                  BLASTX
                  g4580460
NCBI GI
BLAST score
                  392
E value
                  3.0e-38
```

```
Match length
                   100
% identity
                   (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                   thaliana]
                   150191
Seq. No.
                   LIB3175-037-P1-K1-E8
Seq. ID
Method
                   BLASTX
NCBI GI
                   q462579
BLAST score
                   337
E value
                   2.0e-31
Match length
                   93
                   74
% identity
                   MALATE DEHYDROGENASE (NADP), CHLOROPLAST PRECURSOR
NCBI Description
                   (NADP-MDH) >gi_481222_pir__$38346 malate dehydrogenase (NADP+) (EC 1.1.1.82) - garden pea >gi_397475_emb_CAA52614_
                   (X74507) malate dehydrogenase (NADP+) [Pisum sativum]
                   150192
Seq. No.
Seq. ID
                   LIB3175-037-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q4544399
BLAST score
                   318
E value
                   3.0e-29
                   123
Match length
% identity
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   150193
Seq. No.
Seq. ID
                   LIB3175-037-P1-K1-F1
Method
                   BLASTN
NCBI GI
                   q3420042
BLAST score
                   139
E value
                   4.0e-72
Match length
                   458
% identity
                   99
                   Arabidopsis thaliana chromosome II BAC T13E15 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150194
Seq. ID
                   LIB3175-037-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q2829899
BLAST score
                   399
E value
                   7.0e-39
Match length
                   115
% identity
NCBI Description
                   (AC002311) similar to ripening-induced protein,
                   gp AJ001449 2465015 and major#latex protein,
                   gp X91961 1107495 [Arabidopsis thaliana]
Seq. No.
                   150195
                   LIB3175-037-P1-K1-F11
Seq. ID
Method:
                   BLASTN
NCBI GI
                   g2351069
BLAST score
                   309
```

```
1.0e-173
E value
Match length
                   361
                   96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSH12, complete sequence [Arabidopsis thaliana]
                   150196
Seq. No.
                   LIB3175-037-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2961356
BLAST score
                   637
                   1.0e-66
E value
                   135
Match length
% identity
NCBI Description
                   (AL022140) alcohol dehydrogenase like protein [Arabidopsis
                   thaliana]
                   150197
Seq. No.
                   LIB3175-037-P1-K1-F2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2062153
BLAST score
                   272
E value
                   1.0e-151
Match length
                   371
                   97
% identity
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150198
                   LIB3175-037-P1-K1-F3
Seq. ID
Method
                   BLASTX
                   g3859536
NCBI GI
                   371
BLAST score
                   4.0e-36
E value
                   74
Match length
                   93
% identity
                  (AF095453) asparagine synthetase [Arabidopsis thaliana]
NCBI Description
                   150199
Seq. No.
                   LIB3175-037-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4741940
BLAST score
                   242
                   1.0e-20
E value
                   72
Match length
% identity
NCBI Description
                   (AF134120) Lhca2 protein [Arabidopsis thaliana]
Seq. No.
                   150200
                   LIB3175-037-P1-K1-F5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4204277
BLAST score
                   233
                   1.0e-19
E value
Match length
                   79
% identity
                   (AC004146) Hypothetical protein [Arabidopsis thaliana]
NCBI Description
```

Method

BLASTX

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Seq. No.
                  150201
Seq. ID
                  LIB3175-037-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g4490292
BLAST score
                  622
                  5.0e-65
E value
Match length
                  123
% identity
                  99
NCBI Description
                   (AL035678) putative protein [Arabidopsis thaliana]
                  150202
Seq. No.
                  LIB3175-037-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4063737
BLAST score
                  290
E value
                  1.0e-162
Match length
                  425
                  97
% identity
                  Arabidopsis thaliana chromosome II BAC F24D13 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150203
                  LIB3175-037-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2832611
BLAST score
                  295
E value
                   1.0e-165
                   327
Match length
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5
NCBI Description
                   (ESSAII project)
Seq. No.
                  150204
Seq. ID
                  LIB3175-037-P1-K1-G10
Method
                  BLASTX
NCBI GI
                  g2244828
BLAST score
                   472
E value
                   3.0e-50
Match length
                   114
% identity
                   100
                   (Z97336) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150205
                  LIB3175-037-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2244991
BLAST score
                   331
E value
                   0.0e + 00
Match length
                   418
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                  150206
Seq. No.
Seq. ID
                  LIB3175-037-P1-K1-G12
```

```
NCBI GI
                   a3548801
BLAST score
                   210
E value
                   9.0e-17
Match length
                   119
% identity
                   35
NCBI Description
                   (AC005313) putative transmembrane protein [Arabidopsis
                   thaliana] >gi_4335768_gb_AAD17445_ (AC006284) putative
                   integral membrane protein [Arabidopsis thaliana]
Seq. No.
                   150207
Seq. ID
                   LIB3175-037-P1-K1-G2
Method
                   BLASTX
NCBI GI
                   q2506031
BLAST score
                   636
E value
                   1.0e-66
Match length
                   131
% identity
                   95
NCBI Description
                   (D43962) homeodomein containing protein 1 [Arabidopsis
                   thaliana] >gi_3858938_emb_CAA16585.1_ (AL021636)
                   homeodomain containing protein 1 [Arabidopsis thaliana]
Seq. No.
                   150208
Seq. ID
                  LIB3175-037-P1-K1-G4
Method
                   BLASTX
NCBI GI
                   q625977
BLAST score
                   607
E value
                   3.0e-63
Match length
                   118
% identity
                   99
NCBI Description
                  p40 protein homolog - Arabidopsis thaliana >gi 402904
                   (U01955) laminin receptor-like protein [Arabidopsis
                   thaliana]
Seq. No.
                   150209
Seq. ID
                  LIB3175-037-P1-K1-G5
Method
                   BLASTX
NCBI GI
                   q4678261
BLAST score
                   61
E value
                   9.0e-54
Match length
                   124
% identity
                   94
NCBI Description
                   (AL049657) putative proteasome regulatory subunit
                   [Arabidopsis thaliana]
Seq. No.
                   150210
Seq. ID
                  LIB3175-037-P1-K1-G6
Method
                  BLASTN
NCBI GI
                   g3641835
BLAST score
                   184
E value
                   3.0e-99
Match length
                   235
% identity
                   98
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T4L20
                   (ESSAII project)
Seq. No.
                  150211
Seq. ID
                  LIB3175-037-P1-K1-G7
```

```
Method
                  BLASTN
                  q3510343
NCBI GI
BLAST score
                  376
                  0.0e + 00
E value
Match length
                  412
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
                  150212
Seq. No.
                  LIB3175-037-P1-K1-H1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2760606
BLAST score
                  514
                  3.0e-52
E value
Match length
                  99
                  99
% identity
                  (AB001568) phospholipid hydroperoxide glutathione
NCBI Description
                  peroxidase-like protein [Arabidopsis thaliana] >gi_3004869
                  (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis
                  thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500)
                  phospholipid hydroperoxide glutathione peroxidase
                   [Arabidopsis thaliana]
Seq. No.
                  150213
                  LIB3175-037-P1-K1-H10
Seq. ID
Method
                  BLASTX
                  q3298542
NCBI GI
BLAST score
                  133
                  6.0e-15
E value
                  84
Match length
% identity
                  55
                  (AC004681) putative cellulose synthase [Arabidopsis
NCBI Description
                  thaliana]
                  150214
Seq. No.
Seq. ID
                  LIB3175-037-P1-K1-H11
Method
                  BLASTN
NCBI GI
                  q4585891
BLAST score
                  211
                  1.0e-115
E value
Match length
                  258
% identity
                  96
                  Arabidopsis thaliana chromosome II BAC T103 genomic
NCBI Description
                  sequence, complete sequence
                  150215
Seq. No.
                  LIB3175-037-P1-K1-H12
Seq. ID
Method
                  BLASTN
                  g4063756
NCBI GI
BLAST score
                  112
E value
                  1.0e-56
Match length
                  150
% identity
                  Arabidopsis thaliana chromosome II BAC T9F8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                   150216
Seq. ID
                  LIB3175-037-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g4586576
                  235
BLAST score
                   3.0e-20
E value
                   63
Match length
% identity
                   68
NCBI Description
                   (AB024992) multidrug resistance protein [Cicer arietinum]
Seq. No.
                  150217
                  LIB3175-037-P1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3550981
BLAST score
                  77
E value
                   3.0e-35
Match length
                  268
% identity
                   100
NCBI Description
                  Arabidopsis thaliana mutM homologue gene, complete cds
Seq. No.
                   150218
Seq. ID
                  LIB3175-037-P1-K1-H5
Method
                  BLASTN
NCBI GI
                   g2760172
BLAST score
                  297
E value
                   1.0e-166
Match length
                   352
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUB3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150219
                  LIB3175-037-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2565036
BLAST score
                  227
E value
                   6.0e-19
Match length
                  75
% identity
                   53
                   (U75921) APC binding protein EB1 [Rattus norvegicus]
NCBI Description
Seq. No.
                  150220
Seq. ID
                  LIB3175-037-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2645971
BLAST score
                  533
E value
                  1.0e-54
Match length
                  116
% identity
                  83
NCBI Description
                   (AF034255) reversibly glycosylated polypeptide-3
                   [Arabidopsis thaliana]
                  150221
Seq. No.
Seq. ID
                  LIB3175-038-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g4539316
BLAST score
                  457
```

```
E value
                  8.0e-46
                  96
Match length
% identity
                  98
                   (AL035679) putative fructose-bisphosphate aldolase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  150222
                  LIB3175-038-P1-K1-A10
Seq. ID
                  BLASTN
Method
                  g4558656
NCBI GI
                  248
BLAST score
                  1.0e-137
E value
                  477
Match length
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T10F5 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  150223
                  LIB3175-038-P1-K1-A11
Seq. ID
                  BLASTN
Method
NCBI GI
                  g16726
BLAST score
                  38
                  1.0e-11
E value
                  98
Match length
                  91
% identity
NCBI Description
                  ATTS0156 Gif-SeedA+B Arabidopsis thaliana cDNA clone
                  YAP007T, mRNA sequence [Arabidopsis thaliana]
                  >gi 1107498 emb X91953 ATORF007 A.thaliana mRNA for unknown
                  protein (clone YAP007)
                  150224
Seq. No.
                  LIB3175-038-P1-K1-A12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4220641
BLAST score
                  48
                  3.0e-18
E value
                  157
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUL3, complete sequence [Arabidopsis thaliana]
                  150225
Seq. No.
                  LIB3175-038-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2454184
BLAST score
                  305
                  4.0e-28
E value
                  76
Match length
% identity
                  86
                  (U80186) pyruvate dehydrogenase El beta subunit
NCBI Description
                   [Arabidopsis thaliana]
                  150226
Seq. No.
Seq. ID
                  LIB3175-038-P1-K1-A5
Method
                  BLASTX
                  g3170525
NCBI GI
BLAST score
                  378
```

```
E value
                  2.0e-36
Match length
                  125
% identity
                  55
                  (AF054615) cellulase [Fragaria x ananassa]
NCBI Description
                  150227
Seq. No.
                  LIB3175-038-P1-K1-A6
Seq. ID
                  BLASTX
Method
                  g2688824
NCBI GI
                  322
BLAST score
                  9.0e-30
E value
Match length
                  134
                  57
% identity
                  (U93273) putative auxin-repressed protein [Prunus
NCBI Description
                  armeniaca]
                  150228
Seq. No.
                  LIB3175-038-P1-K1-A7
Seq. ID
Method
                  BLASTN
                  g3510343
NCBI GI
                  258
BLAST score
                  1.0e-143
E value
Match length
                  486
% identity
                  99
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150229
Seq. ID
                  LIB3175-038-P1-K1-A8
Method
                  BLASTN
                  q4406805
NCBI GI
                  297
BLAST score
                  1.0e-166
E value
                  466
Match length
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T27K22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150230
                  LIB3175-038-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345655
BLAST score
                  369
                  7.0e-44
E value
                  126
Match length
                  75
% identity
                  CINNAMYL-ALCOHOL DEHYDROGENASE 2 (CAD)
NCBI Description
                  >gi_757535_emb_CAA83508_ (Z31715) cinnamyl alcohol
                  dehydrogenase [Arabidopsis thaliana]
Seq. No.
                  150231
                  LIB3175-038-P1-K1-B1
Seq. ID
Method
                  BLASTN
                  g2827513
NCBI GI
BLAST score
                  270
                  1.0e-150
E value
                  286
Match length
```

Match length

433

```
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8F16
NCBI Description
                   (ESSAII project)
                  150232
Seq. No.
                  LIB3175-038-P1-K1-B10
Seq. ID
                  BLASTX
Method
                  g2062161
NCBI GI
                  642
BLAST score
                  2.0e-67
E value
                  133
Match length
                  46
% identity
                   (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  150233
Seq. No.
Seq. ID
                  LIB3175-038-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  q402551
                  179
BLAST score
                  5.0e-96
E value
                  191
Match length
                  99
% identity
NCBI Description A.thaliana gene for acetohydroxy acid isomeroreductase
Seq. No.
                  150234
Seq. ID
                  LIB3175-038-P1-K1-B4
                  BLASTN
Method
                  q1931636
NCBI GI
                  244
BLAST score
E value
                  1.0e-135
Match length
                  340
                  99
% identity
NCBI Description Arabidopsis thaliana BAC T19D16 genomic sequence
                  150235
Seq. No.
Seq. ID
                  LIB3175-038-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g544425
BLAST score
                  292
E value
                  1.0e-26
Match length
                  59
% identity
                  98
                  GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
NCBI Description
                  >gi_419756_pir__S30148 glycine-rich protein (clone AtGRP8)
                  - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                  glycine rich protein [Arabidopsis thaliana] >gi_166658
                   (L04171) ORF [Arabidopsis thaliana] >gi_166839 (L00649)
                  RNA-binding protein [Arabidopsis thaliana]
                  150236
Seq. No.
                  LIB3175-038-P1-K1-B7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4585952
BLAST score
                  433
                  0.0e + 00
E value
```

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```
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC F26F24,
                  complete sequence
Seq. No.
                  150237
                  LIB3175-038-P1-K1-B8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3335357
BLAST score
                  748
E value
                  1.0e-79
Match length
                  140
                  97
% identity
                  (AC003028) putative diphenol oxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150238
Seq. ID
                  LIB3175-038-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  q3927831
BLAST score
                  602
E value
                  3.0e-80
Match length
                  154
% identity
NCBI Description
                  (AC005727) similar to mouse ankyrin 3 [Arabidopsis
                  thaliana]
Seq. No.
                  150239
Seq. ID
                  LIB3175-038-P1-K1-C1
Method
                  BLASTN
NCBI GI
                  g3510347
BLAST score
                  155
E value
                  1.0e-81
Match length
                  480
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150240
Seq. ID
                  LIB3175-038-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  q3702731
BLAST score
                  178
E value
                  2.0e-95
Match length
                  480
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFC19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150241
Seq. ID
                  LIB3175-038-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  q4507433
BLAST score
                  220
E value
                  8.0e-18
Match length
                  124
                  40
% identity
NCBI Description
                  testis enhanced gene transcript
                  >gi_1729891_sp_P55061_TEGT_HUMAN TEGT PROTEIN (TESTIS
```

ENHANCED GENE TRANSCRIPT) >gi\_2136254\_pir\_\_I38334 TEGT (testis enhanced gene transcript) - human >gi 458545\_emb CAA53472 (X75861) TEGT [Homo sapiens]

Seq. No. 150242

Seq. ID LIB3175-038-P1-K1-C12

Method BLASTX NCBI GI g3929364 BLAST score 280 E value 6.0e-25 Match length 64 % identity

NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR NCBI Description

(COMPLEX I-23KD) (CI-23KD) >gi\_1076356\_pir\_\_S52380 NADH dehydrogenase (EC 1.6.99.3) - Arabidopsis thaliana >gi\_666977\_emb\_CAA59061\_ (X84318) NADH dehydrogenase [Arabidopsis thaliana] >gi\_3152573 (AC002986) Match to NADH: ubiquinone oxidoreductase gb X84318 from A.thaliana. ESTs gb\_ $\overline{2}27005$ , gb\_ $\overline{1}04711$ , gb\_ $\overline{1}45\overline{0}78$  and gb\_ $\overline{2}28689$  come from this gene. [Arabidopsis thaliana]

Seq. No. 150243

Seq. ID LIB3175-038-P1-K1-C2

Method BLASTN NCBI GI q3510347 BLAST score 115 E value 8.0e-58 Match length 338 % identity 92

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MSJ11, complete sequence [Arabidopsis thaliana]

Seq. No. 150244

Seq. ID LIB3175-038-P1-K1-C4

Method BLASTN NCBI GI g2564214 BLAST score 393 E value 0.0e + 00Match length 405 % identity 100

NCBI Description Arabidopsis thaliana mRNA for glycyl-tRNA synthetase

Seq. No. 150245

Seq. ID LIB3175-038-P1-K1-C5

Method BLASTX NCBI GI g4586265 BLAST score 572 E value 4.0e-59 Match length 153 % identity

NCBI Description (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 150246

LIB3175-038-P1-K1-C6 Seq. ID

Method BLASTN NCBI GI q3293583 BLAST score 154

Match length

```
5.0e-81
E value
                  488
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana BAC T27D20
                  150247
Seq. No.
                  LIB3175-038-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3860277
BLAST score
                  540
E value
                  3.0e-55
                  134
Match length
% identity
                   (AC005824) putative ribosomal protein L10 [Arabidopsis
NCBI Description
                  thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative
                  ribosomal protein L10A [Arabidopsis thaliana]
                  150248
Seq. No.
                  LIB3175-038-P1-K1-C9
Seq. ID
Method
                  BLASTX
                  g135467
NCBI GI
                  527
BLAST score
E value
                  1.0e-65
Match length
                  125
% identity
                  99
NCBI Description
                  TUBULIN BETA-4 CHAIN >gi_2129546_pir__S68122 beta-tubulin 4
                  - Arabidopsis thaliana >gi 166640 (M21415) beta-tubulin
                  [Arabidopsis thaliana]
Seq. No.
                  150249
Seq. ID
                  LIB3175-038-P1-K1-D11
Method
                  BLASTN
                  q4678705
NCBI GI
BLAST score
                  185
                  1.0e-99
E value
Match length
                  389
% identity
                  95
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
NCBI Description
                   (ESSA project)
                  150250
Seq. No.
Seq. ID
                  LIB3175-038-P1-K1-D12
Method
                  BLASTX
NCBI GI
                  q3461820
BLAST score
                  564
                  3.0e-58
E value
Match length
                  118
% identity
NCBI Description
                   (AC004138) unknown protein [Arabidopsis thaliana]
                  150251
Seq. No.
Seq. ID
                  LIB3175-038-P1-K1-D3
Method
                  BLASTN
NCBI GI
                  q2760165
BLAST score
                  442
                  0.0e+00
E value
```

```
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MAC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150252
                  LIB3175-038-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2829894
BLAST score
                  191
                  1.0e-14
E value
Match length
                  70
% identity
                  66
                  (AC002311) Unknown protein [Arabidopsis thaliana]
NCBI Description
                  150253
Seq. No.
                  LIB3175-038-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2688820
BLAST score
                  232
E value
                  3.0e-19
                  105
Match length
% identity
                  45
NCBI Description
                  (U93271) enoyl-CoA hydratase [Prunus armeniaca]
Seq. No.
                  150254
Seq. ID
                  LIB3175-038-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  q119350
BLAST score
                  622
E value
                  5.0e-65
Match length
                  132
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                   (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi_16271_{emb_CAA41114_} (X58107) enolase
                   [Arabidopsis thaliana]
                  >gi_4581151_gb_AAD24635.1_AC006919_13 (AC006919) enolase
                   (2-phospho-D-glycerate hydroylase); identical to P25696
                   [Arabidopsis thaliana]
Seq. No.
                  150255
Seq. ID
                  LIB3175-038-P1-K1-D8
Method
                  BLASTX
NCBI GI
                  g1708462
BLAST score
                  669
E value
                  2.0e-70
Match length
                  131
% identity
                  98
NCBI Description
                  IAA-AMINO ACID HYDROLASE HOMOLOG 2 PRECURSOR >gi 902791
                   (U23796) ILL2 [Arabidopsis thaliana]
Seq. No.
                  150256
Seq. ID
                  LIB3175-038-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g113782
BLAST score
                  408
```

Seq. No.

```
5.0e-40
E value
Match length
                   90
                   87
% identity
                   BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE)
NCBI Description
                   >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) -
                   Arabidopsis thaliana >gi_166602 (M73467) beta-amylase
                   [Arabidopsis thaliana] >gi 228699 prf 1808329A beta
                   amylase [Arabidopsis thaliana]
Seq. No.
                   150257
                   LIB3175-038-P1-K1-E10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3914425
BLAST score
                   265
                   3.0e - 23
E value
Match length
                   85
                   65
% identity
NCBI Description
                   PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
                   CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                   >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic
                   endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S
                   proteasome beta subunit PBE1 [Arabidopsis thaliana]
Seq. No.
                   150258
Seq. ID
                   LIB3175-038-P1-K1-E11
Method
                   BLASTN
NCBI GI
                   g2494106
BLAST score
                   419
E value
                   0.0e+00
Match length
                   450
% identity
                   Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   150259
Seq. ID
                   LIB3175-038-P1-K1-E12
Method
                   BLASTN
NCBI GI
                   q4432829
BLAST score
                   265
E value
                   1.0e-147
Match length
                   469
% identity
                   97
                   Arabidopsis thaliana chromosome II BAC T1B3 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150260
Seq. ID
                   LIB3175-038-P1-K1-E2
Method
                   BLASTN
NCBI GI
                   q2959729
BLAST score
                   283
                   1.0e-158
E value
Match length
                   311
% identity
                   Arabidopsis thaliana mRNA for GATA transcription factor
NCBI Description
```

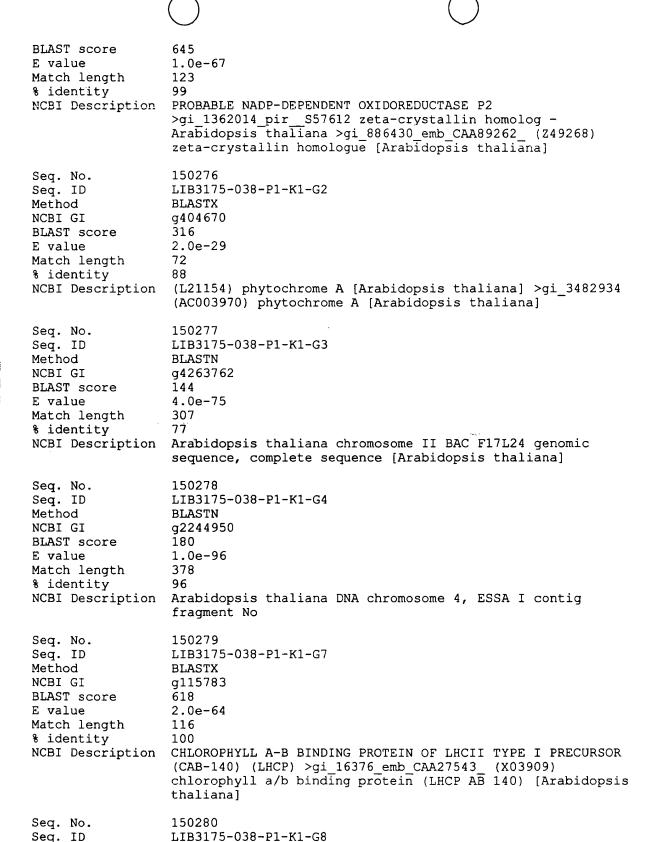
```
LIB3175-038-P1-K1-E3
Seq. ID
                  BLASTX
Method
                  g3892050
NCBI GI
                  289
BLAST score
                   4.0e-26
E value
                  96
Match length
                  61
% identity
                   (ACO02330) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  150262
Seq. No.
                  LIB3175-038-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g543841
BLAST score
                  439
                  1.0e-43
E value
                  85
Match length
                  99
% identity
                  ADP-RIBOSYLATION FACTOR 1 >gi_322518_pir__S28875
NCBI Description
                  ADP-ribosylation factor 1 - Arabidopsis thaliana >gi 166586
                   (M95166) ADP-ribosylation factor [Arabidopsis thaliana]
                  >gi 2275195 (AC002337) ADP-ribosylation factor [Arabidopsis
                  thaliana] >gi 4630747 gb_AAD26597.1_AC007236_2 (AC007236)
                  ADP-ribosylation factor [Arabidopsis thaliana]
Seq. No.
                  150263
                  LIB3175-038-P1-K1-E6
Seq. ID
Method
                  BLASTX
                  g115783
NCBI GI
                  378
BLAST score
                   4.0e-57
E value
Match length
                  115
% identity
                   98
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  150264
Seq. ID
                  LIB3175-038-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g2959729
BLAST score
                  324
E value
                  0.0e + 00
Match length
                  340
                  99
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for GATA transcription factor
                  150265
Seq. No.
                  LIB3175-038-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3769472
BLAST score
                  231
E value
                  4.0e-26
Match length
                  76
                  74
% identity
                   (AF064732) putative phospholipase A2 [Dianthus
NCBI Description
                  caryophyllus]
```

NCBI GI

```
Seq. No.
                   150266
Seq. ID
                   LIB3175-038-P1-K1-E9
Method
                   BLASTX
NCBI GI
                   q3914425
                   665
BLAST score
                   5.0e-70
E value
Match length
                   146
% identity
                   89
                   PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON
NCBI Description
                   CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN)
                   >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic
                   endopeptidase complex, proteasome precursor, beta subunit
[Arabidopsis thaliana] >gi_3421117 (AF043536) 20S
                   proteasome beta subunit PBE1 [Arabidopsis thaliana]
Seq. No.
                   150267
Seq. ID
                   LIB3175-038-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   g115783
                   383
BLAST score
                   7.0e-37
E value
Match length
                   102
% identity
                   CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   150268
Seq. No.
Seq. ID
                   LIB3175-038-P1-K1-F2
Method
                   BLASTN
NCBI GI
                   q3869067
BLAST score
                   264
                   1.0e-147
E value
Match length
                   341
% identity
                   100
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCK7, complete sequence [Arabidopsis thaliana]
                   150269
Seq. No.
Seq. ID
                   LIB3175-038-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q2160168
BLAST score
                   605
E value
                   2.0e-65
Match length
                   131
% identity
NCBI Description
                   (AC000132) Strong similarity to R. communis
                   phosphoglycerate mutase (gb X70652). ESTs
                   gb T41853, gb T76648 come from this gene. [Arabidopsis
                   thalianal
Seq. No.
                   150270
Seq. ID
                   LIB3175-038-P1-K1-F4
Method
                   BLASTX
```

q4539292

```
BLAST score
                   480
                   2.0e-48
E value
Match length
                   111
                   85
% identity
NCBI Description
                   (ALO49480) putative ribosomal protein S10 [Arabidopsis
                   thaliana]
                   150271
Seq. No.
                   LIB3175-038-P1-K1-F5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4468976
BLAST score
                   111
E value
                   2.0e-55
Match length
                   322
                   96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F19F18
NCBI Description
                   (ESSA project)
                   150272
Seq. No.
Seq. ID
                   LIB3175-038-P1-K1-F7
Method
                   BLASTN
NCBI GI
                   g4159704
BLAST score
                   440
E value
                   0.0e+00
Match length
                   476
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                   MCB17, complete sequence
                   150273
Seq. No.
                   LIB3175-038-P1-K1-F8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3142300
BLAST score
                   446
E value
                   3.0e-44
Match length
                   136
% identity
                   60
NCBI Description
                   (AC002411) Contains similarity to pre-mRNA processing
                   protein PRP39 gb_L29224 from S. cerevisiae. ESTs gb_R64908
                   and gb_T88158, gb_N38703 and gb_AA651043 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   150274
                   LIB3175-038-P1-K1-F9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2749918
BLAST score
                   402
E value
                   0.0e + 00
Match length
                   443
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F316 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150275
                   LIB3175-038-P1-K1-G12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2498732
```



```
Method
                  BLASTN
NCBI GI
                  q3063438
BLAST score
                   423
E value
                  0.0e + 00
                   423
Match length
                  100
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                   [Arabidopsis thaliana]
                  150281
Seq. No.
Seq. ID
                  LIB3175-038-P1-K1-G9
Method
                  BLASTX
                  a2160133
NCBI GI
BLAST score
                  373
E value
                  8.0e-36
                  94
Match length
% identity
                  84
NCBI Description
                   (AC000375) Strong similarity to Arabidopsis
                  gb X91953,F19K23.3,F19K23.15. ESTs
                  gb T21984, gb ATTS0219, gb ATTS0207, gb T21984 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  150282
Seq. ID
                  LIB3175-038-P1-K1-H1
Method
                  BLASTN
NCBI GI
                  q4335744
BLAST score
                  71
                  1.0e-31
E value
Match length
                  167
% identity
                  86
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T4M8 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150283
Seq. ID
                  LIB3175-038-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  q115783
BLAST score
                  582
E value
                  2.0e-60
Match length
                  111
                   98
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  150284
Seq. ID
                  LIB3175-038-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  q2677828
BLAST score
                  210
E value
                  9.0e-21
                  79
Match length
% identity
NCBI Description
                  (U93166) cysteine protease [Prunus armeniaca]
Seq. No.
                  150285
```

```
LIB3175-038-P1-K1-H3
Seq. ID
Method
                  BLASTX
                  q132110
NCBI GI
BLAST score
                  466
E value
                  6.0e-63
                  126
Match length
                  97
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1}.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  150286
Seq. No.
Seq. ID
                  LIB3175-038-P1-K1-H4
                  BLASTX
Method
                  g1652082
NCBI GI
                  146
BLAST score
                  3.0e-09
E value
Match length
                  102
% identity
                   (D90902) UDP-3-0-acyl N-acetylglcosamine deacetylase
NCBI Description
                   [Synechocystis sp.]
Seq. No.
                  150287
Seq. ID
                  LIB3175-038-P1-K1-H6
                  BLASTN
Method
                  g16375
NCBI GI
BLAST score
                  35
                  3.0e-10
E value
Match length
                  35
                  100
% identity
                  A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding
NCBI Description
                  protein
Seq. No.
                  150288
Seq. ID
                  LIB3175-038-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  292
E value
                  2.0e-59
Match length
                  114
                  100
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir__JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  150289
                  LIB3175-038-P1-K1-H8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399013
BLAST score
                  102
                  6.0e-23
E value
Match length
                  92
% identity
                  72
```

% identity

```
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                   thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)
                   adenylate translocator [Arabidopsis thaliana]
                   >gi 445607 prf 1909354A adenylate translocator
                   [Arabidopsis thaliana]
Seq. No.
                   150290
                  LIB3175-038-P1-K1-H9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2564046
BLAST score
                   424
E value
                   0.0e + 00
Match length
                   431
% identity
                   100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MGI19, complete sequence [Arabidopsis thaliana]
                   150291
Seq. No.
                  LIB3175-039-P1-K1-A10
Seq. ID
Method
                  BLASTX
                   g2245006
NCBI GI
BLAST score
                   230
E value
                   5.0e-19
Match length
                   87
% identity
                   51
                  (Z97341) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   150292
Seq. No.
Seq. ID
                   LIB3175-039-P1-K1-A11
Method
                   BLASTX
NCBI GI
                   g3158376
BLAST score
                   659
E value
                   3.0e-69
Match length
                   130
% identity
                   (AF035385) unknown [Arabidopsis thaliana]
NCBI Description
                   150293
Seq. No.
                   LIB3175-039-P1-K1-A3
Seq. ID
Method
                   BLASTX
                   g4539324
NCBI GI
BLAST score
                   556
                   3.0e-57
E value
                   137
Match length
% identity
                   86
                   (AL035679) kinesin like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150294
                   LIB3175-039-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                   q1169278
BLAST score
                   305
E value
                   8.0e-28
Match length
                   75
```

```
NCBI Description DEHYDRIN ERD14 >gi_556474_dbj_BAA04569 (D17715) ERD14
                  protein [Arabidopsis thaliana]
                  150295
Seq. No.
                  LIB3175-039-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q82734
BLAST score
                  560
                  9.0e-58
E value
Match length
                  114
                  29
% identity
NCBI Description
                  ubiquitin precursor - maize (fragment)
                  >gi_226763_prf__1604470A poly-ubiquitin [Zea mays]
                  150296
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-A9
Method
                  BLASTN
                  g2618600
NCBI GI
BLAST score
                  221
                  1.0e-121
E value
Match length
                  375
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MDC12, complete sequence [Arabidopsis thaliana]
                  150297
Seq. No.
                  LIB3175-039-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q167012
BLAST score
                  444
E value
                  3.0e-44
Match length
                  124
                  64
% identity
                   (J03897) carboxypeptidase I precursor [Hordeum vulgare]
NCBI Description
                  150298
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  q3241927
BLAST score
                  246
E value
                  1.0e-136
Match length
                  419
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTE17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150299
Seq. ID
                  LIB3175-039-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3123188
BLAST score
                  717
                  4.0e-76
E value
Match length
                  140
% identity
                  CATALASE 3 >gi 2347178 (U43147) catalase 3 [Arabidopsis
NCBI Description
                  thaliana] >gi 2511726 (AF021937) catalase 3 [Arabidopsis ...
                  thaliana]
```

```
Seq. No.
                  150300
                  LIB3175-039-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2887500
BLAST score
                  338
                   1.0e-31
E value
Match length
                  70
% identity
NCBI Description
                   (AC002339) putative AP2 domain-containing protein
                   [Arabidopsis thaliana]
                  150301
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q2673901
BLAST score
                  93
                   3.0e-45
E value
Match length
                  158
% identity
                  Arabidopsis thaliana chromosome II BAC T24P15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150302
                  LIB3175-039-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4584110
BLAST score
                  289
E value
                   5.0e-26
Match length
                  106
% identity
                   54
                   (AJ133639) SAH7 protein [Arabidopsis thaliana]
NCBI Description
                  150303
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  q4154281
BLAST score
                   312
E value
                   8.0e-29
Match length
                  70
% identity
NCBI Description
                  (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
                  150304
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q4204274
BLAST score
                  442
E value
                  8.0e-44
Match length
                  78
% identity
                  100
NCBI Description
                   (AC004146) ribulose bisphosphate carboxylase, small subunit
                   [Arabidopsis thaliana]
Seq. No.
                  150305
                  LIB3175-039-P1-K1-C1
Seq. ID
Method
                  BLASTN
```

```
NCBI GI
                   q3510347
BLAST score
                   434
                   0.0e + 00
E value
Matchalength
                   442
                   60
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MSJ11, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150306
                   LIB3175-039-P1-K1-C10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q2980798
BLAST score
                   559
                   1.0e-57
E value
Match length
                   147
                   73
% identity
NCBI Description
                   (AL022197) putative protein [Arabidopsis thaliana]
                   150307
Seq. No.
Seq. ID
                   LIB3175-039-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g4741940
BLAST score
                   544
E value
                   7.0e-56
                   99
Match length
                   65
% identity
                   (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
                   150308
Seq. No.
                   LIB3175-039-P1-K1-C12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4580460
BLAST score
                   517
E value
                   1.0e-52
Match length
                   118
% identity
NCBI Description
                   (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
                   thaliana]
                   150309
Seq. No.
                   LIB3175-039-P1-K1-C2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2829893
BLAST score
                   385
                   1.0e-37
E value
                   87
Match length
% identity
                   86
NCBI Description
                   (AC002311) phosphoglucomutase [Arabidopsis thaliana]
Seq. No.
                   150310
                   LIB3175-039-P1-K1-C3
Seq. ID
Method
                   BLASTN
                   g4159709
NCBI GI
BLAST score
                   91
                   1.0e-43
E value
Match length
                   195
                   94
% identity
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLN21, complete sequence
Seq. No.
                  150311
                  LIB3175-039-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4678226
BLAST score
                  512
E value
                  3.0e-52
Match length
                  103
                  98
% identity
                   (AC007135) putative 40S ribosomal protein S14 [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  150312
                  LIB3175-039-P1-K1-C7
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3510341
BLAST score
                  405
E value
                  0.0e + 00
Match length
                  442
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MFC16, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150313
                  LIB3175-039-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2160147
BLAST score
                  485
E value
                   7.0e-49
Match length
                  134
                   75
% identity
NCBI Description
                   (AC000375) EST gb ATTS3706 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   150314
                  LIB3175-039-P1-K1-C9
Seq. ID
Method
                  BLASTX
NCBI GI
                   q2702268
BLAST score
                   473
                   2.0e-47
E value
Match length
                  95
% identity
                  (AC003033) putative cellulase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150315
                  LIB3175-039-P1-K1-D1
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4503515
BLAST score
                  202
E value
                   9.0e-16
Matchlength
                  138
% identity
                   33
                  UNKNOWN >gi 2351380 (U54559) translation initiation factor
NCBI Description
```

eIF3 p40 subunit [Homo sapiens]

```
Seq. No.
                   150316
Seq. ID
                   LIB3175-039-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   g2351065
BLAST score
                   359
E value
                   0.0e + 00
                   393
Match length
% identity
                   97
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MHF15, complete sequence [Arabidopsis thaliana]
                   150317
Seq. No.
                   LIB3175-039-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3668069
BLAST score
                   201
E value
                   1.0e-15
Match length
                   74
% identity
NCBI Description
                   (U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
                   150318
Seq. No.
Seq. ID
                   LIB3175-039-P1-K1-D2
Method
                   BLASTX
NCBI GI
                   q231683
BLAST score
                   381
E value
                   5.0e-37
                   72
Match length
% identity
NCBI Description
                   CALNEXIN HOMOLOG PRECURSOR >gi 421825 pir JN0597
                   calnexin-like protein - Arabidopsis thaliana >gi_16211_emb_CAA79144_ (Z18242) calnexin homolog
                    [Arabidopsis thaliana]
Seq. No.
                   150319
Seq. ID
                   LIB3175-039-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q3608261
BLAST score
                   285
E value
                   2.0e-25
Match length
                   69
% identity
NCBI Description
                   (AB017564) dof zinc finger protein [Arabidopsis thaliana]
Seq. No.
                   150320
Seq. ID
                   LIB3175-039-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   q4240116
BLAST score
                   307
E value
                   3.0e-28
                   83
Match length
% identity
NCBI Description
                   (AB007799) NADH-cytochrome b5 reductase [Arabidopsis
                   thaliana] >gi 4240118_dbj_BAA74838_ (AB007800)
                   NADH-cytochrome b5 reductase [Arabidopsis thaliana]
Seq. No.
                   150321
```

```
LIB3175-039-P1-K1-D7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2119927
                  211
BLAST score
                  8.0e-17
E value
                  101
Match length
                  50
% identity
NCBI Description translation elongation factor G, chloroplast - soybean
Seq. No.
                  150322
                  LIB3175-039-P1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q282848
BLAST score
                  409
E value
                  6.0e-40
                  94
Match length
                  79
% identity
                  malate_dehydrogenase (oxaloacetate-decarboxylating) (NADP+)
NCBI Description
                  (EC 1.1.1.40) (clone 064) - western balsam poplar x
                  cottonwood
                  150323
Seq. No.
                  LIB3175-039-P1-K1-D9
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4206210
BLAST score
                  761
E value
                  3.0e-81
                  149
Match length
% identity
                  64
NCBI Description
                  (AF071527) putative calcium channel [Arabidopsis thaliana]
                  >gi 4263043 gb AAD15312 (AC005142) putative calcium
                  channel [Arabidopsis thaliana]
                  150324
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q1486472
BLAST score
                  385
E value
                  3.0e-37
                  92
Match length
% identity
                  (X99853) oxoglutarate malate translocator [Solanum
NCBI Description
                  tuberosum]
                  150325
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-E11
Method
                  BLASTX
NCBI GI
                  g2129597
                  656
BLAST score
E value
                  6.0e-69
Match length
                  130
% identity
                  glutamate dehydrogenase 1 - Arabidopsis thaliana
NCBI Description
                  >gi_1098960 (U37771) glutamate dehydrogenase 1 [Arabidopsis
                  thaliana] >gi_1293095 (U53527) glutamate dehydrogenase 1
```

[Arabidopsis thaliana]

```
Seq. No.
                   150326
Seq. ID
                   LIB3175-039-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   g2829925
BLAST score
                   331
                   5.0e-31
E value
Match length
                   69
                   97
% identity
NCBI Description
                   (AC002291) Similar to dnaj-like protein, gp_Y11969_2230757
                   [Arabidopsis thaliana]
                   150327
Seq. No.
Seq. ID
                   LIB3175-039-P1-K1-E2
Method
                   BLASTX
NCBI GI
                   q4567262
BLAST score
                   450
E value
                   5.0e-45
Match length
                   88
                   95
% identity
NCBI Description
                   (AC006841) putative ubiquitin [Arabidopsis thaliana]
                   150328
Seq. No.
Seq. ID
                   LIB3175-039-P1-K1-E6
Method
                   BLASTX
NCBI GI
                   q4193382
BLAST score
                   423
E value
                   1.0e-41
Match length
                   86
% identity
                   91
                   (AF083336) ribosomal protein S27 [Arabidopsis thaliana]
NCBI Description
                   >qi 4193384 (AF083337) ribosomal protein S27 [Arabidopsis
                   thaliana)
                   150329
Seq. No.
Seq. ID
                   LIB3175-039-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   q4589440
BLAST score
                   388
E value
                   0.0e + 00
Match length
                   411
                   100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MSD21, complete sequence
                   150330
Seq. No.
Seq. ID
                   LIB3175-039-P1-K1-E8
Method
                  BLASTX
NCBI GI
                   q462273
BLAST score
                   380
                   1.0e-36
E value
Match length
                   127
% identity
NCBI Description
                  IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE (IGPD) >qi 437213
                   (U02689) imidazoleglycerolphosphate dehydratase
                   [Arabidopsis thaliana]
Seq. No.
                   150331
```

```
Seq. ID
                   LIB3175-039-P1-K1-E9
Method
                  BLASTX
NCBI GI
                   q2558962
                   437
BLAST score
E value
                   3.0e-43
                   92
Match length
                   97
% identity
NCBI Description
                   (AF025667) histone H2B1 [Gossypium hirsutum]
                   150332
Seq. No.
Seq. ID
                   LIB3175-039-P1-K1-F1
Method
                  BLASTX
NCBI GI
                   q2506277
BLAST score
                   51
E value
                   3.0e-10
Match length
                   99
                   54
% identity
                  RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR 460
NCBI Description
                   KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi 806808
                   (U21139) chaperonin precursor [Pisum sativum]
Seq. No.
                   150333
Seq. ID
                   LIB3175-039-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q4586263
BLAST score
                   337
                   8.0e-32
E value
Match length
                   97
% identity
                   69
                   (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150334
                   LIB3175-039-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q543565
BLAST score
                   205
E value
                   4.0e-16
                   66
Match length
% identity
                  hypothetical 10.0K protein - Zinnia elegans
NCBI Description
                   >gi_493721_dbj_BAA06462_ (D30802) TED4 [Zinnia elegans]
                   >gi_641903 (U19266) putative nonspecific lipid transfer;
                   auxin induced gene [Zinnia elegans]
                   150335
Seq. No.
                   LIB3175-039-P1-K1-F12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4432847
BLAST score
                   348
                   0.0e + 00
E value
                   364
Match length
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F13B15 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   LIB3175-039-P1-K1-F3
Seq. ID
```

```
Method
                  BLASTN
NCBI GI
                  q4417299
BLAST score
                  110
                  3.0e-55
E value
Match length
                  172
% identity
                  Arabidopsis thaliana chromosome II BAC F15011 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150337
                  LIB3175-039-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4741198
BLAST score
                  529
                  4.0e-54
E value
Match length
                  96
                  100
% identity
                  (AL049746) putative protein [Arabidopsis thaliana]
NCBI Description
                  150338
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-F8
                  BLASTX
Method
NCBI GI
                  q2507477
BLAST score
                  182
E value
                  1.0e-13
                  122
Match length
% identity
                  35
                  TRANSALDOLASE A >gi_1788807 (AE000333) transaldolase A
NCBI Description
                  [Escherichia coli] >gi 1799888 dbj BAA16339 (D90875)
                  similar to [PIR Accession Number S40535] [Escherichia coli]
                  >gi 2337774 dbj BAA21821 (D13159) transaldolase
                  [Escherichia coli]
                  150339
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  g2055374
BLAST score
                  209
E value
                  1.0e-16
Match length
                  50
                  82
% identity
NCBI Description
                  (U29095) serine-threonine protein kinase [Triticum
                  aestivum]
                  150340
Seq. No.
                  LIB3175-039-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172872
BLAST score
                  470
E value
                  2.0e-47
Match length
                  111
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi_541856_pir__JN0718
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                  (D13042) thiol protease [Arabidopsis thaliana]
                  >gi 4539328 emb CAB38829.1 (AL035679) drought-inducible
```

```
cysteine proteinase RD19A precursor [Arabidopsis thaliana]
150341
$\frac{1}{5} \text{TB2175-039-P1-K1-C11}
```

```
Seq. No.
                  LIB3175-039-P1-K1-G11
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4432856
                  523
BLAST score
                  2.0e-53
E value
                  109
Match length
                  95
% identity
                  (AC006300) putative 2A6 protein [Arabidopsis thaliana]
NCBI Description
                  150342
Seq. No.
                  LIB3175-039-P1-K1-G12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1175010
BLAST score
                  541
                  2.0e-55
E value
                  119
Match length
                  89
% identity
                  PLASMA MEMBRANE INTRINSIC PROTEIN 1A >gi_629540_pir__S44082
NCBI Description
                  plasma membrane intrinsic protein la - Arabidopsis thaliana
                  >gi_472873_emb_CAA53475_ (X75881) plasma membrane intrinsic
                  protein la [Arabidopsis thaliana]
Seq. No.
                  150343
Seq. ID
                  LIB3175-039-P1-K1-G3
Method
                  BLASTN
NCBI GI
                  q166745
BLAST score
                  136
                  9.0e-71
E value
Match length
                  148
                  98
% identity
                  A.thaliana plasma membrane proton ATPase (PMA) mRNA,
NCBI Description
                  complete cds
Seq. No.
                  150344
Seq. ID
                  LIB3175-039-P1-K1-G5
                  BLASTX
Method
NCBI GI
                  q4583544
BLAST score
                  468
E value
                  5.0e-47
                  97
Match length
                  90
% identity
                  (Z95637) acyl-CoA:1-acylglycerol-3-phosphate
NCBI Description
                  acyltransferase [Brassica napus]
                  150345
Seq. No.
                  LIB3175-039-P1-K1-G7
Seq. ID
```

Seq. No. 130343
Seq. ID LIB3175-039-P1-K1-G7
Method BLASTX
NCBI GI g3193292
BLAST score 577
E value 8.0e-60
Match length 129
% identity 88

NCBI Description (AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91)



## [Arabidopsis thaliana]

```
150346
Seq. No.
                   LIB3175-039-P1-K1-G8
Seq. ID
                   BLASTX
Method
NCBI GI
                   q132110
BLAST score
                   539
                   2.0e-55
E value
                   104
Match length
                   97
```

% identity RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR NCBI Description (RUBISCO SMALL SUBUNIT 3B) >gi\_68060\_pir\_\_RKMUB3

ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702 (X14564) ribulose bisphosphate carboxylase [Arabidopsis

thaliana]

```
150347
Seq. No.
                   LIB3175-039-P1-K1-G9
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4519185
BLAST score
                   280
```

E value 1.0e-156 331 Match length 97 % identity

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K15015, complete sequence

150348 Seq. No. LIB3175-039-P1-K1-H1 Seq. ID Method BLASTX NCBI GI g2894574 BLAST score 607 E value 3.0e-63

Match length 115 100 % identity

NCBI Description (AL021890) peroxidase prxrl [Arabidopsis thaliana]

>gi\_2961341\_emb\_CAA18099.1\_ (AL022140) peroxidase prxr1

[Arabidopsis thaliana]

150349 Seq. No. Seq. ID LIB3175-039-P1-K1-H11

Method BLASTX NCBI GI g2352921 BLAST score 515 1.0e-52 E value Match length 105 % identity

(AF012862) cytosolic glucose-6-phosphate dehydrogenase 1 NCBI Description

[Petroselinum crispum]

150350 Seq. No.

LIB3175-039-P1-K1-H12 Seq. ID

Method BLASTN NCBI GI g4733953 BLAST score 123 7.0e-63 E value

```
163
Match length
% identity
                  Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                  sequence, complete sequence
                  150351
Seq. No.
                  LIB3175-039-P1-K1-H3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2791900
BLAST score
                  231
                  1.0e-19
E value
Match length
                  80
% identity
                  59
NCBI Description
                   (AJ000057) PP7 [Arabidopsis thaliana]
                  150352
Seq. No.
                  LIB3175-039-P1-K1-H7
Seq. ID
Method
                  BLASTX
                  g266693
NCBI GI
BLAST score
                  263
E value
                   6.0e-23
Match length
                  119
                   50
% identity
                  OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis
NCBI Description
                   thaliana >gi_16405_emb_CAA44225_ (X62353) oleosin
                   [Arabidopsis thaliana] >gi_4455257_emb_CAB36756.1_
                   (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
                  150353
Seq. No.
Seq. ID
                  LIB3175-039-P1-K1-H8
Method
                  BLASTN
NCBI GI
                   g3449320
BLAST score
                   191
                   1.0e-103
E value
Match length
                   449
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MRB17, complete sequence [Arabidopsis thaliana]
                  150354
Seq. No.
                  LIB3175-039-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3421094
BLAST score
                   698
E value
                   7.0e-74
Match length
                   141
% identity
NCBI Description
                   (AF043527) 20S proteasome subunit PAF2 [Arabidopsis
                   thaliana]
                  150355
Seq. No.
                  LIB3175-040-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q602764
BLAST score
                  756
                  1.0e-80
E value
                  146
Match length
```

```
% identity
NCBI Description
                  (D43783) beta-amylase [Arabidopsis thaliana]
                  >gi_998369_bbs_163908 (S77076) beta-amylase {EC 3.2.1.2}
                  [Arabidopsis thaliana=thale cress, Heynh., Peptide, 498 aa]
                  [Arabidopsis thaliana]
                  150356
Seq. No.
                  LIB3175-040-P1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3292814
BLAST score
                  292
                  2.0e-26
E value
                  85
Match length
                  75
% identity
NCBI Description
                  (AL031018) putative protein [Arabidopsis thaliana]
                  150357
Seq. No.
                  LIB3175-040-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4220480
BLAST score
                  267
E value
                  2.0e-23
                  99
Match length
                  53
% identity
NCBI Description
                  (AC006069) unknown protein [Arabidopsis thaliana]
Seq. No.
                  150358
Seq. ID
                  LIB3175-040-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q1175012
BLAST score
                  115
                  1.0e-05
E value
Match length
                  137
                  79
% identity
                  PLASMA MEMBRANE INTRINSIC PROTEIN 1C (TRANSMEMBRANE PROTEIN
NCBI Description
                  B) (TMP-B) >gi_396218_emb_CAA49155_ (X69294) transmembrane
                  protein TMP-B [Arabidopsis thaliana]
Seq. No.
                  150359
                  LIB3175-040-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1402874
BLAST score
                  320
                  1.0e-180
E value
                  386
Match length
                  100
% identity
NCBI Description A.thaliana 81kb genomic sequence
                  150360
Seq. No.
Seq. ID
                  LIB3175-040-P1-K1-A6
Method
                  BLASTX
NCBI GI
                  g2829876
BLAST score
                  655
E value
                  7.0e-69
Match length
                  132
% identity
                  98
NCBI Description
                  (AC002396) Unknown protein [Arabidopsis thaliana]
```

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150361
Seq. No.
                  LIB3175-040-P1-K1-A8
Seq. ID
                   BLASTN
Method
                   g2088638
NCBI GI
BLAST score
                   300
                   1.0e-168
E value
                   427
Match length
                   100
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150362
                   LIB3175-040-P1-K1-A9
Seq. ID
                   BLASTX
Method
                   g21913
NCBI GI
BLAST score
                   201
                   1.0e-15
E value
                   83
Match length
                   45
% identity
NCBI Description
                   (X62626) vicilin [Theobroma cacao]
                   150363
Seq. No.
                   LIB3175-040-P1-K1-B10
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3650026
BLAST score
                   223
                   1.0e-122
E value
                   297
Match length
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC T26I20 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   150364
Seq. No.
                   LIB3175-040-P1-K1-B11
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3184285
BLAST score
                   155
E value
                   3.0e-10
Match length
                   59
% identity
NCBI Description
                   (AC004136) hypothetical protein [Arabidopsis thaliana]
                   150365
Seq. No.
                   LIB3175-040-P1-K1-B12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q902200
BLAST score
                   45
E value
                   1.0e-16
                   93
Match length
                   87
% identity
NCBI Description
                  Z.mays complete chloroplast genome
Seq. No.
                   150366
                   LIB3175-040-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g282865
```

% identity
NCBI Description

150371

Seq. No.

```
BLAST score
                  283
E value
                  3.0e-25
Match length
                  95
% identity
                  61
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
NCBI Description
                  >gi_16207_emb_CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi 166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >gi 4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
                  150367
Seq. No.
                  LIB3175-040-P1-K1-B4
Seq. ID
Method
                  BLASTN
                  g4263694
NCBI GI
                  136
BLAST score
                  2.0e-70
E value
                  403
Match length
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC F22D22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  150368
Seq. No.
                  LIB3175-040-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  517
E value
                  1.0e-52
                  118
Match length
                  85
% identity
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150369
                  LIB3175-040-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112682
BLAST score
                  667
                  3.0e-70
E value
                  142
Match length
                  89
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81605 pir S08510
NCBI Description
                  cruciferin precursor (CRB) - Arabidopsis thaliana
                  >gi 166678 (M37248) 12S storage protein CRB [Arabidopsis
                  thaliana] >qi 808937 emb CAA32494 (X14313) 12S seed
                  storage protein [Arabidopsis thaliana]
Seq. No.
                  150370
Seq. ID
                  LIB3175-040-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3478700
BLAST score
                  647
E value
                  6.0e-68
Match length
                  140
```

(AF034387) AFT protein [Arabidopsis thaliana]

```
LIB3175-040-P1-K1-B8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1076316
BLAST score
                   741
                   6.0e-79
E value
                   144
Match length
                   99
% identity
                   drought-induced protein Di19 - Arabidopsis thaliana
NCBI Description
                   >gi 469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis
                   thaliana]
                   150372
Seq. No.
                   LIB3175-040-P1-K1-C10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4519193
BLAST score
                   353
                   0.0e+00
E value
                   406
Match length
                   34
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone:
                   MDC11, complete sequence
Seq. No.
                   150373
Seq. ID
                   LIB3175-040-P1-K1-C11
Method
                   BLASTX
NCBI GI
                   g3132475
BLAST score
                   602
                   1.0e-62
E value
                   141
Match length
% identity
NCBI Description
                   (AC003096) similar to proline-rich protein [Arabidopsis
                   thaliana]
                   150374
Seq. No.
                   LIB3175-040-P1-K1-C12
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4056476
BLAST score
                   224
E value
                   1.0e-123
Match length
                   353
                   98
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F3G5 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   150375
Seq. No.
Seq. ID
                   LIB3175-040-P1-K1-C3
Method
                   BLASTN
NCBI GI
                   q4220636
BLAST score
                   44
                   4.0e-16
E value
Match length
                   88
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MFB16, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                   LIB3175-040-P1-K1-C4
```

```
Method
                  BLASTX
NCBI GI
                  g4557495
                  177
BLAST score
                  8.0e-13
E value
                  101
Match length
                  34
% identity
                  cleavage stimulation factor subunit 3
NCBI Description
                  >gi 1082704 pir S50852 cleavage stimulation factor 77K
                  chain - human >gi 632498 (U15782) cleavage stimulation
                  factor 77kDa subunit [Homo sapiens]
                  >gi 1092656_prf__2024339A cleavage stimulation factor [Homo
                  sapiens]
Seq. No.
                  150377
                  LIB3175-040-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1531762
                  195 %
BLAST score
                  6.0e-15
E value
                  51
Match length
                  75
% identity
NCBI Description
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
                  thaliana]
                  150378
Seq. No.
Seq. ID
                  LIB3175-040-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1174718
BLAST score
                  484
                  7.0e-49
E value
                  128
Match length
                  71
% identity
NCBI Description
                  PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR
                  >gi 322579 pir JQ1674 receptor protein kinase TMK1 (EC
                  2.7.1.-) precursor - Arabidopsis thaliana >gi_166888
                  (L00670) protein kinase [Arabidopsis thaliana]
Seq. No.
                  150379
Seq. ID
                  LIB3175-040-P1-K1-C7
Method
                  BLASTN
NCBI GI
                  g4589439
BLAST score
                  210
E value
                  1.0e-114
                  409
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQM1, complete sequence
Seq. No.
                  150380
Seq. ID
                  LIB3175-040-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  q3883123
BLAST score
                  332
E value
                  0.0e + 00
Match length
                  380
% identity
NCBI Description Arabidopsis thaliana arabinogalactan-protein (AGP3) mRNA,
```

## complete cds

```
150381
Seq. No.
Seq. ID
                  LIB3175-040-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   q3355468
                   429
BLAST score
                   2.0e-42
E value
                   123
Match length
                   76
% identity
                   (AC004218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                   thaliana]
                   150382
Seq. No.
                  LIB3175-040-P1-K1-D10
Seq. ID
Method
                  BLASTX
NCBI GI
                   g2226202
BLAST score
                   174
E value
                   2.0e-12
Match length
                   83
                   51
% identity
NCBI Description
                   (Y14082) hypothetical protein [Bacillus subtilis]
                   >gi 2633281 emb CAB12785 (Z99109) similar to amino acid
                   transporter [Bacillus subtilis]
Seq. No.
                   150383
Seq. ID
                   LIB3175-040-P1-K1-D3
Method
                   BLASTN
NCBI GI
                   q4220638
BLAST score
                   109
                   9.0e-55
E value
Match length
                   125
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MIF21, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150384
Seq. ID
                   LIB3175-040-P1-K1-D4
Method
                  BLASTX
NCBI GI
                   g4160280
BLAST score
                   360
E value
                   3.0e - 34
Match length
                  108
% identity
NCBI Description
                   (AJ006224) purple acid phosphatase [Ipomoea batatas]
                   150385
Seq. No.
Seq. ID
                  LIB3175-040-P1-K1-D5
Method
                  BLASTX
                  g3608263
NCBI GI
BLAST score
                   301
E value
                   2.0e-27
Match length
                  60
% identity
NCBI Description
                   (AB017565) Dof zinc finger protein [Arabidopsis thaliana]
                  150386
Seq. No.
```

Method

BLASTX

```
Seq. ID
                  LIB3175-040-P1-K1-D7
Method
                  BLASTX
NCBI GI
                  g2244750
BLAST score
                  512
                  5.0e-58
E value
Match length
                  127
                  88
% identity
                  (Z97335) adenosylhomocysteinase [Arabidopsis thaliana]
NCBI Description
                  >gi 3088579 (AF059581) S-adenosyl-L-homocysteine hydrolase
                  [Arabidopsis thaliana]
                  150387
Seq. No.
                  LIB3175-040-P1-K1-D8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2668744
BLAST score
                  591
                  2.0e-61
E value
Match length
                  120
                  89
% identity
                  (AF034946) ubiquitin conjugating enzyme [Zea mays]
NCBI Description
                  150388
Seq. No.
                  LIB3175-040-P1-K1-D9
Seq. ID
                  BLASTX
Method
                  g3914740
NCBI GI
BLAST score
                  514
                  2.0e-52
E value
                                     4
Match length
                  131
                  78
% identity
                  60S RIBOSOMAL PROTEIN L26 >gi 2160300 dbj BAA18941_
NCBI Description
                  (D78495) ribosomal protein [Brassica rapa]
Seq. No.
                  150389
                  LIB3175-040-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2564048
BLAST score
                  129
E value
                  3.0e-66
                  335
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MKD15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150390
                  LIB3175-040-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2828188
BLAST score
                  193
E value
                  1.0e-104
                  429
Match length
% identity
                  94
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3K3, complete sequence [Arabidopsis thaliana]
                  150391
Seq. No.
                  LIB3175-040-P1-K1-F10
Seq. ID
```

```
q1864017
NCBI GI
                   508
BLAST score
                   1.0e-51
E value
Match length
                   104
                   92
% identity
                   (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
                   150392
Seq. No.
                   LIB3175-040-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417383
                   376
BLAST score
                   3.0e-36
E value
                   77
Match length
                   97
% identity
NCBI Description
                   NITRILASE 2 >gi_322548_pir__S31969 nitrilase (EC 3.5.5.1) -
                   Arabidopsis thaliana >gi 22656_emb_CAA48377_ (X68305)
                   nitrilase II [Arabidopsis thaliana] >gi_508733 (U09958)
                   nitrilase [Arabidopsis thaliana]
Seq. No.
                   150393
                   LIB3175-040-P1-K1-F12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q544424
BLAST score
                   442
                   6.0e-44
E value
Match length
                   89
% identity
                   GLYCINE-RICH RNA-BINDING PROTEIN 7 >gi_419755_pir__S30147
NCBI Description
                   glycine-rich protein (clone AtGRP7) - Arabidopsis thaliana
                   >gi_16301_emb_CAA78711_ (Z14987) glycine rich protein
[Arabidopsis thaliana] >gi_166837 (L00648) RNA-binding
                   protein [Arabidopsis thaliana]
                   >gi_4567224_gb_AAD23639.1_AC007119_5 (AC007119)
                   glycine-rich RNA binding protein 7 [Arabidopsis thaliana]
Seq. No.
                   150394
                   LIB3175-040-P1-K1-F3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q16249
BLAST score
                   160
E value
                   5.0e-85
Match length
                   176
% identity
                   A.thaliana mRNA for Cu, Zn superoxide dismutase
NCBI Description
                   150395
Seq. No.
Seq. ID
                   LIB3175-040-P1-K1-F4
Method
                   BLASTN
NCBI GI
                   g2618601
BLAST score
                   167
E value
                   3.0e-89
Match length
                   191
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MHJ24, complete sequence [Arabidopsis thaliana]
```

```
150396
Seq. No.
Seq. ID
                  LIB3175-040-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  g112681
                   621
BLAST score
                   7.0e-65
E value
                  141
Match length
                  85
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                   cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                   tha\overline{\text{liana}} >gi 808936_emb_CAA32493 (X14312) 12S seed
                   storage protein [Arabidopsis thaliana]
                  150397
Seq. No.
Seq. ID
                  LIB3175-040-P1-K1-F7
                  BLASTX
Method
NCBI GI
                  q4580394
                   264
BLAST score
                   4.0e-23
E value
                  116
Match length
% identity
NCBI Description
                   (AC007171) putative fatty acid elongase [Arabidopsis
                   thaliana]
                  150398
Seq. No.
                  LIB3175-040-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4469022
                   726
BLAST score
                   3.0e-77
E value
                  142
Match length
                   99
% identity
NCBI Description
                   (AL035602) cytochrome P450-like protein [Arabidopsis
                   thaliana]
Seq. No.
                  150399
                  LIB3175-040-P1-K1-G11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4519195
BLAST score
                  159
                   3.0e-84
E value
                   307
Match length
                  88
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MQC12, complete sequence
                  150400
Seq. No.
                  LIB3175-040-P1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2477521
BLAST score
                  309
E value
                  1.0e-173
                  433
Match length
                  19
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F22K20 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                  150401
Seq. ID
                  LIB3175-040-P1-K1-G6
Method
                  BLASTN
                   g12279
NCBI GI
                   81
BLAST score
E value
                   1.0e-37
                   105
Match length
                   94
% identity
                   Spinach chloroplast genes for the D2 and 44 kd reaction
NCBI Description
                   centre, chlorophyll a-binding protein and for tRNA-Ser
                   (UGA)
                   150402
Seq. No.
Seq. ID
                  LIB3175-040-P1-K1-G7
Method
                  BLASTN
NCBI GI
                   g3319365
BLAST score
                   53
E value
                   7.0e-21
                   192
Match length
                   87
% identity
                  Arabidopsis thaliana BAC T24M8
NCBI Description
Seq. No.
                   150403
Seq. ID
                  LIB3175-040-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g400650
BLAST score
                   203
E value
                   7.0e-16
                   96
Match length
                   43
% identity
                  NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (COMPLEX
NCBI Description
                   I-13KD-B) (CI-13KD-B) (B13) >gi_346535_pir__S28244 NADH
                   dehydrogenase (ubiquinone) (EC 1.6.5.3) chain CI-B13 -
                  bovine >gi 238 emb CAA44903 (X63218) NADH dehydrogenase
                   [Bos taurus]
                   150404
Seq. No.
Seq. ID
                  LIB3175-040-P1-K1-H10
Method
                   BLASTN
NCBI GI
                   q4468103
BLAST score
                   181
E value
                   3.0e-97
Match length
                   321
                   98
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M3E9
NCBI Description
                   (ESSA project)
                   150405
Seq. No.
Seq. ID
                  LIB3175-040-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g4324967
BLAST score
                   289
                   6.0e-26
E value
Match length
                  55
% identity
                   98
                   (AF114796) ADP-ribosylation factor [Glycine max]
NCBI Description
```

```
Seq. No.
                  150406
Seq. ID
                  LIB3175-040-P1-K1-H12
Method
                  BLASTX
                  g3859998
NCBI GI
BLAST score
                  306
                  5.0e-28
E value
                  107
Match length
                  52
% identity
                  (AF091080) unknown [Homo sapiens]
NCBI Description
Seq. No.
                  150407
                  LIB3175-040-P1-K1-H5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q600178
BLAST score
                  578
                  7.0e-60
E value
Match length
                  131
                  87
% identity
                  (L27074) acetyl-CoA carboxylase [Arabidopsis thaliana]
NCBI Description
                  >qi 1090217 prf 2018327A Ac-CoA carboxylase [Arabidopsis
                  thaliana]
                  150408
Seq. No.
                  LIB3175-040-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3128205
BLAST score
                  717
                  4.0e-76
E value
Match length
                  144
                  97
% identity
                  (AC004077) putative pyruvate dehydrogenase complex E1 beta
NCBI Description
                  subunit [Arabidopsis thaliana]
                  150409
Seq. No.
                  LIB3175-040-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172872
BLAST score
                  464
                  1.0e-46
E value
Match length
                  91
% identity
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi 435618 dbj BAA02373_
                  (D13042) thiol protease [Arabidopsis thaliana]
                  >gi 4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                  150410
                  LIB3175-041-P1-K1-A1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q3927822
BLAST score
                  318
E value
                  1.0e-179
                  394
Match length
% identity
                  98
```

```
NCBI Description Arabidopsis thaliana chromosome II BAC F8N16 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150411
                  LIB3175-041-P1-K1-A10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2832625
BLAST score
                  640
                  4.0e-67
E value
                  123
Match length
                  100
% identity
NCBI Description
                   (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  150412
Seq. ID
                  LIB3175-041-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q2832625
BLAST score
                  412
E value
                  2.0e-40
Match length
                  140
% identity
                  66
NCBI Description
                   (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                  150413
                  LIB3175-041-P1-K1-A12
Seq. ID
Method ...
                  BLASTX
NCBI GI
                  g2924779
BLAST score
                  623
E value
                  4.0e-65
Match length
                  124
% identity
                  99
NCBI Description
                   (AC002334) putative 3-ketoacyl-CoA thiolase [Arabidopsis
                  thaliana] >qi 2981616 dbj BAA25248 (AB008854)
                  3-ketoacyl-CoA thiolase [Arabidopsis thaliana]
                  >gi 2981618 dbj BAA25249 (AB008855) 3-ketoacyl-CoA
                  thiolase [Arabidopsis thaliana]
                  150414
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  q3415117
BLAST score
                  82
                  2.0e-38
E value
Match length
                  88
% identity
                  51
                  (AF081203) villin 3 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150415
                  LIB3175-041-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g119350
BLAST score
                  654
E value
                  9.0e-69
Match length
                  127
                  100
% identity
NCBI Description ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi 81608 pir JQ1187
```

Seq. No.

Seq. ID Method

NCBI GI

E value Match length

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

BLAST score

Match length

NCBI Description

% identity

BLAST score

% identity

NCBI Description

```
phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
thaliana >gi_16271_emb_CAA41114_ (X58107) enolase
[Arabidopsis thaliana]
>gi 4581151 gb AAD24635.1 AC006919 13 (AC006919) enolase
(2-phospho-D-glycerate hydroylase); identical to P25696
[Arabidopsis thaliana]
150416
LIB3175-041-P1-K1-A5
BLASTN
g2618599
415
0.0e+00
415
100
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
MBD2, complete sequence [Arabidopsis thaliana]
150417
LIB3175-041-P1-K1-A6
BLASTX
g2739389
389
8.0e-38
106
(AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
150418
LIB3175-041-P1-K1-A7
BLASTN
g3449330
```

Seq. No. Seq. ID Method NCBI GI BLAST score 85 E value 2.0e-40 Match length 105 % identity 95

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]

Seq. No. 150419 Seq. ID LIB3175-041-P1-K1-A8 Method BLASTN NCBI GI q4589435 BLAST score 405 E value 0.0e + 00Match length 425 % identity 99

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MOE17, complete sequence 150420

LIB3175-041-P1-K1-A9 Seq. ID Method BLASTN NCBI GI g1931636 BLAST score 221 E value 1.0e-121 Match length 441

```
% identity
                  Arabidopsis thaliana BAC T19D16 genomic sequence
NCBI Description
                  150421
Seq. No.
                  LIB3175-041-P1-K1-B1
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4689386
                   346
BLAST score
                  1.0e-32
E value
                  91
Match length
                  73
% identity
NCBI Description
                   (AF139468) photosystem I reaction center subunit III [Vigna
                  radiata]
Seq. No.
                  150422
Seq. ID
                  LIB3175-041-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q3421123
BLAST score
                  646
                  8.0e-68
E value
Match length
                  125
% identity
NCBI Description
                   (AF043538) 20S proteasome beta subunit PBG1 [Arabidopsis
                   thaliana]
Seq. No.
                  150423
Seq. ID
                  LIB3175-041-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q2342687 3
BLAST score
                  584
E value
                   1.0e-60
Match length
                  112
% identity
                   100
NCBI Description
                   (AC000106) Similar to Beta integral membrane protein
                   (gb U43629). EST gb W43122 comes from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                  150424
Seq. ID
                  LIB3175-041-P1-K1-B2
Method
                  BLASTX
                  g4455192
NCBI GI
BLAST score
                  241
                   3.0e-20
E value
Match length
                  127
% identity
                  24
                  (AL035440) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150425
                  LIB3175-041-P1-K1-B3
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4678705
BLAST score
                  422
E value
                  0.0e + 00
                  438
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7
                   (ESSA project)
```

19175

```
Seq. No.
                  150426
Seq. ID
                  LIB3175-041-P1-K1-B5
Method
                  BLASTN
NCBI GI
                  q3264774
BLAST score
                  123
                  1.0e-62
E value
Match length
                  207
                  100
% identity
                  Arabidopsis thaliana BAC T8A17 chromosome IV, complete
NCBI Description
                  sequence [Arabidopsis thaliana]
Seq. No.
                  150427
                  LIB3175-041-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g629669
BLAST score
                  165
E value
                  2.0e-11
Match length
                  139
                  31
% identity
NCBI Description hypothetical protein - tomato
Seq. No.
                  150428
                  LIB3175-041-P1-K1-B9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3068713
BLAST score
                  482
E value
                  1.0e-48
Match length
                  140
% identity
NCBI Description
                  (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  150429
Seq. ID
                  LIB3175-041-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  698
                  7.0e-74
E value
Match length
                  146
% identity
                  90
NCBI Description
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  150430
Seq. ID
                  LIB3175-041-P1-K1-C11
Method
                  BLASTN
NCBI GI
                  g2244950
BLAST score
                  176
                  2.0e-94
E value
                  308
Match length
% identity
                  93
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
```

E value

1.0e-24

## fragment No

```
Seq. No.
                  150431
                  LIB3175-041-P1-K1-C12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2827143
BLAST score
                  600
                  2.0e-62
E value
Match length
                  122
% identity
                  (AF027174) cellulose synthase catalytic subunit
NCBI Description
                  [Arabidopsis thaliana]
                  150432
Seq. No.
                  LIB3175-041-P1-K1-C2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585350
BLAST score
                  647
                  7.0e-68
E value
Match length
                  142
% identity
                  86
NCBI Description
                  CASEIN KINASE II, ALPHA CHAIN 2 (CK II)
                  >gi 419753 pir S31099 casein kinase II (EC 2.7.1.-)
                  alpha-type chain (clone ATCKA2) - Arabidopsis thaliana
                  >gi 391605 dbj BAA01091 (D10247) casein kinase II
                  catalytic subunit [Arabidopsis thaliana]
Seq. No.
                  150433
Seq. ID
                  LIB3175-041-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  q3894172
                  399
BLAST score
E value
                  7.0e-39
Match length
                  130
                  57
% identity
NCBI Description
                  (AC005312) putative cinnamoyl-CoA reductase [Arabidopsis
                  thaliana]
Seq. No.
                  150434
Seq. ID
                  LIB3175-041-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g3152587
BLAST score
                  227
E value
                  8.0e-19
                  97
Match length
% identity
NCBI Description
                  (AC002986) Similar to CREB-binding protein homolog
                  gb_U88570 from D. melanogaster and contains similarity to
                  callus-associated protein gb U01961 from Nicotiana tabacum.
                  EST gb W43427 comes from this gene. [Arabidopsis thaliana]
Seq. No.
                  150435
Seq. ID
                  LIB3175-041-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g3860274
BLAST score
                  277
```

```
Match length
                   91
% identity
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   >gi_4314397_gb_AAD15607_ (AC006232) putative zinc finger
                   protein [Arabidopsis thaliana]
                   150436
Seq. No.
                   LIB3175-041-P1-K1-C6
Seq. ID
                   BLASTX
Method
                   q4406777
NCBI GI
                   148
BLAST score
                                                        17.
                   2.0e-09
E value
                   128
Match length
                   31
% identity
                   (AC006532) putative zinc-finger protein [Arabidopsis
NCBI Description
                   thaliana]
                   150437
Seq. No.
                   LIB3175-041-P1-K1-C8
Seq. ID
                   BLASTX
Method
                                               700
NCBI GI
                   g134025
BLAST score
                   511
                    6.0e-52
E value
                   130
Match length
                   80
% identity
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi 70913 pir R3NT8
NCBI Description
                   ribosomal protein S8 - common tobacco chloroplast
                   >gi_11863_emb_CAA77378_ (Z00044) ribosomal protein S8
[Nicotiana tabacum] >gi_225232_prf__1211235BP ribosomal
                    protein S8 [Nicotiana tabacum]
Seq. No.
                    150438
                    LIB3175-041-P1-K1-C9
Seq. ID
                    BLASTX
Method
                    g134025
NCBI GI
                    338
BLAST score
                    8.0e-32
E value
                    107
Match length
                    68
% identity
                   CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 >gi_70913_pir__R3NT8
NCBI Description
                    ribosomal protein S8 - common tobacco chloroplast
                    >gi 11863_emb_CAA77378_ (Z00044) ribosomal protein S8
                    [Nicotiana tabacum] >gi 225232_prf__1211235BP ribosomal
                    protein S8 [Nicotiana tabacum]
                    150439
 Seq. No.
                    LIB3175-041-P1-K1-D12
 Seq. ID
                    BLASTN
Method
                    g4589410
NCBI GI
                    144
BLAST score
                    3.0e-75
E value
                    305
Match length
                    92
 % identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
 NCBI Description
                    F2015, complete sequence
```

Seq. No.

```
Seq. ID
                  LIB3175-041-P1-K1-D2
Method
                  BLASTX
NCBI GI
                  g1170373
BLAST score
                  251
                  1.0e-21
E value
Match length
                  69
                  74
% identity
NCBI Description
                  HEAT SHOCK COGNATE 70 KD PROTEIN 1 >gi 1072473 pir S46302
                  heat shock cognate protein 70-1 - Arabidopsis thaliana
                  >gi_397482_emb_CAA52684 (X74604) heat shock protein 70
                  cognate [Arabidopsis thaliana]
                  150441
Seq. No.
                  LIB3175-041-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1353352
                  326
BLAST score
E value
                  3.0e - 30
Match length
                  86
% identity
                  (U31975) alanine aminotransferase [Chlamydomonas
NCBI Description
                  reinhardtii]
                  150442
Seq. No.
                  LIB3175-041-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2507281
                  646
BLAST score
E value
                  7.0e-68
Match length
                  122
                  95
% identity
                  GTP-BINDING NUCLEAR PROTEIN RAN-2 >gi 1668706 emb CAA66048
NCBI Description
                  (X97380) atran2 [Arabidopsis thaliana]
                  150443
Seq. No.
                  LIB3175-041-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3121853
BLAST score
                  154
                  4.0e-10
E value
Match length
                  141
% identity
                  30
                  CHLORIDE INTRACELLULAR CHANNEL PROTEIN 2 (XAP121)
NCBI Description
                  >gi 2584785 emb CAA73228 (Y12696) p64 bovine chloride
                  channel-like protein [Homo sapiens]
                  150444
Seq. No.
                  LIB3175-041-P1-K1-D7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  572
                  3.0e-59
E value
                  124
Match length
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                  photosystem II type I chlorophyll a /b binding protein
```

...

```
[Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana] >gi_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]
```

```
Seq. No.
                   150445
Seq. ID
                   LIB3175-041-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   q4741954
BLAST score
                   671
                   1.0e-70
E value
Match length
                   130
                   99
% identity
NCBI Description
                   (AF134127) Lhcb4.2 protein [Arabidopsis thaliana]
Seq. No.
                   150446
Seq. ID
                   LIB3175-041-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   q3676294
BLAST score
                   338
E value
                   1.0e-31
Match length
                   112
                   68
% identity
NCBI Description
                   (U96496) mitochondrial ATPase beta subunit [Nicotiana
                   sylvestris]
Seq. No.
                   150447
Seq. ID
                   LIB3175-041-P1-K1-E1
Method
                   BLASTN
NCBI GI
                   q2494110
BLAST score
                   403
                   0.0e + 00
E value
Match length
                   403
% identity
                   90
                   Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150448
Seq. ID
                   LIB3175-041-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g4185515
BLAST score
                   545
                   6.0e-56
E value
Match length
                   105
% identity
                   99
                   (AF102824) actin depolymerizing factor 6 [Arabidopsis
NCBI Description
                   thaliana]
                   150449
Seq. No.
Seq. ID
                   LIB3175-041-P1-K1-E12
                   BLASTX
Method
NCBI GI
                   q4185515
BLAST score
                   190
                   7.0e-19
E value
Match length
                   80
% identity
NCBI Description
                   (AF102824) actin depolymerizing factor 6 [Arabidopsis
```

## thaliana]

```
Seq. No.
                  150450
Seq. ID
                  LIB3175-041-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g3851669
BLAST score
                  210
                  1.0e-114
E value
                  218
Match length
                  99
% identity
                  Arabidopsis thaliana J8 mRNA, nuclear gene encoding plastid
NCBI Description
                  protein, complete cds
Seq. No.
                  150451
Seq. ID
                  LIB3175-041-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g3337361
BLAST score
                   486
                  5.0e-49
E value
Match length
                  110
% identity
                  79
                   (AC004481) ankyrin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150452
                  LIB3175-041-P1-K1-E4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3851636 -
BLAST score
                   452
E value
                   5.0e-45
Match length
                  117
% identity
                   73
                   (AF098519) unknown [Avicennia marina] >gi 4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   150453
Seq. No.
                  LIB3175-041-P1-K1-E5
Seq. ID
Method
                   BLASTX
                   g3851636
NCBI GI
BLAST score
                   480
E value
                   2.0e-48
Match length
                   119
% identity
                   (AF098519) unknown [Avicennia marina] >gi 4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
                   150454
Seq. No.
                  LIB3175-041-P1-K1-E6
Seq. ID
                  BLASTX
Method
                   g3851636
NCBI GI
                   388
BLAST score
                   1.0e-37
E value
Match length
                   113
                   67
% identity
                   (AF098519) unknown [Avicennia marina] >gi 4128206
NCBI Description
                   (AF056316) 40S ribosome protein S7 [Avicennia marina]
```

150455

Seq. No.

```
LIB3175-041-P1-K1-E7
Seq. ID
Method
                  BLASTX
                  g3033375
NCBI GI
BLAST score
                   191
E value
                   2.0e-14
                  135
Match length
                   39
% identity
NCBI Description
                   (AC004238) putative berberine bridge enzyme [Arabidopsis
                  thaliana]
                  150456
Seq. No.
                  LIB3175-041-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586265
                   488
BLAST score
                   3.0e-49
E value
Match length
                  115
% identity
NCBI Description
                  (AL049640) putative protein [Arabidopsis thaliana]
                  150457
Seq. No.
                  LIB3175-041-P1-K1-F1
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129672
BLAST score
                   294
                   1.0e-26
E value
                   117
Match length
% identity
                  photosystem II reaction center protein, 6.1K - Arabidopsis
NCBI Description
                   thaliana >gi 950023 emb CAA62296 (X90769) component of 6.1
                   kDa polypeptide of photosystem II reaction center
                   [Arabidopsis thaliana]
                   150458
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-F10
                   BLASTX
Method
                   q1864017
NCBI GI
BLAST score
                   547
                   2.0e-56
E value
Match length
                   105
                   99
% identity
NCBI Description
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
                   150459
Seq. No.
                   LIB3175-041-P1-K1-F11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g1175013
BLAST score
                   597
                   5.0e-62
E value
Match length
                   131
% identity
                   90
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2A >qi 629542 pir S44084
NCBI Description
                  plasma membrane intrinsic protein 2a - Arabidopsis thaliana
                  >gi 472877 emb CAA53477 (X75883) plasma membrane intrinsic
                  protein 2a [Arabidopsis thaliana]
                  150460
Seq. No.
```

```
LIB3175-041-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267069
BLAST score
                  617
                  2.0e-64
E value
Match length
                  114
                  100
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                  tubulin alpha chain - Arabidopsis thaliana >gi 166914
                  (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi 166916
                  (M84697) alpha-4 tubulin [Arabidopsis thaliana]
                  150461
Seq. No.
                  LIB3175-041-P1-K1-F2
Seq. ID
                  BLASTX
Method
                  g1946362
NCBI GI
                  385
BLAST score
                  3.0e - 37
E value
Match length
                  120
% identity
                  66
                  (U93215) photosystem II reaction center 6.1KD protein
NCBI Description
                  [Arabidopsis thaliana]
                  150462
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-F3
                  BLASTX
Method
NCBI GI
                  g1790922
BLAST score
                  679
                  1.0e-71
E value
Match length
                  135
% identity
                  100
                  (U76670) AtDMC1 [Arabidopsis thaliana]
NCBI Description
                  150463
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  q4220510
BLAST score
                  46
                  1.0e-16
E value
Match length
                  135
                  88
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F22K18
NCBI Description
                  (ESSAII project)
                  150464
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-F5
Method
                  BLASTX
NCBI GI
                  q2062164
BLAST score
                  503
                  4.0e-51
E value
Match length
                  115
% identity
                  (AC001645) jasmonate inducible protein isolog [Arabidopsis
NCBI Description
                  thaliana]
                  150465
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-F6
```

```
Method
                  BLASTX
NCBI GI
                  g3355471
BLAST score
                   496
                   3.0e-50
E value
Match length
                  115
% identity
                   (AC004218) putative lysophospholipase [Arabidopsis
NCBI Description
                  thaliana]
                  150466
Seq. No.
                  LIB3175-041-P1-K1-F7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1170939
                   469
BLAST score
E value
                   5.0e-47
                   97
Match length
                   92
% identity
                  S-ADENOSYLMETHIONINE SYNTHETASE 3 (METHIONINE
NCBI Description
                  ADENOSYLTRANSFERASE 3) (ADOMET SYNTHETASE 3)
                   >gi_1084408_pir__S46540 methionine adenosyltransferase (EC
                   2.5.1.6) - tomato >gi 429108 emb CAA80867 (Z24743)
                   S-adenosyl-L-methionine synthetase [Lycopersicon
                   esculentum]
                   150467
Seq. No.
                   LIB3175-041-P1-K1-F8
Seq. ID
Method
                   BLASTX
                   g4755189
NCBI GI
BLAST score
                   342
E value
                   2.0e-37
                   124
Match length
% identity
                   (ACO07018) putative cytochrome P450 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150468
                  LIB3175-041-P1-K1-G1
Seq. ID
                  BLASTN
Method
                   q2244901
NCBI GI
BLAST score
                   176
E value
                   3.0e-94
                   443
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                   150469
                  LIB3175-041-P1-K1-G10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q345829
BLAST score
                   261
E value
                   1.0e-22
Match length
                  87
                   60
% identity
NCBI Description
                  ubiquitin carrier protein E2 - human
                   150470
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-G12
```

```
Method
                  BLASTX
NCBI GI
                  g2738248
BLAST score
                   631
                   5.0e-66
E value
                  126
Match length
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                  150471
Seq. No.
                  LIB3175-041-P1-K1-G3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4741940
                   627
BLAST score
                   1.0e-65
E value
                   128
Match length
                   65
% identity
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150472
                  LIB3175-041-P1-K1-G5
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4098272
BLAST score
                   353
E value
                   1.0e-33
Match length
                   65
                   97
% identity
                  (U76558) alpha-tubulin [Triticum aestivum]
NCBI Description
                   150473
Seq. No.
                   LIB3175-041-P1-K1-G6
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3047100
BLAST score
                   269
E value
                   1.0e-149
Match length
                   434
                   100
% identity
NCBI Description Arabidopsis thaliana BAC F6N23
                   150474
Seq. No.
                  LIB3175-041-P1-K1-H10
Seq. ID
Method
                   BLASTX
                   g4589398
NCBI GI
BLAST score
                   48
E value
                   1.0e-29
Match length
                   98
% identity
                   68
                  (D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]
NCBI Description
Seq. No.
                   150475
Seq. ID
                  LIB3175-041-P1-K1-H11
                   BLASTN
Method
                   q4760411
NCBI GI
BLAST score
                   364
E value
                   0.0e + 00
                   388
Match length
% identity
                   99
```

```
NCBI Description Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
                  complete sequence
                  150476
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-H2
                  BLASTX
Method
                  g1169598
NCBI GI
                  248
BLAST score
                  3.0e-21
E value
                  58
Match length
                  84
% identity
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
                  150477
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-H5
                  BLASTX
Method
NCBI GI
                  g1561730
BLAST score
                  157
                  1.0e-10
E value
Match length
                  61
                  46
% identity
                   (U65491) Dreg-3 protein [Drosophila melanogaster]
NCBI Description
Seq. No.
                  150478
Seq. ID
                  LIB3175-041-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g4263523
BLAST score
                   454
E value
                  2.0e-45
Match length
                  91
                   67
% identity
                   (AC004044) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150479
Seq. ID
                  LIB3175-041-P1-K1-H7
                  BLASTX
Method
NCBI GI
                  g4689386
BLAST score
                  386
E value
                  3.0e-37
Match length
                  99
% identity
                  74
NCBI Description
                   (AF139468) photosystem I reaction center subunit III [Vigna
                  radiata]
Seq. No.
                  150480
Seq. ID
                  LIB3175-041-P1-K1-H8
                  BLASTX
Method
NCBI GI
                  g4056467
BLAST score
                  656
E value
                  5.0e-69
Match length
                  127
% identity
                   (AC005990) Strong similarity to gb_AB006693 spermidine
NCBI Description
                  synthase from Arabidopsis thaliana. ESTs gb_AA389822,
                  gb_T41794, gb_N38455, gb_AI100106, gb_F14442 and gb_F14256
```

## come from this gene. [Arabidopsis thaliana]

```
150481
Seq. No.
Seq. ID
                  LIB3175-041-P1-K1-H9
                  BLASTX
Method
                  g3395938
NCBI GI
                  474
BLAST score
                  1.0e-47
E value
                  96
Match length
% identity
                  (AF076924) polypyrimidine tract-binding protein homolog
NCBI Description
                  [Arabidopsis thaliana]
                  150482
Seq. No.
                  LIB3175-042-P1-K1-A1
Seq. ID
                  BLASTX
Method
                  g1621268
NCBI GI
BLAST score
                  564
                  3.0e-58
E value
                  131
Match length
                  78
% identity
                  (Z81012) unknown [Ricinus communis]
NCBI Description
                  150483
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-A10
                  BLASTX
Method
                  g417381
NCBI GI
                   665
BLAST score
                   4.0e-70
E value
                  132
Match length
% identity
                   98
                  NITRILASE 1 >gi 99738_pir S22398 nitrilase (EC 3.5.5.1) -
NCBI Description
                  Arabidopsis thaliana >gi 16400 emb CAA45041 (X63445)
                  nitrilase I [Arabidopsis thaliana]
                   150484
Seq. No.
                  LIB3175-042-P1-K1-A4
Seq. ID
                   BLASTX
Method
                   q4758946
NCBI GI
BLAST score
                   186
                   6.0e-14
E value
                   71
Match length
                   55
% identity
                  POP2 (yeast homolog) >gi 4106061_gb AAD02685_ (AF053318)
NCBI Description
                   CCR4-associated factor 1 [Homo sapiens]
                   150485
Seq. No.
                   LIB3175-042-P1-K1-A5
Seq. ID
                   BLASTX
Method
                   q4587564
NCBI GI
BLAST score
                   498
                   2.0e-50
E vàlue
Match length
                   96
% identity
                   (AC006550) Strong similarity to gb_X14017 photosystem I
NCBI Description
                   reaction centre subunit II precursor (psaD) from Spinacia
                   oleracea. ESTs gb_R30423, gb_T42998, gb_Z18178, gb_T14133,
```

```
gb_N65521, gb_T42498, gb_T41918, gb_N38024
                  150486
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-A6
Method
                  BLASTX
                  q2642158
NCBI GI
BLAST score
                  159
                  2.0e-11
E value
                  61
Match length
                  56
% identity
                  (AC003000) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  150487
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-A7
Method
                  BLASTX
                  q114649
NCBI GI
BLAST score
                  205
                  4.0e-16
E value
Match length
                  43
                  100
% identity
                  ATP SYNTHASE C CHAIN (LIPID-BINDING PROTEIN) (SUBUNIT III)
NCBI Description
                  >gi 67899 pir LWLVA H+-transporting ATP synthase (EC
                  3.6.1.34) lipid-binding protein - liverwort (Marchantia
                  polymorpha) chloroplast >gi_11653_emb_CAA28066_ (X04465)
                  atpH [Marchantia polymorpha]
                  150488
Seq. No.
                  LIB3175-042-P1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI ĞI
                  q2244747
BLAST score
                   289
                  1.0e-161
E value
                   415
Match length
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                   150489
Seq. No.
                  LIB3175-042-P1-K1-A9
Seq. ID
Method
                   BLASTN
                   q3985934
NCBI GI
BLAST score
                   163
                   2.0e-86
E value
                   354
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJE7, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150490
                   LIB3175-042-P1-K1-B1
Seq. ID
Method
                   BLASTX
                   g2827529
NCBI GI
BLAST score
                   680
E value
                   8.0e-72
Match length
                   136
% identity
                   (AL021633) putative protein [Arabidopsis thaliana]
NCBI Description
```

E value

```
Seq. No.
                   150491
                   LIB3175-042-P1-K1-B11
Seq. ID
Method
                   BLASTN
                   q4589420
NCBI GI
BLAST score
                   52
E value
                   2.0e-20
                   149
Match length
                   89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                   K3G17, complete sequence
                   150492
Seq. No.
Seq. ID
                   LIB3175-042-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   g132110
BLAST score
                   610
E value
                   1.0e-63
Match length
                   112
                   99
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
NCBI Description
                   (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                   ribulose-bisphosphate carboxylase (\overline{EC} 4.\overline{1.1}.39) small chain
                   B3 precursor - Arabidopsis thaliana >gi 16195 emb CAA32702
                   (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                   thaliana]
Seq. No.
                   150493
Seq. ID
                   LIB3175-042-P1-K1-B2
Method
                   BLASTX
                   q134976
NCBI GI
BLAST score
                   501
                   7.0e-51
E value
Match length
                   96
                   100
% identity
NCBI Description
                  GLUCOSE TRANSPORTER (SUGAR CARRIER) >gi 81619 pir S12042
                   glucose transport protein STP1 - Arabidopsis thaliana
                   >gi_16520_emb_CAA39037_ (X55350) glucose transporter
                   [Arabidopsis thaliana]
Seq. No.
                   150494
                   LIB3175-042-P1-K1-B3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q4432865
BLAST score
                   676
                   2.0e-71
E value
Match length
                   134
% identity
NCBI Description
                   (AC006300) putative cellulose synthase catalytic subunit
                   [Arabidopsis thaliana]
Seq. No.
                   150495
Seq. ID
                  LIB3175-042-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2245087
BLAST score
                   443
```

5.0e-44

BLAST score

E value

594 9.0e-62

```
Match length
                  103
% identity
NCBI Description
                  (Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  150496
                  LIB3175-042-P1-K1-B5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q871991
BLAST score
                  63
                  3.0e-27
E value
Match length
                  139
                  86
% identity
NCBI Description
                  A.thaliana TGG2 gene for myrosinase
                  150497
Seq. No.
                  LIB3175-042-P1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4586241
BLAST score
                  69
                  2.0e-30
E value
                  286
Match length
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
NCBI Description
                  (ESSA project)
                  150498
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q282865
BLAST score
                  203
                  6.0e-16
E value
Match length
                  101
                  48
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >gi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
                  protein [Arabidopsis thaliana] >gi_166644 (M85150)
                  chlorophyll a/b-binding protein [Arabidopsis thaliana]
                  >qi 4678304 emb CAB41095.1 (AL049655) chlorophyll
                  a/b-binding protein [Arabidopsis thaliana]
Seq. No.
                  150499
Seq. ID
                  LIB3175-042-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  q4586241
BLAST score
                  62
E value
                  3.0e-26
Match length
                  218
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                  (ESSA project)
Seq. No.
                  150500
Seq. ID
                  LIB3175-042-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  g119350
```

NCBI GI

```
Match length
                  114
% identity
                  ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE)
NCBI Description
                  (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_81608_pir__JQ1187
                  phosphopyruvate hydratase (EC 4.2.1.11) - Arabidopsis
                  thaliana >gi 16271 emb CAA41114_ (X58107) enolase
                  [Arabidopsis thaliana]
                  >qi 4581151 gb AAD24635.1 AC006919 13 (AC006919) enolase
                  (2-phospho-D-glycerate hydroylase); identical to P25696
                  [Arabidopsis thaliana]
                  150501
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-C10
Method
                  BLASTX
                  q4090884
NCBI GI
BLAST score
                  518
                  7.0e-53
E value
Match length
                  102
                  98
% identity
                  (AF025333) vesicle-associated membrane protein 7B;
NCBI Description
                  synaptobrevin 7B [Arabidopsis thaliana]
                  150502
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-C11
Method
                  BLASTX
                  g4586263
NCBI GI
BLAST score
                  635
                  1.0e-66
E value
                  122
Match length
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
                  150503
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-C12
Method
                  BLASTX
                  g1903357
NCBI GI
                   610
BLAST score
                  1.0e-63
E value
                  132
Match length
% identity
                   (AC000104) Strong similarity to Arabidopsis 2A6
NCBI Description
                   (gb_X83096). [Arabidopsis thaliana]
                   150504
Seq. No.
                  LIB3175-042-P1-K1-C2
Seq. ID
Method
                   BLASTN
                  q1865678
NCBI GI
BLAST score
                   266
                   1.0e-148
E value
                   364
Match length
% identity
                   99
NCBI Description A.thaliana ATB2 gene
Seq. No.
                   150505
Seq. ID
                  LIB3175-042-P1-K1-C3
                  BLASTX
Method
```

q4185505

```
BLAST score
                  343
                  2.0e-32
E value
Match length
                  89
% identity
                  75
                  (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                  [Brassica napus]
Seq. No.
                  150506
                  LIB3175-042-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g267079
BLAST score
                  661
E value
                  1.0e-69
Match length
                  122
% identity
                  99
NCBI Description
                  TUBULIN BETA-6 CHAIN >gi 320187 pir JQ1590 tubulin beta-6
                  chain - Arabidopsis thaliana >gi 166904 (M84703) beta-6
                  tubulin [Arabidopsis thaliana]
Seq. No.
                  150507
Seq. ID
                  LIB3175-042-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1709446
BLAST score
                  486
E value
                  4.0e-49
Match length
                  115
% identity
                  83
NCBI Description
                  PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT
                  PRECURSOR (PDHE1-A) >gi 2117533 pir JC4358 pyruvate
                  dehydrogenase (lipoamide) (EC 1.2.4.1) complex E1 alpha
                  chain - Arabidopsis thaliana mitochondrion >gi 710400
                   (U21214) pyruvate dehydrogenase E1 alpha subunit
                  [Arabidopsis thaliana]
Seq. No.
                  150508
                  LIB3175-042-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586263
BLAST score
                  404
                                   ....
E value
                  2.0e-39
Match length
                  112
% identity
                  (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150509
                  LIB3175-042-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1755162
BLAST score
                  225
E value
                  2.0e-18
                  126
Match length
% identity
NCBI Description
                  (U75192) germin-like protein [Arabidopsis thaliana]
                  150510
Seq. No.
                  LIB3175-042-P1-K1-D10
Seq. ID
Method
                  BLASTN
```

BLAST score

```
q2062153
NCBI GI
BLAST score
                  41
                  9.0e-14
E value
                  188
Match length
                  87
% identity
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  150511
Seq. No.
                  LIB3175-042-P1-K1-D11
Seq. ID
                  BLASTN
Method
                  q4220645
NCBI GI
BLAST score
                  283
                   1.0e-158
E value
                   377
Match length
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYA6, complete sequence [Arabidopsis thaliana]
                   150512
Seq. No.
                   LIB3175-042-P1-K1-D2
Seq. ID
                   BLASTX
Method
                   q1174623
NCBI GI
BLAST score
                   246
                   6.0e-21
E value
                   87
Match length
                   59
% identity
                   T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA)
NCBI Description
                   >gi_529705 (U13070) C. elegans cct-6 (similar to T complex
                   proteins, Tcp-1-related, Cctz) [Caenorhabditis elegans]
                   150513
Seq. No.
                   LIB3175-042-P1-K1-D4
Seq. ID
                   BLASTN
Method
NCBI GI
                   q1209241
                   372
BLAST score
                   0.0e + 00
E value
                   387
Match length
                   99
% identity
                   Arabidopsis thaliana metallothionein mRNA sequence
NCBI Description
                   150514
Seq. No.
Seq. ID
                   LIB3175-042-P1-K1-D5
                   BLASTN
Method
NCBI GI
                   q4063737
BLAST score
                   247
                   1.0e-137
E value
                   287
Match length
                   97
% identity
                   Arabidopsis thaliana chromosome II BAC F24D13 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                   150515
Seq. No.
                   LIB3175-042-P1-K1-D6
Seq. ID
                   BLASTN
Method
NCBI GI
                   q3420042
```

```
2.0e-32
E value
                  176
Match length
% identity
                  85
                  Arabidopsis thaliana chromosome II BAC T13E15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150516
                  LIB3175-042-P1-K1-D7
Seq. ID
                  BLASTX
Method
                  g2317913
NCBI GI
                  533
BLAST score
                  1.0e-54
E value
                  106
Match length
                  99
% identity
NCBI Description
                   (U89959) cathepsin B-like cysteine proteinase [Arabidopsis
                  thaliana]
                  150517
Seq. No.
                  LIB3175-042-P1-K1-D8
Seq. ID
Method
                  BLASTN
                  g3420042
NCBI GI
                  278
BLAST score
E value
                  1.0e-155
Match length
                  349
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T13E15 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150518
                  LIB3175-042-P1-K1-D9
Seq. ID
Method
                  BLASTN
                  g4206764
NCBI GI
BLAST score
                   377
E value
                  0.0e+00
                  393
Match length
                   99
% identity
                  Arabidopsis thaliana putative type 1 membrane protein (PMP)
NCBI Description
                  mRNA, complete cds
Seq. No.
                  150519
Seq. ID
                  LIB3175-042-P1-K1-E1
                  BLASTX
Method
                  g2500430
NCBI GI
BLAST score
                  364
                  8.0e-35
E value
                  73
Match length
                  96
% identity
                  40S RIBOSOMAL PROTEIN S16
NCBI Description
Seq. No.
                  150520
                  LIB3175-042-P1-K1-E10
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4220645
BLAST score
                  34
E value
                  2.0e-09
                  94
Match length
% identity
                  85
```

```
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MYA6, complete sequence [Arabidopsis thaliana]
                  150521
Seq. No.
                  LIB3175-042-P1-K1-E11
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4454036
                  277
BLAST score
                  1.0e-24
E value
                  76
Match length
                  64
% identity
                   (AL035394) putative major latex protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  150522
                  LIB3175-042-P1-K1-E12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4586241
BLAST score
                  45
                  4.0e-16
E value
                  61
Match length
% identity
                  66
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T20K18
                  (ESSA project)
                  150523
Seq. No.
                  LIB3175-042-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1213536
BLAST score
                  151
                  8.0e-10
E value
                  91
Match length
                  41
% identity
                   (U50193) the above GenBank entry begins at aa 120
NCBI Description
                  [Caenorhabditis elegans]
                  150524
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g3080372
BLAST score
                  651
                  2.0e-68
E value
Match length
                  124
% identity
                  (AL022580) putative pectinacetylesterase [Arabidopsis
NCBI Description
                  thaliana]
                  150525
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g4432856
BLAST score
                  695
E value
                  1.0e-73
Match length
                  132
                  100
% identity
NCBI Description (AC006300) putative 2A6 protein [Arabidopsis thaliana]
```

```
Seq. No.
                  150526
                  LIB3175-042-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129672
BLAST score
                  207
                  1.0e-16
E value
                  67
Match length
                   66
% identity
                  photosystem II reaction center protein, 6.1K - Arabidopsis
NCBI Description
                  thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1
                   kDa polypeptide of photosystem II reaction center
                   [Arabidopsis thaliana]
Seq. No.
                  150527
                  LIB3175-042-P1-K1-F1
Seq. ID
                  BLASTN
Method
NCBI GI
                  q4159707
BLAST score
                   98
                  1.0e-47
E value
                  346
Match length
                   94
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJK13, complete sequence
                  150528
Seq. No.
                  LIB3175-042-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4204299
                   709
BLAST score
                   3.0e-75
E value
                  134
Match length
                   100
% identity
                   (AC003027) lcl_prt_seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  150529
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-F11
Method
                  BLASTN
NCBI GI
                   g2062153
BLAST score
                   45
E value
                   3.0e-16
Match length
                  189
% identity
                  85
                  Arabidopsis thaliana chromosome III BAC T02004 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  150530
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g3024526
BLAST score
                   470
E value
                  2.0e-47
Match length
                  105
% identity
                  RAS-RELATED PROTEIN RAB11 >gi 2118459_pir__S59942 small
NCBI Description
                  GTP-binding protein Rabl1 - Arabidopsis thaliana >gi_451860
                   (L18883) small GTP-binding protein [Arabidopsis thaliana]
```

```
Seq. No.
                  150531
                  LIB3175-042-P1-K1-F4
Seq. ID
Method
                  BLASTX
                  g1170639
NCBI GI
BLAST score
                  166
                  1.0e-11
E value
                  130
Match length
                  33
% identity
                  3-DEOXY-D-MANNO-OCTULOSONIC-ACID TRANSFERASE (KDO
NCBI Description
                  TRANSFERASE) >gi_1073787_pir__F64084
                  3-deoxy-d-manno-octulosonic-acid transferase (kdtA) homolog
                  - Haemophilus influenzae (strain Rd KW20) >gi 1573651
                  (U32748) 3-deoxy-d-manno-octulosonic-acid transferase
                  (kdtA) [Haemophilus influenzae Rd]
Seq. No.
                  150532
Seq. ID
                  LIB3175-042-P1-K1-F5
Method
                  BLASTN
                  g2264319
NCBI GI
                  59
BLAST score
                  5.0e-25
E value
                  109
Match length
                  68
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXA21, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150533
Seq. ID
                  LIB3175-042-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q529353
                  202
BLAST score
E value
                  2.0e-23
                  92
Match length
                  60
% identity
                  (U12757) diphenol oxidase [Acer pseudoplatanus]
NCBI Description
                  150534
Seq. No.
Seq. ID
                  LIB3175-042-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g4185505
BLAST score
                  460
                  5.0e-46
E value
Match length
                  112
                  78
% identity
                  (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                  [Brassica napus]
Seq. No.
                  150535
                  LIB3175-042-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q115783
                  561
BLAST score
                  7.0e-58
E value
                  105
Match length
                  100
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
```

(CAB-140) (LHCP) >gi\_16376\_emb\_CAA27543\_ (X03909) chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis thaliana]

Seq. No. 150536

Seq. ID LIB3175-042-P1-K1-F9

Method BLASTX
NCBI GI g2829885
BLAST score 369
E value 2.0e-35
Match length 102
% identity 70

NCBI Description (AC002396) Hypothetical protein [Arabidopsis thaliana]

Seq. No. 150537

Seq. ID LIB3175-042-P1-K1-G10

Method BLASTX
NCBI GI g4567279
BLAST score 498
E value 2.0e-50
Match length 134
% identity 71

NCBI Description (AC006841) putative serine/threonine protein kinase

[Arabidopsis thaliana]

Seq. No. 150538

Seq. ID LIB3175-042-P1-K1-G11

Method BLASTX
NCBI GI g127041
BLAST score 506
E value 2.0e-51
Match length 99
% identity 98

NCBI Description

S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE

ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1)

>gi\_81647\_pir\_\_JN0131 methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana >gi\_166872 (M55077) S-adenosylmethionine synthetase [Arabidopsis thaliana]

Seq. No. 150539

Seq. ID LIB3175-042-P1-K1-G12

Method BLASTX
NCBI GI g130720
BLAST score 277
E value 1.0e-24
Match length 103
% identity 50

NCBI Description PROTEOLIPID PROTEIN PPA1 >gi\_101508\_pir\_\_A34633 probable

H+-transporting ATPase (EC 3.6.1.35) lipid-binding protein - yeast (Saccharomyces cerevisiae) >gi\_172221 (M35294) proteolipid protein of proton ATPase [Saccharomyces

cerevisiae] >gi\_500700 (U10399) Ppalp: Proteolipid protein

of proton ATPase [Saccharomyces cerevisiae]

Seq. No. 150540

Seq. ID LIB3175-042-P1-K1-G2

Method BLASTX

```
NCBI GI
                  g2119846
                  424
BLAST score
                  7.0e-42
E value
                  110
Match length
                  78
% identity
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
NCBI Description
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi_3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  150541
                  LIB3175-042-P1-K1-G3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3540185
BLAST score
                  362
                  2.0e-34
E value
                  133
Match length
                  48
% identity
NCBI Description
                  (AC004122) Highly Similar to branched-chain amino acid
                  aminotransferase [Arabidopsis thaliana]
                  150542
Seq. No.
                  LIB3175-042-P1-K1-G4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1174162
BLAST score
                  476
                  4.0e-48
E value
                  85
Match length
% identity
                  (U44976) ubiquitin-conjugating enzyme [Arabidopsis
NCBI Description
                  thaliana] >gi_3746915 (AF091106) E2
                  ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]
                  150543
Seq. No.
                  LIB3175-042-P1-K1-G5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2564049
                  52
BLAST score
                  1.0e-20
E value
                  76
Match length
                  100
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLE2, complete sequence [Arabidopsis thaliana]
                  150544
Seq. No.
                  LIB3175-042-P1-K1-G7
Seq. ID
Method
                  BLASTN
                  g4760411
NCBI GI
BLAST score
                  42
E value
                  3.0e-14
                  143
Match length
                  71
% identity
                  Arabidopsis thaliana chromosome 1 BAC F25C20 sequence,
NCBI Description
```

complete sequence

```
Seq. No.
                  150545
Seq. ID
                  LIB3175-042-P1-K1-G8
Method
                  BLASTX
                  q2583108
NCBI GI
                   605
BLAST score
E value
                   5.0e-63
                  133
Match length
                   92
% identity
                   (AC002387) putative surface protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150546
                  LIB3175-042-P1-K1-G9
Seq. ID
Method
                  BLASTN
                   g2924728
NCBI GI
BLAST score
                   71
E value
                   1.0e-31
Match length
                   365
                   92
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXH1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150547
                  LIB3175-042-P1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g4263753
                                                 3.5
                   200
BLAST score
E value
                   1.0e-108
Match length
                   357
% identity
                  Arabidopsis thaliana chromosome V map near 60.5 cM,
NCBI Description
                   complete sequence [Arabidopsis thaliana]
Seq. No.
                   150548
                   LIB3175-042-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g462174
BLAST score
                   288
E value
                   6.0e-26
Match length
                  93
% identity
                   67
                  GERANYLGERANYL PYROPHOSPHATE SYNTHETASE PRECURSOR (GGPP
NCBI Description
                   SYNTHETASE) (DIMETHYLALLYLTRANSFERASE /
                   GERANYLTRANSTRANSFERASE / FARNESYLTRANSTRANSFERASE
                   >qi 413730 (L25813) geranylgeranyl pyrophosphate synthase
                   [Arabidopsis thaliana]
                  150549
Seq. No.
                  LIB3175-042-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2342685
BLAST score
                  182
E value
                   7.0e-14
                  72
Match length
                   50
% identity
NCBI Description
                   (AC000106) Contains similarity to Rhodococcus amidase
                   (gb_D16207). ESTs gb_T20504, gb_H36650, gb_N97423, gb_H36595
```

come from this gene. [Arabidopsis thaliana] Seq. No. 150550 Seq. ID LIB3175-042-P1-K1-H12 Method BLASTN NCBI GI g3449327 86 BLAST score 5.0e-41E value 165 Match length 99 % identity NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana] 150551 Seq. No. LIB3175-042-P1-K1-H2 Seq. ID Method BLASTX NCBI GI q2244799 BLAST score 254 8.0e-22 E value 81 Match length 68 % identity (Z97336) carnitine racemase homolog [Arabidopsis thaliana] NCBI Description 150552 Seq. No. LIB3175-042-P1-K1-H3 Seq. ID Method BLASTX NCBI GI g1402912 BLAST score 628 1.0e-65 E value Match length 123 98 % identity (X98317) peroxidase [Arabidopsis thaliana] NCBI Description Seq. No. 150553 LIB3175-042-P1-K1-H4 Seq. ID BLASTN Method NCBI GI g3128136 BLAST score 46 E value 1.0e-16 103 Match length 91 % identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description K1F13, complete sequence [Arabidopsis thaliana] 150554 Seq. No. LIB3175-042-P1-K1-H5 Seq. ID Method BLASTX NCBI GI g2119846 BLAST score 617 2.0e-64 E value

117 Match length % identity 99

chlorophyll a/b-binding protein type I precursor Lhb1B2 -NCBI Description Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460) photosystem II type I chlorophyll a /b binding protein

> [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis

```
thaliana] >gi 3337371 (AC004481) photosystem II type I
                   chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                   150555
                   LIB3175-042-P1-K1-H6
Seq. ID
                   BLASTX
Method
NCBI GI
                   q3043415
BLAST score
                   287
E value
                   4.0e-26
                   54
Match length
% identity
                   100
                   (Y17053) At-hsc70-3 [Arabidopsis thaliana]
NCBI Description
                   150556
Seq. No.
Seq. ID
                   LIB3175-042-P1-K1-H7
                   BLASTN
Method
NCBI GI
                   q547390
                   361
BLAST score
                   0.0e + 00
E value
Match length
                   369
                   99
% identity
                  Arabidopsis thaliana TRAP mRNA, partial cds
NCBI Description
                   150557
Seq. No.
                   LIB3175-042-P1-K1-H8
Seq. ID
Method
                   BLASTN
NCBI GI
                   q2264317
BLAST score
                   192
                   1.0e-104
E value
Match length
                   398
% identity
                   47
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MUG13, complete sequence [Arabidopsis thaliana]
                   150558
Seq. No.
Seq. ID
                   LIB3175-042-P1-K1-H9
Method
                   BLASTX
NCBI GI
                   q3063445
BLAST score
                   147
E value
                   2.0e-09
Match length
                   132
% identity
NCBI Description
                   (AC003981) F22013.7 [Arabidopsis thaliana]
                   150559
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-A10
Method
                   BLASTN
NCBI GI
                   q2815404
BLAST score
                   155
E value
                   1.0e-81
Match length
                   392
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MMG4, complete sequence [Arabidopsis thaliana]
                   150560
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-A12
```

```
Method
                  BLASTX
NCBI GI
                  q3355468
                  492
BLAST score
E value
                  1.0e-49
                  123
Match length
% identity
                   (ACO04218) putative ribosomal protein L35 [Arabidopsis
NCBI Description
                  thaliana]
                  150561
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-A3
Method
                  BLASTX
                  a3063470
NCBI GI
                  328
BLAST score
E value
                  7.0e-33
                  121
Match length
                   63
% identity
                   (AC003981) F22013.32 [Arabidopsis thaliana]
NCBI Description
                  150562
Seq. No.
                  LIB3175-043-P1-K1-A5
Seq. ID
Method
                  BLASTN
                  q547390
NCBI GI
BLAST score
                   258
                   1.0e-143
E value
Match length
                   298
                   97
% identity
                  Arabidopsis thaliana TRAP mRNA, partial cds
NCBI Description
                   150563
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-A6
Method
                   BLASTX
                   q2642159
NCBI GI
                   456
BLAST score
                   9.0e-46
E value
Match length
                   104
% identity
                   (AC003000) putative mannose-1-phosphate guanyltransferase
NCBI Description
                   [Arabidopsis thaliana] >gi_3598958 (AF076484) GDP-mannose
                   pyrophosphorylase [Arabidopsis thaliana] >gi_4151925
                   (AF108660) CYT1 protein [Arabidopsis thaliana]
                   150564
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-A7
Method
                   BLASTX
NCBI GI
                   q4218123
BLAST score
                   325
E value
                   3.0e-30
Match length
                   95
% identity
                   (AL035353) photosystem I subunit PSI-E-like protein
NCBI Description
                   [Arabidopsis thaliana]
                   150565
Seq. No.
                   LIB3175-043-P1-K1-A8
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2275202
```

Seq. No.

150570

```
BLAST score
                   419
E value
                   3.0e-41
Match length
                   78
                   100
% identity
NCBI Description
                   (AC002337) acyl-CoA synthetase isolog [Arabidopsis
                   thaliana]
                   150566
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-A9
Method
                   BLASTN
NCBI GI
                   g4049332
BLAST score
                   170
E value
                   6.0e-91
Match length
                   185
                   98
% identity
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
                   (ESSAII project)
Seq. No.
                   150567
Seq. ID
                   LIB3175-043-P1-K1-B1
Method
                   BLASTN
NCBI GI
                   g2760167
BLAST score
                   65
E value
                   2.0e-28
Match length
                   101
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MCO15, complete sequence [Arabidopsis thaliana]
                   150568
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-B10
Method
                   BLASTN
NCBI GI
                   g2264305
BLAST score
                   278
E value
                   1.0e-155
Match length
                   320
% identity
NCBI Description
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                   MBK23, complete sequence [Arabidopsis thaliana]
                   150569
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-B11
Method
                   BLASTX
NCBI GI
                   q2119846
BLAST score
                   576
                   8.0e-60
E value
Match length
                   110
% identity
NCBI Description
                   chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                   Arabidopsis thaliana >gi_16364_emb_CAA45790_ (X64460)
                   photosystem II type I chlorophyll a /b binding protein
                   [Arabidopsis thaliana] >gi_3128230 (AC004077) photosystem
                   II type I chlorophyll a/b binding protein [Arabidopsis
                   thaliana] >gi_3337371 (AC004481) photosystem II type I
```

19204

chlorophyll a/b binding protein [Arabidopsis thaliana]

```
Seq. ID
                  LIB3175-043-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  q3157934
BLAST score
                  321
                  1.0e-29
E value
Match length
                  63
                  98
% identity
NCBI Description
                  (AC002131) Similar to hypothetical protein F09E5.8
                  gb U37429 from C. elegans. ESTs gb_T42019 and gb_N97000
                  come from this gene. [Arabidopsis thaliana]
Seq. No.
                  LIB3175-043-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q730864
BLAST score
                  165
E value
                  2.0e-11
Match length
                  139
                  32
% identity
NCBI Description
                  SPORULATION PROTEIN SPS19 (SPORULATION-SPECIFIC PROTEIN
                  SPX19) >gi_2117442_pir__S50729 sporulation protein SPS19 -
                  yeast (Saccharomyces cerevisiae) >gi 600063 emb CAA55506_
                   (X78898) N1362 [Saccharomyces cerevisiae]
                  >gi 1302205 emb_CAA96103_ (Z71479) ORF YNL202w
                   [Saccharomyces cerevisiae]
                  150572
Seq. No.
                  LIB3175-043-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q481132
BLAST score
                  369
                  2.0e-35
E value
Match length
                  87
% identity
                  sucrose transport protein SUC1 - Arabidopsis thaliana
NCBI Description
                   >gi_407094_emb_CAA53147_ (X75365) sucrose-proton symporter
                   [Arabidopsis thaliana]
                  150573
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-B4
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  333
E value
                   0.0e+00
Match length
                  390
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  150574
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q481914
BLAST score
                  264
E value
                   3.0e-55
Match length
                  127
                  85
% identity
```

% identity

NCBI Description

```
NCBI Description
                  glutamate--ammonia ligase (EC 6.3.1.2) - rape
                  >gi_436422_emb_CAA54151.1_ (X76736) glutamine [Brassica
                  napus]
Seq. No.
                  150575
                  LIB3175-043-P1-K1-B7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3367516
BLAST score
                   586
                  7.0e-61
E value
Match length
                  118
% identity
                   (AC004392) Similar to beta-glucosidase BGQ60 precursor
NCBI Description
                  gb L41869 from Hordeum vulgare. [Arabidopsis thaliana]
Seq. No.
                  150576
                  LIB3175-043-P1-K1-B8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3702731
BLAST score
                  282
E value
                  1.0e-157
Match length
                  332
                   95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFC19, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150577
                  LIB3175-043-P1-K1-C1
Seq. ID
Method
                  BLASTX
                  g3913418
NCBI GI
BLAST score
                   796
E value
                   2.0e-85
Match length
                  154
                   97
% identity
                  S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC)
NCBI Description
                   (SAMDC) >gi_1531763_emb_CAA69073_ (Y07765)
                  S-adenosylmethionine decarboxylase [Arabidopsis thaliana]
Seq. No.
                  150578
Seq. ID
                  LIB3175-043-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q1916613
BLAST score
                  294
                  1.0e-26
E value
Match length
                  126
% identity
NCBI Description
                 (U62029) acetyl-CoA carboxylase [Arabidopsis thaliana]
Seq. No.
                  150579
                  LIB3175-043-P1-K1-C11
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3080430
BLAST score
                  221
                  1.0e-121
E value
Match length
                  404
```

Arabidopsis thaliana DNA chromosome 4, BAC clone T19P19

## (ESSAII project)

150580 Seq. No. Seq. ID LIB3175-043-P1-K1-C12 Method BLASTX NCBI GI a2119846 BLAST score 657 4.0e-69 E value Match length 138 % identity

150581

NCBI Description chlorophyll a/b-binding protein type I precursor Lhb1B2 -Arabidopsis thaliana >gi\_16364\_emb\_CAA45790\_ (X64460) photosystem II type I chlorophyll a /b binding protein [Arabidopsis thaliana] >gi\_3128230 (AC004077) photosystem II type I chlorophyll a/b binding protein [Arabidopsis

thaliana] >gi\_3337371 (AC004481) photosystem II type I chlorophyll a/b binding protein [Arabidopsis thaliana]

Seq. No. Seq. ID LIB3175-043-P1-K1-C3 Method BLASTN NCBI GI q4757395 BLAST score 35 E value 4.0e-10 95 Match length

% identity Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: NCBI Description

K21L13, complete sequence

150582 Seq. No.

Seq. ID LIB3175-043-P1-K1-C5

Method BLASTX NCBI GI g1175013 BLAST score 467 6.0e-47 E value

Match length 111 % identity 83

PLASMA MEMBRANE INTRINSIC PROTEIN 2A >gi\_629542\_pir\_\_S44084 NCBI Description

plasma membrane intrinsic protein 2a - Arabidopsis thaliana >gi\_472877\_emb\_CAA53477\_ (X75883) plasma membrane intrinsic

protein 2a [Arabidopsis thaliana]

150583 Seq. No.

Seq. ID LIB3175-043-P1-K1-C6

Method BLASTX NCBI GI q4467097 BLAST score 486 E value 3.0e-49 Match length 118 % identity

(AL035538) heat shock protein 70 like protein [Arabidopsis NCBI Description

thaliana]

150584 Seq. No.

Seq. ID LIB3175-043-P1-K1-C7

Method BLASTN NCBI GI q2264305

```
BLAST score
                   325
E value
                   0.0e + 00
Match length
                   325
% identity
                   100
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MBK23, complete sequence [Arabidopsis thaliana]
                   150585
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-C8
Method
                   BLASTN
NCBI GI
                   q4678196
BLAST score
                   362
E value
                   0.0e + 00
Match length
                   494
% identity
                   93
                   Arabidopsis thaliana chromosome II BAC F7H1 genomic
NCBI Description
                   sequence, complete sequence
                   150586
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   q3935181
BLAST score
                   808
E value
                   9.0e-87
Match length
                   153
% identity
NCBI Description
                   (AC004557) F17L21.24 [Arabidopsis thaliana]
Seq. No.
                   150587
Seq. ID
                   LIB3175-043-P1-K1-D1
Method
                   BLASTN
NCBI GI
                   g2696018
BLAST score
                   62
E value
                   2.0e-26
Match length
                   235
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150588
Seq. ID
                   LIB3175-043-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   g950022
BLAST score
                   48
E value
                   6.0e-18
Match length
                   237
% identity
                   88
NCBI Description
                  A.thaliana psbW gene
Seq. No.
                   150589
                   LIB3175-043-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3298443
BLAST score
                   327
E value
                   2.0e-30
Match length
                   84
% identity
                   71
```

Method

NCBI GI

BLASTX

g1402906

```
(AB010880) chloroplast ribosomal protein L17 [Nicotiana
NCBI Description
                   tabacuml
Seq. No.
                   150590
                   LIB3175-043-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   q115783
                   341
BLAST score
E value
                   3.0e-32
                   91
Match length
                   78
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   150591
Seq. No.
                   LIB3175-043-P1-K1-D2
Seq. ID
Method
                   BLASTN
NCBI GI
                   g1402905
BLAST score
                   52
E value
                   5.0e-21
Match length
                   52
                   100
% identity
NCBI Description A.thaliana mRNA for peroxidase, prxr2
Seq. No.
                   150592
                   LIB3175-043-P1-K1-D3
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1709535
BLAST score
                   717
                   5.0e-76
E value
Match length
                   161
% identity
                   DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE B (P5CS B)
NCBI Description
                   [CONTAINS: GLUTAMATE 5-KINASE (GAMMA-GLUTAMYL KINASE) (GK);
                   GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR)
                   (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE)
                   (GLUTAMYL-GAMMA-SEMIALDE... >gi_887388_emb_CAA60447_
                   (X86778) pyrroline-5-carboxylate synthetase B [Arabidopsis
                  thaliana] >gi_1669658_emb_CAA70527 (Y09355)
pyrroline-5-carboxlyate synthetase [Arabidopsis thaliana]
Seq. No.
                   150593
Seq. ID
                   LIB3175-043-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q4678308
BLAST score
                   583
E value
                   1.0e-60
Match length
                   113
% identity
NCBI Description
                   (AL049655) putative protein [Arabidopsis thaliana]
                   150594
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-D7
```

Method

BLASTX

```
BLAST score
E value
                    4.0e-77
Match length
                    159
% identity
                    90
NCBI Description
                    (X98314) peroxidase [Arabidopsis thaliana]
                    >gi_4468977_emb_CAB38291_ (AL035605) peroxidase, prxr2
                    [Arabidopsis thaliana]
Seq. No.
                    150595
Seq. ID
                    LIB3175-043-P1-K1-D8
Method
                    BLASTX
NCBI GI
                    g4567311
BLAST score
                    531
E value
                    3.0e - 54
Match length
                    97
                    97
% identity
NCBI Description
                    (AC005956) putative protein kinase [Arabidopsis thaliana]
                    150596
Seq. No.
Seq. ID
                    LIB3175-043-P1-K1-D9
Method
                    BLASTN
NCBI GI
                    q2245031
BLAST score
                    430
E value
                    0.0e + 00
Match length
                    451
% identity
                    98
NCBI Description
                    Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                    fragment No
                    150597
Seq. No.
Seq. ID
                    LIB3175-043-P1-K1-E1
Method
                    BLASTX
NCBI GI
                    g3540183
BLAST score
                    545
E value
                    7.0e-56
Match length
                    104
% identity
                    100
NCBI Description
                    (AC004122) Highly Similar to branched-chain amino acid
                    aminotransferase [Arabidopsis thaliana]
Seq. No.
                    150598
                    LIB3175-043-P1-K1-E10
Seq. ID
Method
                    BLASTX
NCBI GI
                    g4056469
BLAST score
                    298
E value
                    3.0e-27
Match length
                    68
% identity
                    (AC005990) Strong similarity to gb_M95166 ADP-ribosylation factor from Arabidopsis thaliana. ESTs gb_Z25826, gb_R90191, gb_N65697, gb_AA713150, gb_T46332, gb_AA040967,
NCBI Description
                    gb_AA712956, gb_T46403, gb_T46050, gb_AI100391 and
                    gb Z25043 come from t
Seq. No.
                    150599
Seq. ID
                    LIB3175-043-P1-K1-E11
```

```
NCBI GI
                  g3287691
BLAST score
                  350
E value
                  2.0e-33
Match length
                  105
% identity
                  67
NCBI Description
                   (AC003979) Contains similarity to RING zinc finger protein
                  gb X95455 from Gallus gallus. [Arabidopsis thaliana]
                  150600
Seq. No.
                  LIB3175-043-P1-K1-E12
Seq. ID
Method
                  BLASTN
                  g3449313
NCBI GI
BLAST score
                  38
E value
                  1.0e-12
Match length
                  54
% identity
                  93
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21P3, complete sequence [Arabidopsis thaliana]
                  150601
Seq. No.
                  LIB3175-043-P1-K1-E3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1504020
BLAST score
                  308
E value
                  4.0e-28
Match length
                  147
% identity
                  28
                  (D86973) similar to Yeast translation activator GCN1
NCBI Description
                  (P1:A48126) [Homo sapiens]
                  150602
Seq. No.
                  LIB3175-043-P1-K1-E4
Seq. ID
Method
                  BLASTX
                  g113782
NCBI GI
BLAST score
                  802
E value
                  4.0e-86
Match length
                  147
% identity
NCBI Description
                  BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE)
                  >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2)
                  Arabidopsis thaliana >gi_166602 (M73467) beta-amylase
                  [Arabidopsis thaliana] >gi 228699 prf 1808329A beta
                  amylase [Arabidopsis thaliana]
Seq. No.
                  150603
                  LIB3175-043-P1-K1-E5
Seq. ID
Method
                  BLASTX
                  g3600058
NCBI GI
BLAST score
                  570
E value
                  7.0e-59
Match length
                  118
% identity
NCBI Description
                  (AF080120) similar to vacuolar ATPases [Arabidopsis
                  thaliana]
                  150604
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-E6
```

```
Method
                   BLASTN
NCBI GI
                   g2459406
BLAST score
                   139
                   3.0e-72
E value
                   373
Match length
                   99
% identity
                   Arabidopsis thaliana chromosome II BAC F4P9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150605
                   LIB3175-043-P1-K1-E7
Seq. ID
                   BLASTX
Method
NCBI GI
                   q1351272
                   192
BLAST score
                   3.0e-15
E value
                   36
Match length
                   100
% identity
                   TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550
NCBI Description
                   (U02949) cytosolic triose phosphate isomerase [Arabidopsis thaliana] >gi_742408_prf__2009415A triose phosphate
                   isomerase [Arabidopsis thaliana]
Seq. No.
                   150606
                   LIB3175-043-P1-K1-E9
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4733953
BLAST score
                   332
E value
                   0.0e + 00
Match length
                   332
% identity
                   100
                   Arabidopsis thaliana chromosome I BAC F13011 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   150607
Seq. ID
                   LIB3175-043-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   q1702986
BLAST score
                   451
E value
                   5.0e-45
Match length
                   111
% identity
                   86
                   14-3-3-LIKE PROTEIN GF14 CHI >gi 1255987 (U09377) GF14chi
NCBI Description
                   isoform [Arabidopsis thaliana] >gi 1256534 (L09112) GF14
                   chi chain [Arabidopsis thaliana]
Seq. No.
                   150608
Seq. ID
                   LIB3175-043-P1-K1-F11
Method
                   BLASTN
NCBI GI
                   q469109
BLAST score
                   35
E value
                   9.0e-11
Match length
                   63
% identity
                   89
NCBI Description
                   A.thaliana (Columbia) Di19 mRNA
                   150609
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-F12
```

Seq. No.

```
Method
                    BLASTX
NCBI GI
                    q119975
BLAST score
                    172
E value
                    1.0e-17
Match length
                    83
                    70
% identity
NCBI Description
                    FERREDOXIN PRECURSOR >gi 99692 pir S09979 ferredoxin
                    [2Fe-2S] precursor - Arabidopsis thaliana
                    >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                    [Arabidopsis thaliana]
Seq. No.
                    150610
Seq. ID
                    LIB3175-043-P1-K1-F2
Method
                    BLASTX
NCBI GI
                    q121907
BLAST score
                    413
E value
                    2.0e-40
Match length
                    145
% identity
                    HISTONE H1.2 >gi_70682_pir__HSMU12 histone H1.2 -
NCBI Description
                    Arabidopsis thaliana >gi_1\overline{163}20 emb_CAA44316_ (X62459)
Histone H1-2 [Arabidopsis thaliana] >gi_1946357 (U93215)
                    histone H1-2C [Arabidopsis thaliana]
Seq. No.
                    150611
Seq. ID
                    LIB3175-043-P1-K1-F3
Method
                    BLASTX
NCBI GI
                    g2832625
BLAST score
                    558
E value
                    2.0e-57
Match length
                    157
                    69
% identity
NCBI Description
                    (AL021711) putative protein [Arabidopsis thaliana]
Seq. No.
                    150612
Seq. ID
                    LIB3175-043-P1-K1-F4
Method
                    BLASTX
NCBI GI
                    g2832625
BLAST score
                    90
E value
                    5.0e-14
Match length
                    105
% identity
                    47
NCBI Description
                    (AL021711) putative protein [Arabidopsis thaliana]
                    150613
Seq. No.
Seq. ID
                    LIB3175-043-P1-K1-F5
Method
                    BLASTN
NCBI GI
                    g3980374
BLAST score
                    142
E value
                    5.0e-74
Match length
                    279
% identity
                    94
                    Arabidopsis thaliana chromosome II BAC F16P2 genomic
NCBI Description
                    sequence, complete sequence [Arabidopsis thaliana]
```

```
LIB3175-043-P1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3510343
BLAST score
                  336
                  0.0e + 00
E value
                  351
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MJC20, complete sequence [Arabidopsis thaliana]
                  150615
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g121907
                  349
BLAST score
                  1.0e-33
E value
                  136
Match length
                  64
% identity
                  HISTONE H1.2 >gi 70682 pir HSMU12 histone H1.2 -
NCBI Description
                  Arabidopsis thaliana >gi 16320 emb CAA44316 (X62459)
                  Histone H1-2 [Arabidopsis thaliana] >gi 1946357 (U93215)
                  histone H1-2C [Arabidopsis thaliana]
                  150616
Seq. No.
                  LIB3175-043-P1-K1-F8
Seq. ID
                  BLASTX
Method
NCBI GI
                  g4581114
                                                                             ...
                  577
BLAST score
E value
                  1.0e-59
Match length
                  118
% identity
                  96
NCBI Description
                  (AC005825) putative HesB-like protein; required for
                  efficient nitrogen fixation in Cyanobacteria [Arabidopsis
                  thaliana]
                  150617
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-F9
                  BLASTX
Method
NCBI GI
                  q4154281
                  300
BLAST score
                  2.0e-27
E value
                  78
Match length
% identity
                  (AF082347) C13 endopeptidase NP1 precursor [Zea mays]
NCBI Description
Seq. No.
                  150618
Seq. ID
                  LIB3175-043-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q4006827
BLAST score
                  409
E value
                  6.0e-40
Match length
                  159
% identity
                  50
                  (AC005970) subtilisin-like protease [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150619
                  LIB3175-043-P1-K1-G10
Seq. ID
```

Seq. No.

```
Method
                   BLASTX
NCBI GI
                   g629692
BLAST score
                   418
                   3.0e-41
E value
                   93
Match length
                   84
% identity
NCBI Description
                   hypothetical protein - common tobacco
                   >gi 506471_emb_CAA56189_ (X79794) unnamed protein product
                   [Nicotiana tabacum]
                   150620
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-G11
Method
                   BLASTX
NCBI GI
                   q3860247
BLAST score
                   468
E value
                   7.0e-47
Match length
                   109
% identity
                   84
                   (AC005824) unknown protein [Arabidopsis thaliana]
NCBI Description
                   150621
Seq. No.
Seq. ID
                   LIB3175-043-P1-K1-G12
Method
                   BLASTX
NCBI GI
                   g119975
BLAST score
                   514
E value
                   2.0e-52
Match length
                   120
% identity
                   88
NCBI Description
                   FERREDOXIN PRECURSOR >gi_99692_pir__S09979 ferredoxin
                   [2Fe-2S] precursor - Arabidopsis thaliana
                   >gi_16437_emb_CAA35754_ (X51370) ferredoxin precursor
[Arabidopsis thaliana] >gi_166698 (M35868) ferrodoxin A
                   [Arabidopsis thaliana]
Seq. No.
                   150622
                   LIB3175-043-P1-K1-G2
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4756967
BLAST score
                   149
E value
                   3.0e-78
                   209
Match length
                   95
% identity
                   Arabidopsis thaliana partial mRNA for hypothetical protein,
NCBI Description
                   clone g19
Seq. No.
                   150623
                   LIB3175-043-P1-K1-G4
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4733953
BLAST score
                   332
E value
                   0.0e+00
                   402
Match length
                   96
% identity
NCBI Description
                   Arabidopsis thaliana chromosome I BAC F13011 genomic
                   sequence, complete sequence
```

```
Seq. ID
                  LIB3175-043-P1-K1-G6
                  BLASTX
Method
NCBI GI
                  g3738339
BLAST score
                  337
                  1.0e-31
E value
                  125
Match length
                  63
% identity
                  (AC005170) putative kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150625
                  LIB3175-043-P1-K1-G7
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4337206
BLAST score
                  303
E value
                  1.0e-27
Match length
                  131
% identity
                   44
                   (AC006403) putative replication factor-A protein
NCBI Description
                   [Arabidopsis thaliana]
                  150626
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  428
E value
                  0.0e + 00
Match length
                  481
                  99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                  fragment No
                  150627
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  q2435519
BLAST score
                  512
                   4.0e-52
E value
Match length
                  123
% identity
                  83
                   (AF024504) similar to mouse MEM3 (GB:U47024 and S.
NCBI Description
                   cerevisiae vacuolar sorting protein 35 (SW; P34110)
                   [Arabidopsis thaliana]
                  150628
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g2062167
BLAST score
                  261
E value
                  1.0e-25
                  59
Match length
% identity
                  (ACO01645) Proline-rich protein APG isolog [Arabidopsis
NCBI Description
                  thaliana]
                  150629
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-H2
Method
                  BLASTX
```

```
NCBI GI
                  q2275196
BLAST score
                  329
E value
                  5.0e-31
Match length
                  69
                  96
% identity
                   (AC002337) water stress-induced protein, WSI76 isolog
NCBI Description
                   [Arabidopsis thaliana] >gi_4630746_gb_AAD26596.1 AC007236 1
                   (AC007236) water stress-induced protein [Arabidopsis
                  thaliana]
                  150630
Seq. No.
Seq. ID
                  LIB3175-043-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  q4584841
BLAST score
                  280
E value
                  1.0e-156
Match length
                  328
% identity
                  96
                  Genomic sequence for Arabidopsis thaliana BAC T23E23,
NCBI Description
                  complete sequence
Seq. No.
                  150631
                  LIB3175-043-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076348
BLAST score
                  551
E value
                  8.0e-57
Match length
                  109
                  98
% identity
NCBI Description
                  myosin MYA1, class V - Arabidopsis thaliana
                  >gi 433663 emb CAA82234 (Z28389) myosin [Arabidopsis
                  thaliana]
Seq. No.
                  150632
Seq. ID
                  LIB3175-043-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q132074
BLAST score
                  618
E value
                  1.0e-64
Match length
                  117
                  96
% identity
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A PRECURSOR
NCBI Description
                  (RUBISCO SMALL SUBUNIT 1A) >gi 68063 pir RKMUA1
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  Al precursor - Arabidopsis thaliana
Seq. No.
                  150633
Seq. ID
                  LIB3175-044-P1-K1-A1
                  BLASTX
Method
NCBI GI
                  q2654122
BLAST score
                  202
                  5.0e-16
E value
Match length
                  59
% identity
                  (AF034694) ribosomal protein L23a [Arabidopsis thaliana]
NCBI Description
```

Seq. No.

```
Seq. ID
                  LIB3175-044-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  g2494299
BLAST score
                  341
E value
                  6.0e-32
Match length
                  145
% identity
                  52
                  EUKARYOTIC TRANSLATION INITIATION FACTOR 2 BETA SUBUNIT
NCBI Description
                  (EIF-2-BETA) >gi 1732361 (U80269) translation initiation
                  factor 2 beta [Malus domestica]
Seq. No.
                  150635
Seq. ID
                  LIB3175-044-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1706186
BLAST score
                  224
E value
                  3.0e-18
Match length
                  138
% identity
                  37
                  HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1)
NCBI Description
                  (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC
                  RETROVIRAL LEUKEMIA RECEPTOR) (ERR) (ECOTROPIC RETROVIRUS
                  RECEPTOR) >gi 110721 pir A32742 murine ecotropic
                  retrovirus receptor protein - mouse >gi 532612 (M26687)
                  ecotropic retrovirus receptor [Mus musculus]
Seq. No.
                  150636
Seq. ID
                  LIB3175-044-P1-K1-A12
Method
                  BLASTX
NCBI GI
                  g99699
BLAST score
                  373
E value
                  7.0e-36
Match length
                  101
% identity
                  68
                  glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone
NCBI Description
                  lambdaAtgsr1) - Arabidopsis thaliana
                  150637
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g3721926
BLAST score
                  410
E value
                  1.0e-40
Match length
                  125
% identity
NCBI Description (AB017480) chloroplast FtsH protease [Nicotiana tabacum]
                  150638
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g629557
BLAST score
                  554
E value
                  6.0e-57
Match length
                  144
% identity
                  50
NCBI Description
                  RNA-binding protein rnpD - Arabidopsis thaliana (fragment)
                  >gi 510240_emb_CAA43420_ (X61108) RNA binding protein
```

% identity

NCBI Description

```
[Arabidopsis thaliana]
Seq. No.
                    150639
Seq. ID
                   LIB3175-044-P1-K1-A5
Method
                   BLASTX
NCBI GI
                    q899608
BLAST score
                    728
E value
                    2.0e-77
Match length
                   146
% identity
                    22
                   (U29158) polyubiquitin [Zea mays]
NCBI Description
                    150640
Seq. No.
Seq. ID
                   LIB3175-044-P1-K1-A6
Method
                   BLASTX
NCBI GI
                    g2317906
BLAST score
                   867
E value
                    1.0e-93
Match length
                   169
% identity
                    99
                   (U89959) ARA-5 [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    150641
                    LIB3175-044-P1-K1-A7
Seq. ID
Method
                    BLASTX
NCBI GI
                    g3046700
BLAST score
                    367
E value
                    2.0e-35
                    78
Match length
% identity
NCBI Description
                    (AJ005261) cytidine deaminase [Arabidopsis thaliana]
                   >gi_3093276_emb_CAA06671_ (AJ005687) cytidine deaminase
[Arabidopsis thaliana] >gi_4191787 (AC005917) putative
                    cytidine deaminase [Arabidopsis thaliana]
Seq. No.
                    150642
Seq. ID
                   LIB3175-044-P1-K1-B10
Method
                   BLASTN
NCBI GI
                    g4206762
BLAST score
                    239
E value
                    1.0e-132
Match length
                    409
                    54
% identity
NCBI Description
                   Arabidopsis thaliana cell wall-plasma membrane linker
                   protein homolog (CWLP) mRNA, complete cds
Seq. No.
                   150643
Seq. ID
                   LIB3175-044-P1-K1-B12
Method
                   BLASTX
NCBI GI
                   q4262156
BLAST score
                    466
E value
                   1.0e-46
Match length
                   121
```

[Arabidopsis thaliana]

(AC005275) putative component of cytochrome B6-F complex

```
Seq. No.
                  150644
Seq. ID
                  LIB3175-044-P1-K1-B2
Method
                  BLASTX
                  g2129650
NCBI GI
                  520
BLAST score
                  5.0e-53
E value
                  109
Match length
% identity
                  myb-related transcription factor 24,7K - Arabidopsis
NCBI Description
                  thaliana >gi 1197190 emb CAA92280 (Z68157) myb-related
                  transcription factor [Arabidopsis thaliana]
                  150645
Seq. No.
                  LIB3175-044-P1-K1-B3
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1169476
BLAST score
                  858
E value
                  2.0e-92
                  170
Match length
                  98
% identity
                  ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) (VITRONECTIN-LIKE
NCBI Description
                  ADHESION PROTEIN 1) (PVN1) >gi 439577 (U04632)
                  vitronectin-like adhesion protein [Nicotiana tabacum]
                  150646
Seq. No.
                  LIB3175-044-P1-K1-B4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1170203
                  556
BLAST score
                  3.0e-57
E value
                  142
Match length
                  79
% identity
                  GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi 454359
NCBI Description
                  (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]
                  150647
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-B5
                  BLASTX
Method
NCBI GI
                  g1931644
BLAST score
                  269
E value
                  1.0e-23
Match length
                  123
                  45
% identity
NCBI Description
                  (U95973) membrane protein PTM1 precursor isolog
                  [Arabidopsis thaliana]
                  150648
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g3367567
BLAST score
                  258
E value
                  1.0e-143
                  500
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20
                  (ESSAII project)
```

```
150649
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g3892712
                  340
BLAST score
                  8.0e-32
E value
Match length
                  66
                  100
% identity
                   (AL033545) adenine phosphoribosyltransferase (EC
NCBI Description
                  2.4.2.7) -like protein [Arabidopsis thaliana]
                  150650
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-C1
                  BLASTN
Method
                  g2947056
NCBI GI
BLAST score
                  239
E value
                   1.0e-132
Match length
                  299
                  95
% identity
                  Arabidopsis thaliana chromosome II BAC T20F6 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150651
Seq. ID
                  LIB3175-044-P1-K1-C10
Method
                  BLASTX
NCBI GI
                  q2765081
                  705
BLAST score
                  1.0e-74
E value
Match length
                  153
% identity
                  91
NCBI Description
                  (Y10557) g5bf [Arabidopsis thaliana]
Seq. No.
                  150652
Seq. ID
                  LIB3175-044-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g1532135
BLAST score
                  300
                  3.0e-27
E value
                  74
Match length
% identity
                  76
                   (U49442) chloroplast mRNA-binding protein CSP41 precursor
NCBI Description
                   [Spinacia oleracea]
                  150653
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-C12
Method
                  BLASTX
NCBI GI
                  g4741960
BLAST score
                  620
E value
                  1.0e-64
                  137
Match length
% identity
                  86
NCBI Description
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
                  150654
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g4581146
```

```
BLAST score
                   4.0e-81
E value
Match length
                   153
                   99
% identity
                   (ACO06919) putative fructose-bisphosphate aldolase,
NCBI Description
                  cytoplasmic [Arabidopsis thaliana]
Seq. No.
                  150655
                  LIB3175-044-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g404668
BLAST score
                  142
E value
                   7.0e-09
Match length
                  88
% identity
                   42
                  (L22568) cor78 [Arabidopsis thaliana]
NCBI Description
                  150656
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-C5
Method
                  BLASTN
NCBI GI
                  g3201608
BLAST score
                  61
E value
                   2.0e-25
Match length
                  89
                   92
% identity
                  Arabidopsis thaliana chromosome II BAC F7F1 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  150657
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g4512656
                  35
BLAST score
E value
                   1.0e-10
Match length
                  83
                   86
% identity
                  Arabidopsis thaliana chromosome II BAC F7D19 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  150658
Seq. ID
                  LIB3175-044-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g4406767
BLAST score
                  393
E value
                  2.0e-38
Match length
                  75
% identity
                  (AC006836) putative flavonol sulfotransferase [Arabidopsis
NCBI Description
                  thaliana]
                  150659
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-C8
Method
                  BLASTN
NCBI GI
                  g3695400
BLAST score
                  94
E value
                  2.0e-45
Match length
                  302
```

Seq. No.

150665

```
% identity
NCBI Description Arabidopsis thaliana BAC T9A4
                   150660
                   LIB3175-044-P1-K1-C9
Seq. ID
                   BLASTX
Method
NCBI GI
                   g4586265
BLAST score
                   310
E value
                   2.0e-28
Match length
                   145
                   45
% identity
                   (AL049640) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150661
                   LIB3175-044-P1-K1-D1
Seq. ID
                   BLASTX
Method
NCBI GI
                   g1652297
BLAST score
                   210
E value
                   2.0e-16
                   131
Match length
                   37
% identity
NCBI Description
                   (D90904) hypothetical protein [Synechocystis sp.]
Seq. No.
                   150662
Seq. ID
                   LIB3175-044-P1-K1-D10
                   BLASTN
Method
NCBI GI
                   g2244747
BLAST score
                   134
E value
                   2.0e-69
Match length
                   142
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                   150663
Seq. ID
                   LIB3175-044-P1-K1-D11
Method
                   BLASTN
NCBI GI
                   g3341671
BLAST score
                   142
                   6.0e-74
E value
Match length
                   415
                   97
% identity
                  Arabidopsis thaliana chromosome II BAC F16B22 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150664
Seq. ID
                  LIB3175-044-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g3096931
BLAST score
                   360
E value
                   3.0e - 34
Match length
                   112
% identity
                   58
                   (AL023094) putative ribosomal protein S16 [Arabidopsis
NCBI Description
                   thaliana]
```

19223

```
Seq. ID
                  LIB3175-044-P1-K1-D4
Method
                  BLASTX
NCBI GI
                  q3122673
BLAST score
                  407
E value
                  6.0e-40
                  96
Match length
                  83
% identity
                  60S RIBOSOMAL PROTEIN L15 >gi_2245027_emb_CAB10447_
NCBI Description
                  (Z97341) ribosomal protein [Arabidopsis thaliana]
                  150666
Seq. No.
                  LIB3175-044-P1-K1-D6
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2244896
BLAST score
                  47
                  6.0e-70
E value
Match length
                  138
% identity
                  94
NCBI Description
                  (Z97338) similar to HSR201 protein N.tabacum [Arabidopsis
                  thaliana]
Seq. No.
                  150667
Seq. ID
                  LIB3175-044-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q1532167
BLAST score
                  181
E value
                  3.0e-13
Match length
                  64
% identity
NCBI Description
                  (U63815) localized according to blastn similarity to EST
                  sequences; therefore, the coding span corresponds only to
                  an area of similarity since the initation codon and stop
                  codon could not be precisely determined [Arabidopsis
                  thaliana]
Seq. No.
                  150668
Seq. ID
                  LIB3175-044-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  q4503169
BLAST score
                  214
E value
                  5.0e-17
                  93
Match length
% identity
                  42
                  cut (Drosophila)-like 1 (CCAAT displacement protein)
NCBI Description
                  >gi 457517 (L12579) alternatively spliced [Homo sapiens]
Seq. No.
                  150669
Seq. ID
                  LIB3175-044-P1-K1-E10
Method
                  BLASTN
NCBI GI
                  g4415928
BLAST score
                  97
E value
                  3.0e-47
                  331
Match length
% identity
                  Arabidopsis thaliana chromosome II BAC F13A10 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
                   150670
Seq. ID
                   LIB3175-044-P1-K1-E12
Method
                   BLASTN
NCBI GI
                   g2245073
BLAST score
                   342
E value
                   0.0e + 00
Match length
                   406
% identity
                   99
NCBI Description
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   150671
Seq. No.
                   LIB3175-044-P1-K1-E2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2865394
BLAST score
                   180
E value
                   4.0e-13
Match length
                   50
% identity
                   60
                   (AF036949) basic leucine zipper protein [Zea mays]
NCBI Description
Seq. No.
                   150672
                   LIB3175-044-P1-K1-E3
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3399678
BLAST score
                   152
E value
                   3.0e - 80
Match length
                   212
% identity
                   94
NCBI Description
                   Arabidopsis thaliana chromosome 1 BAC F13M7 sequence,
                   complete sequence [Arabidopsis thaliana]
                   150673
Seq. No.
                   LIB3175-044-P1-K1-E4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q1353352
                   233
BLAST score
                   1.0e-19
E value
Match length
                   61
                   77
% identity
NCBI Description
                   (U31975) alanine aminotransferase [Chlamydomonas
                   reinhardtii]
Seq. No.
                   150674
Seq. ID
                   LIB3175-044-P1-K1-E5
Method
                   BLASTX
NCBI GI
                   g3600058
BLAST score
                   529
E value
                   4.0e-54
Match length
                   117
                   94
% identity
                   (AF080120) similar to vacuolar ATPases [Arabidopsis
NCBI Description
                   thaliana]
                   150675
Seq. No.
Seq. ID
                   LIB3175-044-P1-K1-E6
Method
                   BLASTX
```

19225

```
NCBI GI
                   q4115337
BLAST score
                   815
E value
                   2.0e-87
Match length
                   165
% identity
                   18
NCBI Description
                   (L81141) ubiquitin [Pisum sativum]
                  150676
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-E8
Method
                  BLASTN
NCBI GI
                   g4581138
                   393
BLAST score
                   0.0e + 00
E value
Match length
                   401
                   100
% identity
                  Arabidopsis thaliana chromosome II BAC F1011 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   150677
                  LIB3175-044-P1-K1-F1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3335356
                   79
BLAST score
E value
                   6.0e-37
Match length
                   123
% identity
                   92
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150678
                   LIB3175-044-P1-K1-F10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3135611
BLAST score
                   727
E value
                   3.0e-77
Match length
                   150
% identity
                   93
                   (AF062485) cellulose synthase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150679
Seq. ID
                   LIB3175-044-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   g2501578
BLAST score
                   740
E value
                   1.0e-78
Match length
                   164
% identity
                   87
                  ETHYLENE-INDUCIBLE PROTEIN HEVER >gi 2129913 pir $60047
NCBI Description
                   ethylene-responsive protein 1 - Para rubber tree
                   >qi 1209317 (M88254) ethylene-inducible protein [Hevea
                  brasiliensis]
                   150680
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g4406783
BLAST score
                   591
```

```
E value
                   2.0e-61
Match length
                   114
% identity
                   100
                   (AC006532) putative glutamate decarboxylase [Arabidopsis
NCBI Description
                   thaliana]
                   150681
Seq. No.
Seq. ID
                   LIB3175-044-P1-K1-F3
Method
                  BLASTX
NCBI GI
                   g4006941
                   596
BLAST score
                   6.0e-62
E value
Match length
                   127
% identity
                   91
                   (AJ131391) voltage-dependent anion-selective channel
NCBI Description
                  protein [Arabidopsis thaliana]
                   150682
Seq. No.
Seq. ID
                   LIB3175-044-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   q3451071
BLAST score
                   377
E value
                   1.0e-36
Match length
                   89
% identity
NCBI Description
                   (ALO31326) beta adaptin - like protein [Arabidopsis...
                  thaliana]
Seq. No.
                   150683
Seq. ID
                   LIB3175-044-P1-K1-F6
Method
                   BLASTN
NCBI GI
                   g2351065
BLAST score
                   358
E value
                   0.0e + 00
Match length
                   486
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MHF15, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150684
Seq. ID
                  LIB3175-044-P1-K1-F7
Method
                  BLASTX
NCBI GI
                   g4586256
BLAST score
                   643
E value
                   2.0e-67
Match length
                   133
% identity
NCBI Description
                   (AL049640) probable photosystem I chain XI precursor
                   [Arabidopsis thaliana]
Seq. No.
                   150685
Seq. ID
                  LIB3175-044-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  g2894603
BLAST score
                  423
E value
                  1.0e-41
Match length
                  96
```

NCBI GI

```
% identity
NCBI Description
                  (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                   150686
Seq. ID
                   LIB3175-044-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   q2160184
BLAST score
                   608
E value
                   3.0e-63
Match length
                   113
                   100
% identity
                   (AC000132) ESTs gb H37208, gb H36853 come from this gene.
NCBI Description
                   [Arabidopsis thaliana]
                   150687
Seq. No.
Seq. ID
                   LIB3175-044-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g112741
BLAST score
                   58
E value
                   2.0e-68
Match length
                   164
% identity
                   84
NCBI Description
                   2S SEED STORAGE PROTEIN 3 PRECURSOR (2S ALBUMIN STORAGE
                   PROTEIN) >gi_68855_pir__NWMU3 2S albumin 3 precursor -
                   Arabidopsis thaliana >gi_166616 (M22033) albumin 2S subunit 3 precursor [Arabidopsis thaliana] >gi_395201_emb_CAA80868_
                   (Z24744) 2S albumin isoform 3 [Arabidopsis thaliana]
                   >gi_4490712_emb_CAB38846.1_ (AL035680) NWMU3-2S albumin 3
                   precursor [Arabidopsis thaliana]
Seq. No.
                   150688
Seq. ID
                   LIB3175-044-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g2347098
BLAST score
                   337
E value
                   1.0e-31
Match length
                   80
% identity
NCBI Description
                   (U76845) ubiquitin-specific protease [Arabidopsis thaliana]
                   >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific
                   protease (AtUBP3) [Arabidopsis thaliana]
Seq. No.
                   150689
Seq. ID
                   LIB3175-044-P1-K1-G11
Method
                   BLASTN
NCBI GI
                   q2062153
BLAST score
                   48
E value
                   4.0e-18
Match length
                   125
% identity
NCBI Description
                   Arabidopsis thaliana chromosome III BAC T02004 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150690
Seq. ID
                   LIB3175-044-P1-K1-G2
Method
                   BLASTX
```

g3785986

```
BLAST score
                   413
                   2.0e-40
E value
                  107
Match length
                   78
% identity
                  (AC005560) RGA1 protein [Arabidopsis thaliana]
NCBI Description
                  150691
Seq. No.
                  LIB3175-044-P1-K1-G3
Seq. ID
                  BLASTN
Method
NCBI GI
                  g3790580
BLAST score
                  383
E value
                  0.0e + 00
Match length
                  411
% identity
                  98
NCBI Description
                  Arabidopsis thaliana RING-H2 finger protein RHB1a mRNA,
                  complete cds
                  150692
Seq. No.
                  LIB3175-044-P1-K1-G6
Seq. ID
                  BLASTN
Method
NCBI GI
                  g4531433
BLAST score
                  478
E value
                  0.0e+00
Match length
                  481
% identity
                  100
NCBI Description
                  Arabidopsis thaliana chromosome II P1 MFL8 genomic
                  sequence, complete sequence
Seq. No.
                  150693
Seq. ID
                  LIB3175-044-P1-K1-G7
Method
                  BLASTX
NCBI GI
                  g1495269
BLAST score
                  636
E value
                  1.0e-66
Match length
                  141
% identity
                  (X97829) product similar to ccr protein, Citrus paradisi;
NCBI Description
                  PIR: S52663 [Arabidopsis thaliana]
                  >gi 1550735 emb CAA66824 (X98130) unknown [Arabidopsis
                  thaliana]
                  150694
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g4204300
BLAST score
                  246
E value
                  8.0e-21
                  147
Match length
% identity
                  41
                 (AC003027) Unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150695
Seq. ID
                  LIB3175-044-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4185505
                  467
BLAST score
E value
                  8.0e-47
```

```
Match length
                   115
% identity
                   (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                   [Brassica napus]
Seq. No.
                   150696
                  LIB3175-044-P1-K1-H11
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4689316
BLAST score
                   545
E value
                   5.0e-56
Match length
                   113
% identity
                   (AF130973) peroxisomal targeting signal type 2 receptor
NCBI Description
                   [Arabidopsis thaliana]
                   150697
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-H3
Method
                  BLASTN
NCBI GI
                   g3098611
                                                - P.
BLAST score
                   295
                   1.0e-165
E value
Match length
                   360
                   97
% identity
                  Arabidopsis thaliana senescence associated gene (SAG20)
NCBI Description
                  mRNA, partial cds
                   150698
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-H4
Method
                  BLASTX
NCBI GI
                   g1432083
BLAST score
                   695
E value
                   2.0e-73
Match length
                   155
                   89
% identity
                   (U60981) homolog to Skplp, an evolutionarily conserved
NCBI Description
                   kinetochore protein in budding yeast [Arabidopsis thaliana]
                   >gi 3068807 (AF059294) Skp1 homolog [Arabidopsis thaliana]
                   >gi 3719209 (U97020) UIP1 [Arabidopsis thaliana]
                   150699
Seq. No.
Seq. ID
                  LIB3175-044-P1-K1-H5
Method
                  BLASTX
NCBI GI
                   g1419090
BLAST score
                   279
E value
                   1.0e-24
                  108
Match length
                   53
% identity
NCBI Description
                   (X94968) 37kDa chloroplast inner envelope membrane
                  polypeptide precursor [Nicotiana tabacum]
                  150700
Seq. No.
                  LIB3175-044-P1-K1-H6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q486784
BLAST score
                   338
                   9.0e-32
E value
```

```
Match length
                   107
% identity
                   58
NCBI Description Golgi-associated particle 102K chain - human
Seq. No.
                   150701
Seq. ID
                   LIB3175-044-P1-K1-H7
Method
                   BLASTX
NCBI GI
                   g4063570
BLAST score
                   767
E value
                   6.0e-82
Match length
                   155
                   98
% identity
                   (AF035917) ATP synthase beta subunit [Tropaeolum tricolor]
NCBI Description
Seq. No.
                   150702
Seq. ID
                   LIB3175-044-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g3328231
BLAST score
                   87
E value
                   3.1e-02
Match length
                   112
% identity
                   19
                   (AF051784) 14S cohesin SMC1 subunit; SMC protein [Xenopus
NCBI Description
                   laevis]
                   150703
Seq. No.
                   LIB3175-044-P1-K1-H9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4689316
BLAST score
                   856
E value
                   3.0e-92
Match length
                   163
                   52
% identity
NCBI Description
                   (AF130973) peroxisomal targeting signal type 2 receptor
                   [Arabidopsis thaliana]
                   150704
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-A10
Method
                  BLASTX
NCBI GI
                   g1172873
BLAST score
                   428
E value
                   3.0e-42
Match length
                  133
                   67
% identity
NCBI Description
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__JN0719
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374
                   (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  150705
Seq. ID
                  LIB3175-045-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g1172873
BLAST score
                  438
E value
                  2.0e-43
Match length
                  135
% identity
                   67
```

19231 -

```
NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
                  drought-inducible cysteine proteinase (\overline{EC} \ 3.4.\overline{22.-)} \ RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                  (D13043) thiol protease [Arabidopsis thaliana]
                  150706
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g266693
                  244
BLAST score
E value
                  4.0e-21
                  72
Match length
% identity
                  69
                  OLEOSIN >gi_282875_pir__S22538 oleosin - Arabidopsis
NCBI Description
                  thaliana >gi 16405 emb CAA44225 (X62353) oleosin
                   [Arabidopsis thaliana] >gi 4455257 emb CAB36756.1
                   (AL035523) oleosin, 18.5K [Arabidopsis thaliana]
Seq. No.
                  150707
Seq. ID
                  LIB3175-045-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  q4038037
                  239
BLAST score
                  4.0e-20
E value
Match length
                  48
                  100
% identity
NCBI Description (AC005936) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  150708
                  LIB3175-045-P1-K1-A5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g1871173
BLAST score
                  367
E value
                  0.0e + 00
Match length
                  421
                  100
% identity
                  Arabidopsis thaliana chromosome II BAC T06D20 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  150709
                  LIB3175-045-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g585536
BLAST score
                  771
E value
                  2.0e-82
Match length
                  142
% identity
                  99
                  MYROSINASE PRECURSOR (SINIGRINASE) (THIOGLUCOSIDASE)
NCBI Description
                  >gi 1362006 pir S56653 thioglucosidase (EC 3.2.3.1) -
                  Arabidopsis thaliana >qi 304115 (L11454) thioglucosidase
                  [Arabidopsis thaliana] >gi 871990 emb CAA55786 (X79194)
                  thioglucosidase [Arabidopsis thaliana]
```

Seq. No. 150710 Seq. ID LIB3175-045-P1-K1-A7

Method BLASTX NCBI GI g1172873

NCBI Description

```
BLAST score
E value
                  1.0e-25
Match length
                  89
% identity
                  65
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374
                  (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  150711
                  LIB3175-045-P1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2815404
BLAST score
                  103
E value
                  9.0e-51
                  339
Match length
                  83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MMG4, complete sequence [Arabidopsis thaliana]
                  150712
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-A9
Method
                  BLASTX
NCBI GI
                  q1172873
BLAST score
                  208
                  8.0e-17
E value
                  80
Match length
                  57
% identity
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi_541857_pir__
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374
                  (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  150713
Seq. ID
                  LIB3175-045-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  q1172873
BLAST score
                  416
E value
                  7.0e-41
Match length
                  133
% identity
                  66
NCBI Description
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374
                  (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  150714
Seq. ID
                  LIB3175-045-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q2815404
BLAST score
                  60
E value
                  4.0e-25
Match length
                  188
% identity
                  83
```

MMG4, complete sequence [Arabidopsis thaliana]

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:

```
150715
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g2827143
BLAST score
                  287
E value
                  1.0e-54
Match length
                  132
                  78
% identity
                  (AF027174) cellulose synthase catalytic subunit
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  150716
Seq. ID
                  LIB3175-045-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g1518540
BLAST score
                  180
E value
                  1.0e-13
Match length
                  45
% identity
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
                  150717
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g1172873
BLAST score
                  178
E value
                  4.0e-39
Match length
                  135
% identity
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374
                  (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  150718
                  LIB3175-045-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172873
BLAST score
                  428
E value
                  3.0e-42
Match length
                  135
% identity
NCBI Description
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374
                  (D13043) thiol protease [Arabidopsis thaliana]
                  150719
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g1172873
BLAST score
                  436
                  3.0e-43
E value
Match length
                  135
% identity
                  CYSTEINE PROTEINASE RD21A PRECURSOR >qi 541857 pir JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
```

Seq. No.

BLAST score

% identity

Seq. No.

Seq. ID Method

NCBI GI

E value

Seq. No.

Seq. ID Method

NCBI GI

E value

BLAST score

Match length

% identity

BLAST score

Match length

% identity

Seq. ID

E value Match length

Method NCBI GI

```
precursor - Arabidopsis thaliana >gi_435619_dbj_BAA02374_
                  (D13043) thiol protease [Arabidopsis thaliana]
                  150720
                  LIB3175-045-P1-K1-B8
                  BLASTX
                  g1172873
                  382
                  6.0e-37
                  115
                  67
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619 dbj BAA02374
                  (D13043) thiol protease [Arabidopsis thaliana]
                  150721
                  LIB3175-045-P1-K1-B9
                  BLASTX
                  g1172873
                  325
                  3.0e-30
                  118
                  56
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi_435619_dbj&BAA02374
                  (D13043) thiol protease [Arabidopsis thaliana]
                  150722
                  LIB3175-045-P1-K1-C1
                  BLASTN
                  g2337888
                  140
                  5.0e-73
                  230
                  47
                  Genomic sequence for Arabidopsis thaliana BAC F14J16,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  150723
                  LIB3175-045-P1-K1-C10
                  BLASTN
                  g2245031
                  124
                  3.0e-63
                  427
                  99
```

Seq. No. Seq. ID Method NCBI GI BLAST score E value Match length

% identity Arabidopsis thaliana DNA chromosome 4, ESSA I contig NCBI Description

fragment No

150724 Seq. No. LIB3175-045-P1-K1-C11 Seq. ID Method BLASTX

NCBI GI g1175014 BLAST score 557 E value 2.0e-57

```
Match length
% identity
                  89
                  PLASMA MEMBRANE INTRINSIC PROTEIN 2B >gi 629543 pir S44085
NCBI Description
                  plasma membrane intrinsic protein 2b - Arabidopsis thaliana
                  >gi_472879_emb_CAA53478_ (X75884) plasma membrane intrinsic
                  protein 2b [Arabidopsis thaliana]
Seq. No.
                  150725
Seq. ID
                  LIB3175-045-P1-K1-C12
                  BLASTX
Method
NCBI GI
                  g4220535
BLAST score
                  489
E value
                  2.0e-49
Match length
                  97
% identity
NCBI Description
                  (AL035356) clathrin coat assembly like protein [Arabidopsis
                  thaliana]
                  150726
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1172873
BLAST score
                  239
E value
                  4.0e-20
                  97
Match length
                  55
% identity
                  CYSTEINE PROTEINASE RD21A PRECURSOR >gi 541857 pir JN0719
NCBI Description
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A
                  precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374_
                  (D13043) thiol protease [Arabidopsis thaliana]
Seq. No.
                  150727
Seq. ID
                  LIB3175-045-P1-K1-C3
Method
                  BLASTN
NCBI GI
                  q4455229
BLAST score
                  407
E value
                  0.0e + 00
Match length
                  425
                  99
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F13M23
                  (ESSAII project)
Seq. No.
                  150728
Seq. ID
                  LIB3175-045-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g1703115
BLAST score
                  223
                  2.0e-18
E value
Match length
                  81
                  57
% identity
```

ACTIN 3 >gi 2129526 pir S68112 actin 3 - Arabidopsis NCBI Description thaliana >gi 1145695 (U39480) actin [Arabidopsis thaliana]

>qi 3236244 (AC004684) actin 3 protein [Arabidopsis

thaliana]

Seq. No. 150729

Seq. ID LIB3175-045-P1-K1-C5

```
Method
                  BLASTX
NCBI GI
                  q2464899
BLAST score
                  390
E value
                  8.0e-38
Match length
                  112
% identity
                  73
                  (Z99708) geranylgeranyl pyrophosphate synthase (Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  150730
                  LIB3175-045-P1-K1-C6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1172872
BLAST score
                  614
E value
                  4.0e-64
Match length
                  135
% identity
                  89
NCBI Description
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir JN0718
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi_435618_dbj_BAA02373_
                  (D13042) thiol protease [Arabidopsis thaliana]
                  >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
Seq. No.
                  150731
                  LIB3175-045-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q421826
BLAST score
                  403
E value
                  2.0e-39
                  78
Match length
% identity
                  100
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
NCBI Description
                  >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis
                  thaliana]
                  150732
Seq. No.
                  LIB3175-045-P1-K1-C8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2342688
BLAST score
                  411
E value
                  3.0e-40
Match length
                  90
% identity
NCBI Description
                  (AC000106) Similar to Beta integral membrane protein
                  (gb U43629). [Arabidopsis thaliana]
                  150733
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-C9
                  BLASTX
Method
NCBI GI
                  g2244760
BLAST score
                  315
                  3.0e-29
E value
Match length
                  86
                  70
% identity
NCBI Description (Z97335) selenium-binding protein [Arabidopsis thaliana]
```

```
150734
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g3128187
BLAST score
                  331
                  6.0e-31
E value
Match length
                  77
                  77
% identity
NCBI Description (AC004521) putative beta-glucosidase [Arabidopsis thaliana]
                  150735
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q1345595
                  527
BLAST score
                  6.0e-54
E value
Match length
                  110
% identity
                  98
                  14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
NCBI Description
                  >gi 1084332 pir _S53727 14-3-3-like protein (ATF1) -
                  Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like
                  protein 1 [Arabidopsis thaliana] >gi_1549404 (U68545) GF14
                  lambda [Arabidopsis thaliana]
Seq. No.
                  150736
                  LIB3175-045-P1-K1-D5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3449331
                  98
BLAST score
                  4.0e-48
E value
                  150
Match length
                  45
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MNC17, complete sequence [Arabidopsis thaliana]
                  150737
Seq. No.
                  LIB3175-045-P1-K1-D6
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4544419
BLAST score
                  656
E value
                  5.0e-69
Match length
                  128
% identity
NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]
Seq. No.
                  150738
Seq. ID
                  LIB3175-045-P1-K1-D7
                  BLASTX
Method
NCBI GI
                  g2213592
BLAST score
                  271
E value
                  6.0e-24
Match length
                  115
% identity
NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]
Seq. No.
                  150739
Seq. ID
                  LIB3175-045-P1-K1-D8
```

```
BLASTX
Method
NCBI GI
                  g1076301
                  159
BLAST score
                  1.0e-10
E value
                  54
Match length
                  35
% identity
                  CONSTANS protein - Arabidopsis thaliana
NCBI Description
                  >gi_1161514_emb_CAA64407_ (X94937) CONSTANS protein
                  [Arabidopsis thaliana]
                  150740
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  q399013
                  511
BLAST score
                  5.0e-52
E value
                  100
Match length
                  100
% identity
                  ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
NCBI Description
                   (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi 99658 pir S21313 ADP, ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi 16175 emb CAA46518 (X65549)
                  adenylate translocator [Arabidopsis thaliana]
                  >gi 445607 prf 1909354A adenylate translocator
                  [Arabidopsis thaliana]
Seq. No.
                  150741
Seq. ID
                  LIB3175-045-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g3021336
BLAST score
                  630
E value
                  6.0e-66
Match length
                  138
% identity
                  91
NCBI Description
                  (AJ224957) RGA-like [Arabidopsis thaliana]
                  150742
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g4757409
BLAST score
                  364
E value
                  0.0e + 00
Match length
                  364
                  100
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MVC8, complete sequence
Seq. No.
                  150743
Seq. ID
                  LIB3175-045-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g2213592
BLAST score
                  293
E value
                  2.0e-26
Match length
                  119
                  25
% identity
NCBI Description (AC000348) T7N9.12 [Arabidopsis thaliana]
```

```
Seq. No.
                  150744
Seq. ID
                  LIB3175-045-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g115767
BLAST score
                  680
E value
                  8.0e-72
Match length
                  134
                  97
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  150745
Seq. ID
                  LIB3175-045-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  g2462929
BLAST score
                  554
                  4.0e-57
E value
Match length
                  116
                  93
% identity
                  (Y12295) glutathione transferase [Arabidopsis thaliana]
NCBI Description
                  150746
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-E7
                  BLASTX
Method
NCBI GI
                  g1170028
BLAST score
                  518
E value
                  8.0e-53
                  118
Match length
% identity
                  86
                  GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE 1 PRECURSOR (GSA
NCBI Description
                  1) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE 1) (GSA-AT 1)
                  >gi 454357 (U03773)
                  glutamate-1-semialdehyde-2,1-aminomutase [Arabidopsis
                  thaliana]
Seq. No.
                  150747
Seq. ID
                  LIB3175-045-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g2462748
BLAST score
                  622
E value
                  5.0e-65
Match length
                  122
                  99
% identity
                  (AC002292) putative Clathrin Coat Assembly protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  150748
Seq. ID
                  LIB3175-045-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q3123188
BLAST score
                  479
E value
                  2.0e-48
```

```
Match length
% identity
NCBI Description
                  CATALASE 3 >gi 2347178 (U43147) catalase 3 [Arabidopsis
                  thaliana] >gi \overline{2}511726 (AF021937) catalase 3 [Arabidopsis
                  thaliana]
                  150749
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-F11
Method
                  BLASTX
NCBI GI
                  g1402912
BLAST score
                  518
                   6.0e-53
E value
                  116
Match length
% identity
                  88
                  (X98317) peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150750
                  LIB3175-045-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1076361
BLAST score
                  442
E value
                  3.0e-44
                  92
Match length
% identity
NCBI Description
                  oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14) -
                  Arabidopsis thaliana >gi 2129660 pir S69197
                  oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14)
                   (clone TE 1-7) - Arabidopsis thaliana
                  >gi 804946 emb CAA85389 (Z36912) acyl-(acyl carrier
                  protein) thioesterase [Arabidopsis thaliana]
Seq. No.
                  150751
Seq. ID
                  LIB3175-045-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g3024426
BLAST score
                  277
                   5.0e-25
E value
                  75
Match length
% identity
                  PYRUVATE, PHOSPHATE DIKINASE PRECURSOR
NCBI Description
                   (PYRUVATE,ORTHOPHOSPHATE DIKINASE) >gi 1084302_pir_ S55478
                  pyruvate, orthophosphate dikinase (EC 2.7.9.1) - common ice
                  plant >gi 854265 emb CAA57872 (X82489)
                  pyruvate, orthophosphate dikinase [Mesembryanthemum
                  crystallinum]
Seq. No.
                  150752
Seq. ID
                  LIB3175-045-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  q2338712
BLAST score
                  262
E value
                  9.0e-23
Match length
                  69
% identity
                   (AF013959) metallothionein-like protein [Arabidopsis
NCBI Description
```

thaliana]

```
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-F4
Method
                  BLASTN
NCBI GI
                  g3176693
BLAST score
                  49
                  2.0e-18
E value
                  57
Match length
                  96
% identity
                  Arabidopsis thaliana chromosome I BAC T27I1 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-F5
                  BLASTX
Method
NCBI GI
                  g3834309
BLAST score
                  102
E value
                  7.0e-75
Match length
                  141
% identity
NCBI Description
                  (AC005679) Strong similarity to glycoprotein EP1 gb_L16983
                  Daucus carota and a member of S locus glycoprotein family
                  PF_00954. ESTs gb_F13813, gb_T21052, gb_R30218 and
                  gb W43262 come from this gene. [Arabidopsis thaliana]
Seq. No.
                  150755
Seq. ID
                  LIB3175-045-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  q2088654
BLAST score
                  549
E value
                  2.0e-56
Match length
                  121
% identity
NCBI Description
                  (AF002109) 60S acidic ribosomal protein PO isolog
                  [Arabidopsis thaliana]
Seq. No.
                  150756
                  LIB3175-045-P1-K1-F8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4757409
BLAST score
                  116
E value
                  2.0e-58
Match length
                  417
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MVC8, complete sequence
                  150757
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  q4581146
BLAST score
                  580
E value
                  4.0e-60
Match length
                  118
% identity
NCBI Description
                  (AC006919) putative fructose-bisphosphate aldolase,
                  cytoplasmic [Arabidopsis thaliana]
```

```
150758
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-G1
Method
                  BLASTN
NCBI GI
                  g3297806
                  152
BLAST score
                  7.0e-80
E value
Match length
                  433
% identity
                  95
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F1715
NCBI Description
                   (ESSA project)
                  150759
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-G11
                  BLASTX
Method
NCBI GI
                  g4586254
BLAST score
                  408
E value
                   4.0e-40
                  109
Match length
% identity
                  82
                  (AL049640) auxilin-like protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150760
                  LIB3175-045-P1-K1-G12
Seq. ID
                  BLASTX
Method
NCBI GI
                  g113782
BLAST score
                  490
                  2.0e-49
E value
Match length
                  110
                  89
% identity
NCBI Description
                  BETA-AMYLASE (1,4-ALPHA-D-GLUCAN MALTOHYDROLASE)
                  >gi_486824_pir__S36094 beta-amylase (EC 3.2.1.2) -
                  Arabidopsis thaliana >gi_166602 (M73467) beta-amylase
                   [Arabidopsis thaliana] >gi_228699_prf__1808329A beta
                  amylase [Arabidopsis thaliana]
                  150761
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-G3
                  BLASTX
Method
NCBI GI
                  q4510424
BLAST score
                  203
                  2.0e-27
E value
                  71
Match length
% identity
NCBI Description
                  (AC006929) putative carboxypeptidase [Arabidopsis thaliana]
Seq. No.
                  150762
Seq. ID
                  LIB3175-045-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  g3242730
BLAST score
                  656
E value
                  5.0e-69
                  128
Match length
                  99
% identity
                   (AC003040) putative host response protein (Pir7)
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  150763
```

```
Seq. ID
                   LIB3175-045-P1-K1-G5
Method
                   BLASTN
NCBI GI
                   g3985955
BLAST score
                   377
                   0.0e + 00
E value
Match length
                   393
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MTH16, complete sequence [Arabidopsis thaliana]
                   150764
Seq. No.
                   LIB3175-045-P1-K1-G6
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4760577
BLAST score
                   186
E value
                   7.0e-14
Match length
                   111
                   32
% identity
NCBI Description (AB019602) IDN3-B [Homo sapiens]
                   150765
Seq. No.
Seq. ID
                   LIB3175-045-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q2827621
BLAST score
                   405
                   1.0e-39
E value
Match length
                   134
% identity
                   60
NCBI Description (AL021636) putative protein [Arabidopsis thaliana]
                   150766
Seq. No.
Seq. ID
                   LIB3175-045-P1-K1-G8
Method
                   BLASTX
NCBI GI
                   g1084335
BLAST score
                   543
E value
                   9.0e-56
Match length
                   114
% identity
                   89
NCBI Description
                   calcium-dependent protein kinase (EC 2.7.1.-) 2 -
                   Arabidopsis thaliana >gi_604881_dbj_BAA04830_ (D21806) calcium-dependent protein kinase [Arabidopsis thaliana]
Seq. No.
                   150767
Seq. ID
                   LIB3175-045-P1-K1-G9
Method
                   BLASTX
NCBI GI
                   g114330
                   233
BLAST score
E value
                   7.0e-22
Match length
                   63
% identity
                   84
NCBI Description
                   PLASMA MEMBRANE ATPASE 1 (PROTON PUMP)
                   >gi_67972_pir__PXMUP1 H+-transporting ATPase (EC 3.6.1.35)
                   type 1, plasma membrane - Arabidopsis thaliana >gi_166746
                   (M24107) plasma membrane proton pump H+ ATPase [Arabidopsis
                   thaliana]
                   150768
Seq. No.
```

```
Seq. ID
                  LIB3175-045-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  342
                  1.0e-60
E value
Match length
                  125
% identity
                  94
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  150769
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g1769905
BLAST score
                  126
E value
                  3.0e-39
Match length
                  127
% identity
                  69
                   (X98108) 23 kDa polypeptide of oxygen-evolving comlex (OEC)
NCBI Description
                   [Arabidopsis thaliana]
                  150770
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-H11
                  BLASTX
Method
NCBI GI
                  g2129648
BLAST score
                  665
                  5.0e-70
E value
Match length
                  121
                  99
% identity
NCBI Description
                  MYB-related protein 33,3K - Arabidopsis thaliana
                  >gi 1263095 emb CAA90809 (Z54136) MYB-related protein
                  [Arabidopsis thaliana]
                  150771
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-H12
                  BLASTX
Method
NCBI GI
                  g2499811
BLAST score
                  533
                  1.0e-57
E value
Match length
                  116
                  98
% identity
NCBI Description
                  PROFILIN 2 >gi 1353766 (U43323) profilin 2 [Arabidopsis
                  thaliana] >gi 1353772 (U43326) profilin 2 [Arabidopsis
                  thaliana]
                  150772
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g3819710
BLAST score
                  463
                  2.0e-46
E value
Match length
                  84
% identity
NCBI Description
                  (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
                  thaliana]
```

```
150773
Seq. No.
Seq. ID
                  LIB3175-045-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g4510346
BLAST score
                  198
E value
                  7.0e-58
                  125
Match length
% identity
                  (AC006921) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150774
                  LIB3175-045-P1-K1-H4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4587986
BLAST score
                  58
E value
                  5.0e-24
Match length
                  70
% identity
                  96
                  Arabidopsis thaliana ABA-regulated gene cluster, complete
NCBI Description
                  sequence
Seq. No.
                  150775
Seq. ID
                  LIB3175-045-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  q421826
BLAST score
                  424
E value
                  7.0e-42
Match length
                  122
% identity
NCBI Description
                  chlorophyll a/b-binding protein CP29 - Arabidopsis thaliana
                  >gi 298036 emb CAA50712 (X71878) CP29 [Arabidopsis
                  thaliana]
Seq. No.
                  150776
Seq. ID
                  LIB3175-045-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g3510254
BLAST score
                  233
E value
                  2.0e-19
Match length
                  54
% identity
NCBI Description
                  (AC005310) putative zinc transporter [Arabidopsis thaliana]
Seq. No.
                  150777
Seq. ID
                  LIB3175-045-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  q3183185
BLAST score
                  231
E value
                  4.0e~19
Match length
                  62
% identity
NCBI Description
                  GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG
                  >gi_2224766_emb_CAB09712_ (Z97025) product highly similar
```

elongation factor [Bacillus subtilis]

to elongation factor EF-G [Bacillus subtilis]

>gi\_2633848 emb CAB13350 (Z99111) similar to GTP-binding

```
150778
Seq. No.
Seq. ID
                   LIB3175-045-P1-K1-H8
Method
                   BLASTX
NCBI GI
                   g1076317
BLAST score
                   632
                   3.0e-66
E value
                   138
Match length
                   89
% identity
                   dihydrodipicolinate synthase (EC 4.2.1.52) precursor -
NCBI Description
                   Arabidopsis thaliana
                   150779
Seq. No.
Seq. ID
                   LIB3175-046-P1-K1-A11
Method
                   BLASTN
NCBI GI
                   g1669388
BLAST score
                   137
E value
                   3.0e-71
                   238
Match length
% identity
                   97
NCBI Description Arabidopsis thaliana actin 8 (ACT8) gene, complete cds
Seq. No.
                   150780
                   LIB3175-046-P1-K1-A12
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2245073
BLAST score
                   414
                   0.0e+00
E value
Match length
                   426
% identity
                   99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
                   150781
Seq. No.
Seq. ID
                   LIB3175-046-P1-K1-A2
Method
                   BLASTX
NCBI GI
                   g115767
BLAST score
                   398
E value
                   9.0e-39
Match length
                   80
% identity
                   96
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-165/180) (LHCP) >gi_81603_pir__A29280 chlorophyll
                   a/b-binding protein ab16\overline{5} - Arabidopsis thaliana
                   >gi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                   protein (LHCP AB 65) [Arabidopsis thaliana]
                   >gi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                   150782
                  LIB3175-046-P1-K1-A4
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2494110
BLAST score
                   408
E value
                   0.0e + 00
                   420
Match length
                   90
% identity
```

```
NCBI Description Sequence of BAC T1G11 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
                  150783
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  q498038
                  400
BLAST score
                  6.0e-39
E value
                  142
Match length
% identity
                  (L33792) lipid transfer protein [Senecio odorus]
NCBI Description
                  150784
Seq. No.
                  LIB3175-046-P1-K1-A6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4337189
BLAST score
                  725
E value
                  4.0e-77
Match length
                  139
% identity
NCBI Description
                  (AC006403) putative calmodulin-binding protein [Arabidopsis
                  thaliana]
                  150785
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g3641252
BLAST score
                  115
E value
                  7.0e-06
Match length
                  88
% identity
                  6
NCBI Description
                  (AF053127) leucine-rich receptor-like protein kinase [Malus
                  domestica]
                  150786
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g2052379
BLAST score
                  727
E value
                  2.0e-77
Match length
                  135
% identity
NCBI Description
                 (U66343) calreticulin [Arabidopsis thaliana]
Seq. No.
                  150787
Seq. ID
                  LIB3175-046-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g2129648
BLAST score
                  316
E value
                  3.0e-29
Match length
                  69
% identity
                  52
NCBI Description
                  MYB-related protein 33,3K - Arabidopsis thaliana
```

[Arabidopsis thaliana]

>gi\_1263095\_emb\_CAA90809\_ (Z54136) MYB-related protein

```
150788
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-B12
Method
                  BLASTX
NCBI GI
                   g4581116
BLAST score
                   463
                   2.0e-46
E value
                   121
Match length
% identity
                   61
                   (AC005825) putative beta-galactosidase [Arabidopsis
NCBI Description
                   thaliana]
                   150789
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-B2
Method
                  BLASTX
                   g1465368
NCBI GI
BLAST score
                   316
E value
                   4.0e-29
                   143
Match length
% identity
                   57
                   (X99548) bHLH protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   150790
                  LIB3175-046-P1-K1-B4
Seq. ID
Method
                  BLASTX
NCBI GI
                   q4586265
BLAST score
                   506
E value
                   2.0e-51
Match length
                  138
                   73
% identity
NCBI Description
                   (AL049640) putative protein [Arabidopsis thaliana]
                   150791
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-B5
                  BLASTX
Method
NCBI GI
                   g267069
BLAST score
                   572
E value
                   4.0e-59
Match length
                  108
                   98
% identity
                  TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi 320183 pir JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi 166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                  150792
                  LIB3175-046-P1-K1-B6
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2462749
BLAST score
                  362
E value
                  2.0e-34
                  109
Match length
% identity
                   (AC002292) Putative Serine/Threonine protein kinase
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                  150793
Seq. ID
                  LIB3175-046-P1-K1-B8
```

```
Method
                   BLASTX
 NCBI GI
                   g3184100
 BLAST score
                   232
                   3.0e-19
E value
Match length
                   72
 % identity
                   57
                   (AL023777) rna binding protein [Schizosaccharomyces pombe]
NCBI Description
                   150794
 Seq. No.
 Seq. ID
                   LIB3175-046-P1-K1-C1
 Method
                   BLASTX
 NCBI GI
                   q3929364
 BLAST score
                   455
                   2.0e-45
E value
                   96
Match length
 % identity
                   91
 NCBI Description
                   NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR
                   (COMPLEX I-23KD) (CI-23KD) >gi 1076356 pir S52380 NADH
                   dehydrogenase (EC 1.6.99.3) - Arabidopsis Thaliana
                   >gi 666977 emb CAA59061 (X84318) NADH dehydrogenase
                   [Arabidopsis thaliana] >gi 3152573 (AC002986) Match to
                   NADH: ubiquinone oxidoreductase gb X84318 from A.thaliana.
                   ESTs gb_Z27005, gb_T04711, gb T45\overline{0}78 and gb_Z28689 come
                   from this gene. [Arabidopsis thaliana]
                   150795
 Seq. No.
 Seq. ID
                   LIB3175-046-P1-K1-C2
 Method
                   BLASTX
NCBI GI
                   g2218152
 BLAST score
                   77
                   1.0e-65
E value
Match length
                   131
 % identity
                   (AF005279) type IIIa membrane protein cp-wap13 [Vigna
NCBI Description
                   unguiculata]
 Seq. No.
                   150796
 Seq. ID
                   LIB3175-046-P1-K1-C3
Method
                   BLASTN
NCBI GI
                  -g2281648
 BLAST score
                   140
E value
                   8.0e-73
Match length
                   140
 % identity
                   Arabidopsis thaliana AP2 domain containing protein RAP2.12
NCBI Description
                   mRNA, partial cds
                   150797
 Seq. No.
 Seq. ID
                   LIB3175-046-P1-K1-C4
Method
                   BLASTX
∵NCBI GI
                   g2723477
BLAST score
                   203
E value
                   7.0e-16
Match length
                   45
% identity
NCBI Description
                  (D89824) GTP-binding protein [Arabidopsis thaliana]
```

```
150798
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-C5
                  BLASTX
Method
NCBI GI
                  g2252857
                  276
BLAST score
E value
                  9.0e-25
Match length
                  63
% identity
NCBI Description (AF013294) similar to acidic ribosomal protein p1
                  [Arabidopsis thaliana]
                  150799
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-C6
                  BLASTX
Method
NCBI GI
                  g1351272
BLAST score
                  95
E value
                  9.0e-58
Match length
                  140
% identity
                  87
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_414550
                  (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                  thaliana] >gi 742408 prf 2009415A triose phosphate
                  isomerase [Arabidopsis thaliana]
                  150800
Seq. No.
                  LIB3175-046-P1-K1-C7
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3928134
BLAST score
                  474
                  1.0e-47
E value
                  130
Match length
                  45
% identity
NCBI Description (AJ130956) annexin P38 [Capsicum annuum]
Seq. No.
                  150801
                  LIB3175-046-P1-K1-C8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2497886
BLAST score
                  300
                  3.0e-27
E value
Match length
                  54
                  100
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)
NCBI Description
                  >gi 1361999 pir S57862 metallothionein 2b - Arabidopsis
                  thaliana >gi 1086463 (U11256) metallothionein [Arabidopsis
                  thaliana]
                  150802
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  g4522012
BLAST score
                  403
E value
                  8.0e-45
Match length
                  131
% identity
NCBI Description (AC007069) hypothetical protein [Arabidopsis thaliana]
```

```
Seq. No.
                  150803
Seq. ID
                  LIB3175-046-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g1351272
BLAST score
                  562
E value
                  6.0e-58
Match length
                  129
                  87
% identity
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550
NCBI Description
                  (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                  thaliana] >gi 742408 prf 2009415A triose phosphate
                  isomerase [Arabidopsis thaliana]
                  150804
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  g21913
BLAST score
                  213
E value
                  5.0e-17
                  88
Match length
% identity
                  44
NCBI Description
                  (X62626) vicilin [Theobroma cacao]
Seq. No.
                  150805
Seq. ID
                  LIB3175-046-P1-K1-D11
Method
                  BLASTN
NCBI GI
                  g4220636
BLAST score
                  331
E value
                  0.0e+00
                  400
Match length
                  95
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFB16, complete sequence [Arabidopsis thaliana]
                  150806
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g2351068
BLAST score
                  80
                  2.0e-37
E value
Match length
                  116
% identity
                  94
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MRH10, complete sequence [Arabidopsis thaliana]
                  150807
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-D3
Method
                  BLASTX
NCBI GI
                  q4006834
BLAST score
                  554
E value
                  4.0e-57
Match length
                  108
% identity
NCBI Description
                  (AC005970) enoyl-ACP reductase (enr-A) [Arabidopsis
                  thaliana]
Seq. No.
                  150808
```

Seq. ID

```
Seq. ID
                   LIB3175-046-P1-K1-D4
Method
                   BLASTX
NCBI GI
                   q1737218
BLAST score
                   386
E value
                   3.0e-37
Match length
                   73
% identity
                   100
NCBI Description
                   (U79959) vacuolar sorting receptor homolog [Arabidopsis
                   thalianal
Seq. No.
                   150809
Seq. ID
                   LIB3175-046-P1-K1-D5
Method
                   BLASTX
NCBI GI
                   q2887500
BLAST score
                   287
E value
                   1.0e-25
Match length
                   60
% identity
                   87
NCBI Description
                   (AC002339) putative AP2 domain-containing protein
                   [Arabidopsis thaliana]
Seq. No.
                   150810
Seq. ID
                   LIB3175-046-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   q2388578
BLAST score
                   718
E value
                   3.0e-76
Match length
                   144
% identity
NCBI Description
                   (AC000098) Similar to Mycobacterium RlpF (gb Z84395). ESTs
                   gb T75785,gb R30580,gb T04698 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   150811
Seq. ID
                   LIB3175-046-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q3335365
BLAST score
                   595
E value
                   8.0e-62
Match length
                   145
% identity
NCBI Description
                   (AC003028) high affinity calcium antiporter [Arabidopsis
                   thalianal
Seq. No.
                   150812
Seq. ID
                   LIB3175-046-P1-K1-D8
Method
                   BLASTN
NCBI GI
                   q3449321
BLAST score
                   223
E value
                   1.0e-122
Match length
                   366
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTG10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150813
```

LIB3175-046-P1-K1-D9

Method BLASTX NCBI GI g1710581 BLAST score 491 E value 9.0e-50 Match length 105 % identity 91 60S RIBOSOMAL PROTEIN L9 >gi\_2129720\_pir\_\_S71255 ribosomal NCBI Description protein L9 - Arabidopsis thaliana >gi 1107489 emb CAA63024 (X91958) 60S ribosomal protein L9 [Arabidopsis thaliana] Seq. No. 150814 Seq. ID LIB3175-046-P1-K1-E1 Method BLASTX NCBI GI q4519671 BLAST score 251 E value 2.0e-21 Match length 80 % identity 65 NCBI Description (AB017693) transfactor [Nicotiana tabacum] 150815 Seq. No. Seq. ID LIB3175-046-P1-K1-E10 Method BLASTN NCBI GI q3402745 BLAST score 155 E value 1.0e-81 Match length 341 % identity 100 Arabidopsis thaliana DNA chromosome 4, BAC clone F18E5 NCBI Description (ESSAII project) Seq. No. 150816 Seq. ID LIB3175-046-P1-K1-E11 Method BLASTX NCBI GI g2829899 BLAST score 162 E value 2.0e-11 Match length 50 % identity 66 (AC002311) similar to ripening-induced protein, NCBI Description gp\_AJ001449\_2465015 and major#latex protein, gp\_X91961\_1107495 [Arabidopsis thaliana] Seq. No. 150817 Seq. ID LIB3175-046-P1-K1-E12 Method BLASTX NCBI GI g417073 BLAST score 546 E value 4.0e-56 Match length 120 % identity 86 NCBI Description GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) >gi\_484529\_pir\_\_JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa >gi\_166412 (L01660) NADH-glutamate

Seq. No. 150818

synthase [Medicago sativa]

```
Seq. ID
                  LIB3175-046-P1-K1-E2
                  BLASTN
Method
NCBI GI
                  q2760165
BLAST score
                  53
E value
                  4.0e-21
Match length
                  161
                  83
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAC9, complete sequence [Arabidopsis thaliana]
                  150819
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  q3913518
BLAST score
                  358
E value
                  4.0e-34
                  77
Match length
                  97
% identity
                  3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE
NCBI Description
                  (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE)
                   (DPNPASE) >gi 1103921 (U40433) 3'(2'),5'-bisphosphate
                  nucleotidase [Arabidopsis thaliana]
                  150820
Seq. No.
                  LIB3175-046-P1-K1-E4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3860243
BLAST score
                  268
E value
                  1.0e-149
Match length
                  346
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F15K20 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150821
                  LIB3175-046-P1-K1-E5
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3287679
BLAST score
                  ×607
E value
                  3.0e-63
                  137
Match length
% identity
NCBI Description (AC003979) T22J18.6 [Arabidopsis thaliana]
Seq. No.
                  150822
                  LIB3175-046-P1-K1-E6
Seq. ID
                  BLASTX
Method
NCBI GI
                  g2104957
BLAST score
                  605
E value
                  5.0e-63
Match length
                  112
% identity
                  100
NCBI Description (U96924) immunophilin [Arabidopsis thaliana]
                  150823
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-E7
Method
                  BLASTN
```

19255

```
q3985952
NCBI GI
BLAST score
                  46
                  7.0e-17
E value
Match length
                  123
                  83
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MRC8, complete sequence [Arabidopsis thaliana]
                  150824
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-E8
                  BLASTX
Method
NCBI GI
                  q3157924
                  291
BLAST score
E value
                  3.0e-26
                  56
Match length
                  100
% identity
NCBI Description
                  (AC002131) Contains homology to extensin-like protein
                  gb_D83227 from Populus nigra. ESTs gb_H76425, gb_T13883,
                  gb_T45348, gb_H37743, gb_AA042634, gb_Z26960 and gb Z25951
                  come from this gene. There is a similar ORF on the
                  opposite strand. [... >gi_4063707 (AF104327) extensin-like
                  protein [Arabidopsis thaliana]
Seq. No.
                  150825
Seq. ID
                  LIB3175-046-P1-K1-E9
                  BLASTX
Method
NCBI GI
                  g4741960
BLAST score
                  769
E value
                  3.0e-82
                  141
Match length
                  99
% identity
                  (AF134130) Lhcb6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  150826
Seq. ID
                  LIB3175-046-P1-K1-F1
                  BLASTX
Method
NCBI GI
                  g4589398
BLAST score
                  394
E value
                  3.0e-38
                  86
Match length
% identity
NCBI Description (D89972) asparaginyl endopeptidase (VmPE-1A) [Vigna mungo]
                  150827
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-F10
Method
                  BLASTX
NCBI GI
                  g4732123
BLAST score
                  331
E value
                  3.0e - 34
                  93
Match length
% identity
                  (AF129087) mitogen-activated protein kinase homologue
NCBI Description
                  [Medicago sativa]
                  150828
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-F12
Method
                  BLASTX
```

```
NCBI GI
                   q2738248
BLAST score
                   196
E value
                   1.0e-15
Match length
                   46
% identity
                   (U97200) cobalamin-independent methionine synthase
NCBI Description
                   [Arabidopsis thaliana]
                   150829
Seq. No.
Seq. ID
                   LIB3175-046-P1-K1-F2
                   BLASTN
Method
NCBI GI
                   q1865682
BLAST score
                   240
                   1.0e-132
E value
                   404
Match length
                   95
% identity
                  A.thaliana 16 kb chromosome 1 DNA fragment
NCBI Description
Seq. No.
                   150830
                   LIB3175-046-P1-K1-F4
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3176874
                   249
BLAST score
E value
                   7.0e-22
                   56
Match length
                   91
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   150831
                   LIB3175-046-P1-K1-F5
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2623295
BLAST score
                   252
E value
                   1.0e-21
Match length
                   68
                   71
% identity
                   (AC002409) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   150832
Seq. No.
                   LIB3175-046-P1-K1-F6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g2245031
BLAST score
                   412
E value
                   0.0e+00
Match length
                   433
                   98
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                   fragment No
Seq. No.
                  150833
Seq. ID
                   LIB3175-046-P1-K1-F8
Method
                   BLASTX
NCBI GI
                   g2245144
BLAST score
                   265
E value
                   2.0e-23
Match length
                   63
```

```
% identity
NCBI Description
                  (Y10846) O-acetylserine(thiol) lyase [Brassica juncea]
                  150834
Seq. No.
                  LIB3175-046-P1-K1-F9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3860420
BLAST score
                  208
                  2.0e-16
E value
                  53
Match length
                  75
% identity
NCBI Description (AJ011047) exo galactanase [Lupinus angustifolius]
                  150835
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  g4263774
BLAST score
                  52
E value
                  2.0e-20
Match length
                  132
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC T20F21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  150836
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-G12
Method
                  BLASTX
NCBI GI
                  g3953473
BLAST score
                  608
E value
                  2.0e-63
Match length
                  123
                  100
% identity
                  (AC002328) F2202.18 [Arabidopsis thaliana]
NCBI Description
                  150837
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-G2
                  BLASTN
Method
NCBI GI
                  g3785968
BLAST score
                  39
E value
                  5.0e-13
Match length
                  130
% identity
                  Arabidopsis thaliana chromosome II BAC F2I9 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  150838
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-G4
Method
                  BLASTX
NCBI GI
                  q4538963
BLAST score
                  534
E value
                  1.0e-54
Match length
                  131
% identity
                  62
NCBI Description
                   (AL049488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi 4741958_gb_AAD28776.1_AF134129_1
                   (AF134129) Lhcb5 protein [Arabidopsis thaliana]
```

```
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  q4263711
BLAST score
                  208
E value
                  2.0e-16
                  45
Match length
                  84
% identity
                   (AC006223) putative CCR4-associated transcription factor
NCBI Description
                  [Arabidopsis thaliana]
                  150840
Seq. No.
Seq. ID
                  LIB3175-046-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q731529
BLAST score
                  189
E value
                  3.0e-14
Match length
                  127
                  37
% identity
                  HYPOTHETICAL 92.5 KD PROTEIN IN BEM2-NCB1 INTERGENIC REGION
NCBI Description
                  >gi 1077719 pir S50660 hypothetical protein YER157w -
                  yeast (Saccharomyces cerevisiae) >qi 603397 (U18917)
                  Yer157wp [Saccharomyces cerevisiae]
                  150841
Seq. No.
                  LIB3175-046-P1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4376087
BLAST score
                  314
E value
                  1.0e-176
Match length
                  428
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
                  150842
Seq. No.
                  LIB3175-046-P1-K1-G8
Seq. ID
Method
                  BLASTX
                  g3928103
NCBI GI
BLAST score
                  481
                  2.0e-48
E value
Match length
                  102
% identity
NCBI Description
                  (AC005770) putative water channel protein [Arabidopsis
                  thalianal
                  150843
Seq. No.
                  LIB3175-046-P1-K1-H10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1708420
BLAST score
                  349
                  3.0e-33
E value
Match length
                  107
% identity
                  72
NCBI Description
                  ISOFLAVONE REDUCTASE HOMOLOG P3 >gi 1361992 pir S57613
                  isoflavonoid reductase homolog - Arabidopsis thaliana
                  >gi_886432_emb_CAA89859_ (Z49777) isoflavonoid reductase
```

## homologue [Arabidopsis thaliana]

150844 Seq. No. Seq. ID LIB3175-046-P1-K1-H11 Method BLASTX NCBI GI q122781 BLAST score 183 1.0e-13 E value Match length 47 68 % identity POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229) NCBI Description >gi 82210 pir A05198 hypothetical protein 229 - common tobacco chloroplast >gi 11844 emb CAA77364 (Z00044) hypothetical protein [Nicotiana tabacum] >gi\_225212\_prf\_\_1211235AT ORF 229 [Nicotiana tabacum] Seq. No. 150845 Seq. ID LIB3175-046-P1-K1-H12 Method BLASTN NCBI GI q4544381 BLAST score 65 E value 3.0e-28 Match length 88 100 % identity Arabidopsis thaliana chromosome II BAC F16F14 genomic NCBI Description sequence, complete sequence Seq. No. 150846 Seq. ID LIB3175-046-P1-K1-H3 Method BLASTX g1351411 NCBI GI BLAST score 144 E value 6.0e-25 Match length 92 % identity VACUOLAR PROCESSING ENZYME PRECURSOR (VPE) (PROTEINASE B) NCBI Description >gi 1076553 pir S49175 cysteine proteinase precursor spring vetch >gi 2129906 pir S68984 cysteine proteinase precursor - spring vetch >gi 510358 emb CAA84383 (Z34899) cysteine proteinase [Vicia sativa] 150847 Seq. No. Seq. ID LIB3175-046-P1-K1-H4 Method BLASTX NCBI GI g4325346 BLAST score 586 E value 9.0e-61 Match length 134 % identity NCBI Description (AF128393) similar to N-ethylmaleimide sensitive fusion proteins; contains similarity to ATPases (Pfam: PF00004,

Score=307.7, E=1.4e-88n N=1) [Arabidopsis thaliana]

Seq. No. 150848 Seq. ID LIB3175-046-P1-K1-H5

Method BLASTX NCBI GI g2842469

NCBI GI

```
BLAST score
                  168
                  9.0e-12
E value
Match length
                  80
                  40
% identity
NCBI Description (AL021747) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.
                  150849
                  LIB3175-046-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2160135
BLAST score
                  349
E value
                  5.0e-33
Match length
                  91
                  79
% identity
                  (AC000375) Strong similarity to Arabidopsis
NCBI Description
                  gb_X91953,F19K23.1,F19K23.15. EST gb_ATTS0156 comes from
                  this gene. [Arabidopsis thaliana]
                  150850
Seq. No.
Seq. ID
                  LIB3175-047-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  g2842474
                  46
BLAST score
E value
                  3.0e-17
Match length
                  103
                  83
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F2009
NCBI Description
                  (ESSAII project)
                  150851
Seq. No.
Seq. ID
                  LIB3175-047-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  g16375
BLAST score
                  50
E value
                  2.0e-19
Match length
                  169
                  79
% identity
NCBI Description A.thaliana gene (LHCP AB 140) for chlorophyll a/b binding
                  protein
                  150852
Seq. No.
                  LIB3175-047-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  q2129672
BLAST score
                  192
                  8.0e-15
E value
                  89
Match length
% identity
                  52
NCBI Description
                  photosystem II reaction center protein, 6.1K - Arabidopsis
                  thaliana >gi 950023 emb CAA62296 (X90769) component of 6.1
                  kDa polypeptide of photosystem II reaction center
                  [Arabidopsis thaliana]
Seq. No.
                  150853
Seq. ID
                  LIB3175-047-P1-K1-B6
Method
                  BLASTN
```

19261

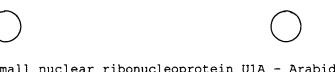
q4559375

E value

5.0e-18

```
BLAST score
                   3.0e-87
E value
Match length
                   194
% identity
                   96
                  Arabidopsis thaliana chromosome II BAC F11C10 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   150854
                  LIB3175-047-P1-K1-D11
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2564049
                  50
BLAST score
E value
                  2.0e-19
Match length
                  165
                   78
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MLE2, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150855
Seq. ID
                  LIB3175-047-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g1184164
BLAST score
                   37
E value
                  1.0e-11
Match length
                  130
                   78
% identity
                  Arabidopsis thaliana syntaxin-related knolle mRNA, complete
NCBI Description
Seq. No.
                  150856
                  LIB3175-047-P1-K1-D6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q905390
BLAST score
                   45
E value
                  1.0e-16
Match length
                  141
                   79
% identity
NCBI Description
                  Arabidopsis thaliana serine acetyltransferase (Sat-52)
                  mRNA, complete cds
Seq. No.
                  150857
Seq. ID
                  LIB3175-047-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g3342804
BLAST score
                  107
                  9.0e-18
E value
                  59
Match length
% identity
                   (AF061839) putative 6-phosphogluconate dehydrogenase [Zea
NCBI Description
                  mays]
                  150858
Seq. No.
Seq. ID
                  LIB3175-047-P1-K1-E3
                  {\tt BLASTX}
Method
NCBI GI
                  g3548811
BLAST score
                  218
```

```
Match length
                   86
% identity
                   53
                   (AC005313) kinetochore (SKPlp)-like protein [Arabidopsis
NCBI Description
                   thaliana]
                   150859
Seq. No.
Seq. ID
                   LIB3175-047-P1-K1-E4
Method
                   BLASTN
NCBI GI
                   g4159700
                   58
BLAST score
E value
                   4.0e-24
                   204
Match length
% identity
                   87
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K1L20, complete sequence
                   150860
Seq. No.
Seq. ID
                   LIB3175-047-P1-K1-E7
Method
                   BLASTN
NCBI GI
                   g2961335
BLAST score
                   44
E value
                   1.0e-15
Match length
                   99
                   83
% identity
                   Arabidopsis thaliana DNA chromosome 4, BAC clone F1N20
NCBI Description
                   (ESSAII project)
Seq. No.
                   150861
Seq. ID
                   LIB3175-047-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   g4220633
BLAST score
                   161
E value
                   1.0e-85
Match length
                   167
% identity
                   99
                   Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K7J8, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150862
Seq. ID
                   LIB3175-047-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   g4490291
BLAST score
                   155
E value
                   6.0e-82
Match length
                   231
% identity
                   92
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F17M5
NCBI Description
                   (ESSA project)
Seq. No.
                   150863
Seq. ID
                   LIB3175-047-P1-K1-F7
                   BLASTX
Method
NCBI GI
                   g2119046
BLAST score
                   463
E value
                   2.0e-46
Match length
                   101
% identity
                   92
```



NCBI Description small nuclear ribonucleoprotein U1A - Arabidopsis thaliana >gi\_1050430\_emb\_CAA90283\_ (Z49991) U1snRNP-specific protein [Arabidopsis thaliana] >gi\_2529669 (AC002535) U1snRNP-specific protein, U1A [Arabidopsis thaliana]

Seq. No. 150864

Seq. ID LIB3175-047-P1-K1-F9

Method BLASTX
NCBI GI 94753655
BLAST score 284
E value 1.0e-25
Match length 80
% identity 66

NCBI Description (AL049751) pectate lyase like protein [Arabidopsis

thaliana]

Seq. No.

150865

Seq. ID

LIB3175-047-P1-K1-G1

Method BLASTN
NCBI GI g4519192
BLAST score 107
E value 4.0e-53
Match length 206
% identity 97

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

MBK21, complete sequence

Seq. No. 150866

Seq. ID LIB3175-047-P1-K1-G2

Method BLASTX
NCBI GI g3834312
BLAST score 492
E value 6.0e-50
Match length 114
% identity 81

NCBI Description (AC005679) Strong similarity to glycoprotein EP1 gb L16983

Daucus carota and a member of S locus glycoprotein family

PF\_00954. ESTs gb\_AA067487, gb\_Z35737, gb\_Z30815, gb\_Z35350, gb\_AA713171, gb\_AI100553, gb\_Z34248,

gb AA728536, gb Z30816 an

Seq. No. 150867

Seq. ID LIB3175-047-P1-K1-G6

Method BLASTN
NCBI GI g2245126
BLAST score 45
E value 1.0e-16
Match length 126
% identity 81

NCBI Description Arabidopsis thaliana DNA chromosome 4, ESSA I contig

fragment No

Seq. No. 150868

Seq. ID LIB3175-047-P1-K1-G9

Method BLASTX NCBI GI g4512675 BLAST score 254

```
E value
                  2.0e-22
Match length
                  63
% identity
                  83
                  (AC006931) putative citrate synthase [Arabidopsis thaliana]
NCBI Description
                  150869
Seq. No.
                  LIB3175-047-P1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924257
BLAST score
                  65
                  3.0e-28
E value
Match length
                  159
                  43
% identity
NCBI Description
                  Tobacco chloroplast genome DNA
                  150870
Seq. No.
Seq. ID
                  LIB3175-047-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  g4757403
BLAST score
                  94
                  2.0e-45
E value
                  303
Match length
                  95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MJL12, complete sequence
                  150871
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g2981620
BLAST score
                  138
E value
                  7.0e-09
Match length
                  27
% identity
                  100
                  (AB008856) mutated 3-ketoacyl-CoA thiolase [Arabidopsis
NCBI Description
                  thaliana]
                  150872
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  g4733984
BLAST score
                  42
E value
                  7.0e-15
Match length
                  60
% identity
                  92
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F1404 genomic
                  sequence, complete sequence
Seq. No.
                  150873
Seq. ID
                  LIB3175-048-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g4056469
BLAST score
                  348
E value
                  5.0e-33
Match length
                  71
% identity
                  (AC005990) Strong similarity to gb M95166 ADP-ribosylation
NCBI Description
```

```
) (
```

factor from Arabidopsis thaliana. ESTs gb\_Z25826, gb\_R90191, gb\_N65697, gb\_AA713150, gb\_T46332, gb\_AA040967, gb\_AA712956, gb\_T46403, gb\_T46050, gb\_AI100391 and gb\_Z25043 come from t

Seq. No. 150874

Seq. ID LIB3175-048-P1-K1-A7

Method BLASTN
NCBI GI g2842474
BLAST score 260
E value 1.0e-144
Match length 295
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F2009

(ESSAII project)

Seq. No. 150875

Seq. ID LIB3175-048-P1-K1-A8

Method BLASTN
NCBI GI g4455262
BLAST score 157
E value 3.0e-83
Match length 181
% identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F17L22

(ESSAII project)

Seq. No. 150876

Seq. ID LIB3175-048-P1-K1-A9

Method BLASTN
NCBI GI g4584531
BLAST score 163
E value 1.0e-86
Match length 314
% identity 96

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T9E8

(ESSA project)

Seq. No. 150877

Seq. ID LIB3175-048-P1-K1-B1

Method BLASTX
NCBI GI g3319349
BLAST score 176
E-value 3.0e-13
Match length 38
% identity 95

NCBI Description (AF077407) No definition line found [Arabidopsis thaliana]

Seq. No. 150878

Seq. ID LIB3175-048-P1-K1-B10

Method BLASTX
NCBI GI g602764
BLAST score 240
E value 8.0e-21
Match length 51
% identity 92

NCBI Description (D43783) beta-amylase [Arabidopsis thaliana]

Seq. No. Seq. ID

Method

NCBI GI

E value

Seq. No. Seq. ID

NCBI GI ...

E value

Seq. No.

Seq. ID

Method

NCBI GI

E value

BLAST score

Match length

% identity

BLAST score

Match length % identity

Method

BLAST score

Match length

% identity

```
>gi 998369 bbs 163908 (S77076) beta-amylase {EC 3.2.1.2}
                  [Arabidopsis thaliana=thale cress, Heynh., Peptide, 498 aa]
                  [Arabidopsis thaliana]
                  150879
                  LIB3175-048-P1-K1-B11
                  BLASTN
                  g2618605
                  113
                  9.0e-57
                  262
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MUK11, complete sequence [Arabidopsis thaliana]
                  150880
                  LIB3175-048-P1-K1-B3
                  BLASTX
                  g120667
                  275
                  5.0e-41
                  97
NCBI Description
                  GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                  >gi 81622 pir JQ1287 glyceraldehyde-3-phosphate
                  dehydrogenase (EC 1.2.1.12), cytosolic - Arabidopsis
                  thaliana >gi_166706 (M64116) cystolic
                  glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis
                  thaliana] >gi_166710 (M64119) glyceraldehyde-3-phosphate
                  dehydrogenase [Arabidopsis thaliana]
                  150881
                  LIB3175-048-P1-K1-B4
                  BLASTX
                  g1922944
                  155
                  7.0e-11
                  32
                  100
                  (AC000106) Strong similarity to Picea histone H2A
NCBI Description
                  (gb_X67819). ESTs gb_ATTS3874, gb T46627, gb_T14194 come from
                  this gene. [Arabidopsis thaliana]
                  150882
                  LIB3175-048-P1-K1-B5
                  BLASTX
                  q542157
                  254
                  2.0e-22
```

Seq. No. Seq. ID Method

NCBI GI BLAST score E value Match length 62 81 % identity

NCBI Description ribosomal 5S RNA-binding protein - Rice

150883 Seq. No.

Seq. ID LIB3175-048-P1-K1-B6

Method BLASTX NCBI GI q3395425

```
BLAST score
                   444
                   2.0e-44
E value
                   96
Match length
                   54
% identity
                   (ACO04683) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
                   150884
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-C1
                  BLASTN
Method
NCBI GI
                   g4662640
BLAST score
                   275
                   1.0e-153
E value
                   324
Match length
                   25
% identity
                  Arabidopsis thaliana chromosome II BAC F15K19 genomic
NCBI Description
                  sequence, complete sequence
                   150885
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-C10
Method
                  BLASTX
NCBI GI
                   q557472
BLAST score
                   163
                   4.0e-11
E value
                   94
Match length
% identity
NCBI Description (U15178) arabinosidase [Bacteroides ovatus]
                   150886
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-C4
                  BLASTN
Method
NCBI GI
                   g16363
BLAST score
                   32
E value
                   1.0e-08
                   96
Match length
                   82
% identity
                  A.thaliana Lhb1B2 gene for photosystem II chlorophyll a/b
NCBI Description
                  binding protein
                   150887
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-C5
Method
                  BLASTN
NCBI GI
                   g4522002
BLAST score
                   78
E value
                   4.0e-36
Match length
                  98
                   96
% identity
                  Arabidopsis thaliana chromosome II BAC T23K3 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  150888
                  LIB3175-048-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g399013
BLAST score
                  444
E value
                  2.0e-44
Match length
                  105
```

```
% identity
NCBI Description ADP, ATP CARRIER PROTEIN 1 PRECURSOR (ADP/ATP TRANSLOCASE 1)
                  (ADENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1)
                  >gi_99658_pir__S21313 ADP,ATP carrier protein - Arabidopsis
                  thaliana (fragment) >gi_16175_emb_CAA46518_ (X65549)
                  adenylate translocator [Arabidopsis thaliana]
                  >gi 445607 prf 1909354A adenylate translocator
                  [Arabidopsis thaliana]
                  150889
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-D1
Method
                  BLASTX
NCBI GI
                  g115767
                  295
BLAST score
E value
                  6.0e-27
Match length
                  81
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-165/180) (LHCP) >gi 81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >qi 16368 emb CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >qi 16372 emb CAA27541 (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
Seq. No.
                  150890
Seq. ID
                  LIB3175-048-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g1172635
BLAST score
                  466
E value
                  5.0e-47
Match length
                  97
% identity
                  96
                  26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING
NCBI Description
                  PROTEIN HOMOLOG 2) >gi 556558 dbj BAA04615 (D17789) rice
                  homologue of Tat binding protein [Oryza sativa]
Seq. No.
                  150891
                  LIB3175-048-P1-K1-D12
Seq. ID
Method
                  BLASTN
NCBI GI
                  q2529657
BLAST score
                  42
E value
                  1.0e-14
Match length
                  135
% identity
                  78
                  Arabidopsis thaliana chromosome II BAC T30B22 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150892
                  LIB3175-048-P1-K1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519192
BLAST score
                  112
E value
                  4.0e-56
Match length
                  334
% identity
```

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

. .

## MBK21, complete sequence

```
150893
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-D6
Method
                  BLASTX
NCBI GI
                   g3913651
BLAST score
                   227
                   7.0e-19
E value
                   104
Match length
                   46
% identity
NCBI Description FERREDOXIN--NADP REDUCTASE, LEAF-TYPE ISOZYME PRECURSOR
                   (FNR) >gi 2225993 emb CAA74359 (Y14032)
                   ferredoxin--NADP(+) reductase [Nicotiana tabacum]
Seq. No.
                   150894
Seq. ID
                   LIB3175-048-P1-K1-D7
                   BLASTX
Method
NCBI GI
                   g2181180
BLAST score
                   178
                   4.0e-13
E value
                   91
Match length
% identity
                   42
NCBI Description (Z84377) xylosidase [Aspergillus niger]
                   150895
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-E1
Method
                  BLASTX
NCBI GI
                   g2832661
BLAST score
                   265
                   2.0e-23
E value
Match length
                   101
                   59
% identity
                   (AL021710) pherophorin - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   150896
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-E2
Method
                  BLASTN
                   g4063730
NCBI GI
BLAST score
                   73
E value
                   2.0e-33
Match length
                   119
                   97
% identity
NCBI Description
                  Arabidopsis thaliana BAC F21J6 from chromosome V,
                   containing KNAT3 and mapping near 60.5 cM, complete
                   sequence [Arabidopsis thaliana]
Seq. No.
                   150897
Seq. ID
                  LIB3175-048-P1-K1-E5
Method
                  BLASTN
NCBI GI
                   g4454587
BLAST score
                   39
E value
                   5.0e-13
Match length
                   109
% identity
                   89
NCBI Description
                  Arabidopsis thaliana BAC F21A20 from chromosome V near 61
```

cM, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                   150898
Seq. ID
                   LIB3175-048-P1-K1-E8
Method
                   BLASTN
NCBI GI
                   g3785968
BLAST score
                   163
E value
                   1.0e-86
                   280
Match length
                   97
% identity
                  Arabidopsis thaliana chromosome II BAC F2I9 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150899
Seq. ID
                   LIB3175-048-P1-K1-F10
Method
                   BLASTN
NCBI GI
                   g2244950
BLAST score
                   318
E value
                   1.0e-179
                   341
Match length
                   99
% identity
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
Seq. No.
                   150900
Seq. ID
                   LIB3175-048-P1-K1-F12
Method
                   BLASTN
NCBI GI
                   g472876
BLAST score
                   52
E value
                   2.0e-20
Match length
                   119
                   82
% identity
NCBI Description A.thaliana mRNA for plasma membrane intrinsic protein 2a
Seq. No.
                   150901
Seq. ID
                   LIB3175-048-P1-K1-F3
Method
                   BLASTN
NCBI GI
                   g2749918
BLAST score
                   33
E value
                   6.0e-09
Match length
                   124
                   86
% identity
                  Arabidopsis thaliana chromosome I BAC F3I6 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150902
Seq. ID
                  LIB3175-048-P1-K1-F4
Method
                  BLASTN
NCBI GI
                   g3327922
                   60
BLAST score
E value
                   2.0e-25
Match length
                  124
                   84
% identity
                  Arabidopsis thaliana chromosome II BAC T31E10 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150903
Seq. ID
                  LIB3175-048-P1-K1-F5
```

BLASTX Method NCBI GI g2499610 BLAST score 537 E value 4.0e-55 Match length 120 % identity 88 MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG 6 (MAP KINASE 6) NCBI Description (ATMPK6) >gi\_629547\_pir\_\_S40472 mitogen-activated protein kinase 6 (EC 2.7.1.-) - Arabidopsis thaliana >gi 457404 dbj BAA04869 (D21842) MAP kinase [Arabidopsis thaliana] >gi 2281091 (AC002333) MAP Kinase 6 [Arabidopsis thaliana] 150904 Seq. No. Seq. ID LIB3175-048-P1-K1-F7 Method BLASTN NCBI GI q3033373 BLAST score 101 1.0e-49 E value 309 Match length 95 % identity NCBI Description Arabidopsis thaliana chromosome II BAC F19I3 genomic sequence, complete sequence [Arabidopsis thaliana] 150905 Seq. No. Seq. ID LIB3175-048-P1-K1-G1 Method BLASTN NCBI GI g531378 BLAST score 58 2.0e-24 E value 149 Match length % identity 81 NCBI Description A.thaliana RCI1B mRNA 150906 Seq. No. Seq. ID LIB3175-048-P1-K1-G8 Method **BLASTX** NCBI GI g3983125 BLAST score 214 9.0e-18 E value Match length 52 % identity NCBI Description (AF097648) phosphate/triose-phosphate translocator precursor [Arabidopsis thaliana] 150907 Seq. No. Seq. ID LIB3175-048-P1-K1-H1 Method BLASTN NCBI GI g4165340 BLAST score 90 E value 4.0e-43 Match length 266 80 % identity NCBI Description Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 150908

```
Seq. ID
                  LIB3175-048-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2119846
BLAST score
                  526
                  5.0e-54
E value
Match length
                  98
% identity
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >gi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >gi 3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >gi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
                  150909
Seq. No.
Seq. ID
                  LIB3175-048-P1-K1-H5
Method
                  BLASTN
                                     . 'S
NCBI GI
                  g2656031
BLAST score
                  67
E value
                  2.0e-29
Match length
                  139
% identity
                  83
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MXC20
Seq. No.
                  150910
Seq. ID
                  LIB3175-048-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g3763932
BLAST score
                  333
E value
                  3.0e-31
                  94
Match length
% identity
NCBI Description (AC004450) putative protein kinase [Arabidopsis thaliana]
Seq. No.
                  150911
Seq. ID
                  LIB3175-049-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  g4376087
BLAST score
                  65
E value
                  3.0e-28
Match length
                  153
% identity
                  82
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
                  fragment No
Seq. No.
                  150912
Seq. ID
                  LIB3175-049-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  g4467094
BLAST score
                  39
E value
                  5.0e-13
Match length
                  117
% identity
NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone F20D10
                  (ESSA project)
```

```
150913
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g2832717
BLAST score
                  470
                  3.0e-47
E value
                  118
Match length
                  75
% identity
                  (AJ003114) alkaline/neutral invertase [Lolium temulentum]
NCBI Description
                  150914
Seq. No.
                  LIB3175-049-P1-K1-A3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1345595
BLAST score
                  386
E value
                  2.0e-37
Match length
                  110
% identity
                  62
NCBI Description
                  14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
                  >gi_1084332_pir__ S53727 14-3-3-like protein (ATF1) -
                  Arabidopsis thaliana >gi 953221 (U02565) 14-3-3-like
                  protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14
                  lambda [Arabidopsis thaliana]
                  150915
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g4454004
BLAST score
                  318
E value
                  1.0e-179
Match length
                  345
% identity
                  99
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F24A6
                  (ESSAII project)
                  150916
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  q4646229
BLAST score
                  82
E value
                  2.0e-38
Match length
                  209
% identity
                  Arabidopsis thaliana chromosome II BAC F27A10 genomic
NCBI Description
                  sequence, complete sequence
                  150917
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  g4510338
BLAST score
                  88
E value
                  6.0e-42
Match length
                  259
% identity
                  79
                  Arabidopsis thaliana chromosome II BAC F2H17 genomic
NCBI Description
                  sequence, complete sequence
```

```
150918
Seq. No.
                  LIB3175-049-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3915823
BLAST score
                  159
E value
                  3.0e-11
Match length
                  30
                  100
% identity
NCBI Description [Segment 1 of 2] 60S RIBOSOMAL PROTEIN L5
                  150919
Seq. No.
                  LIB3175-049-P1-K1-B5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2306917
BLAST score
                  425
E value
                  4.0e-42
                  96
Match length
% identity
                  (AF003728) plasma membrane intrinsic protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  150920
                  LIB3175-049-P1-K1-B6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924505
BLAST score
                  252
E value
                  1.0e-139
Match length
                  349
                  96
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone M4E13
NCBI Description
                   (ESSAII project)
Seq. No.
                  150921
Seq. ID
                  LIB3175-049-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g1628582
BLAST score
                  50
E value
                  3.0e-19
Match length
                  116
                  48
% identity
NCBI Description
                  Arabidopsis thaliana 12S cruciferin seed storage protein
                   (ATCRU3) gene, complete cds
Seq. No.
                  150922
                  LIB3175-049-P1-K1-C12
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2894557
BLAST score
                  48
E value
                  4.0e-18
Match length
                  119
% identity
                  82
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T805
NCBI Description
                  (ESSAII project)
Seq. No.
                  150923
                  LIB3175-049-P1-K1-D2
Seq. ID
```

```
Method
                  BLASTN
NCBI GI
                  g4589427
BLAST score
                  116
E value
                  1.0e-58
                  136
Match length
% identity
                  96
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MFG13, complete sequence
                  150924
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-D3
Method
                  BLASTX
                  q2145358
NCBI GI
BLAST score
                  388
E value
                  8.0e-38
                  95
Match length
% identity
                  81
NCBI Description (Y10922) HD-Zip protein [Arabidopsis thaliana]
Seq. No.
                  150925
Seq. ID
                  LIB3175-049-P1-K1-E10
Method
                  BLASTX
NCBI GI
                  g2842477
BLAST score
                  481
E value
                  1.0e-48
Match length
                  111
                  79
% identity
NCBI Description
                  (AL021749) copper-binding protein-like [Arabidopsis
                  thaliana]
Seq. No.
                  150926
Seq. ID
                  LIB3175-049-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g16446
BLAST score
                  38
E value
                  3.0e-12
Match length
                  151
                  85
% identity
NCBI Description A.thaliana gene for photosystem II 10 kDa polypeptide
                  150927
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-F7
Method
                  BLASTN
NCBI GI
                  g3510343
BLAST score
                  36
E value
                  6.0e-11
Match length
                  132
% identity
                  81
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
                  150928
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-F8
Method
                  BLASTN
NCBI GI
                  g4006885
BLAST score
                  61
E value
                  6.0e-26
```

```
104
Match length
% identity
                  87
                  Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig
NCBI Description
                  fragment No
                  150929
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-G5
                  BLASTN
Method
                  g2244991
NCBI GI
BLAST score
                  47
                  2.0e-17
E value
Match length
                  182
                  79
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
                  150930
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  g58298
                  38
BLAST score
                  2.0e-12
E value
                  154
Match length
                  79
% identity
                  Synthetic DNA for A.thaliana ats1A leader spliced to
NCBI Description
                  B.thuringiensis CryIA(c)
                  150931
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-H11
                  BLASTN
Method
NCBI GI
                  g2924652
BLAST score
                  74
                  5.0e-34
E value
Match length
                  80
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K9L2, complete sequence [Arabidopsis thaliana]
                  150932
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g99688
BLAST score
                  299
E value
                  2.0e-27
Match length
                  94
% identity
                  translation elongation factor eEF-1 alpha chain (gene A4) -
NCBI Description
                  Arabidopsis thaliana >gi_295789_emb_CAA34456_ (X16432)
                  elongation factor 1-alpha [Arabidopsis thaliana]
                  150933
Seq. No.
Seq. ID
                  LIB3175-049-P1-K1-H3
Method
                  BLASTN
NCBI GI
                  g3250673
BLAST score
                  46
E value
                  3.0e-17
Match length
                  109
```

```
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5
                  (ESSAII project)
                  150934
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-A11
Method
                  BLASTN
NCBI GI
                  g3309276
BLAST score
                  63
                  2.0e-27
E value
Match length
                  71
% identity
                  97
                  Arabidopsis thaliana BAC T26N6 from chromosome IV at 19.3
NCBI Description
                  cM, complete sequence
                  150935
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g1527221
BLAST score
                  576
E value
                  3.0e-60
                  114
Match length
% identity
                  97
NCBI Description (U68219) catalase [Brassica napus]
                  150936
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-A3
Method
                  BLASTX
NCBI GI
                  g3451065
BLAST score
                  530
E value
                  2.0e-54
Match length
                  104
% identity
                  98
NCBI Description
                  (AL031326) water channel - like protein [Arabidopsis
                  thaliana]
                  150937
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  g3849811
BLAST score
                  174
                  2.0e-93
E value
Match length
                  178
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC T2P11 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150938
Seq. ID
                  LIB3175-050-P1-K1-B6
Method
                  BLASTX
NCBI GI
                  q1076387
BLAST score
                  439
E value
                  1.0e-43
Match length
                  100
% identity
                  88
NCBI Description
                  protein kinase homolog - Arabidopsis thaliana
                  >gi_717180_emb_CAA55866_ (X79279) protein kinase homologous
```

NCBI Description

```
to shaggy and glycogen synthase kinase-3 [Arabidopsis
                  thaliana]
                  150939
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  q4220638
BLAST score
                  62
E value
                   9.0e-27
                  85
Match length
                   95
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MIF21, complete sequence [Arabidopsis thaliana]
                   150940
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g1490552
BLAST score
                  265
E value
                   1.0e-147
                  284
Match length
% identity
                   99
                  Arabidopsis thaliana S-adenosylmethionine decarboxylase
NCBI Description
                   (SAMdc) mRNA, complete cds
                   150941
Seq. No.
                  LIB3175-050-P1-K1-E11
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4519192
BLAST score
                  62
E value
                   2.0e-26
Match length
                  173
                   97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MBK21, complete sequence
                   150942
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g2584827
BLAST score
                  360
E value
                  0.0e+00
                  453
Match length
                   96
% identity
NCBI Description
                  Arabidopsis thaliana chromosome 1 BAC F12F1 sequence,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  150943
Seq. ID
                  LIB3175-050-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g3776559
BLAST score
                  232
E value
                  7.0e-20
                  58
Match length
                  71
% identity
                  (ACO05388) Strong similarity to gene F14J9.26 gi_3482933
```

cdc2 protein kinase homolog from A. thaliana BAC

```
gb AC003970. ESTs gb Z35332 and gb F19907 come from this
                  gene. [Arabidopsis thaliana]
                  150944
Seq. No.
                  LIB3175-050-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g115480
BLAST score
                  434
                   3.0e-43
E value
Match length
                  88
% identity
NCBI Description
                  CALMODULIN-1 >gi 166649 (M38379) calmodulin-1 [Arabidopsis
                  thaliana]
                  150945
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-E6
Method
                  BLASTN
NCBI GI
                  g4199934
BLAST score
                  167
                   4.0e-89
E value
                  229
Match length
                  95
% identity
NCBI Description
                  Genomic sequence for Arabidopsis thaliana BAC T3P18,
                  complete sequence [Arabidopsis thaliana]
Seq. No.
                  150946
Seq. ID
                  LIB3175-050-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g99699
BLAST score
                  606
E value
                  3.0e-63
Match length
                  116
                  96
% identity
NCBI Description
                  glutamate--ammonia ligase (EC 6.3.1.2), cytosolic (clone
                  lambdaAtgsr1) - Arabidopsis thaliana
                  150947
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  g4757404
BLAST score
                  73
E value
                  3.0e-33
Match length
                  77
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MLJ15, complete sequence
                  150948
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-F1
Method
                  BLASTN
                g4519193
NCBI GI
BLAST score
                  139
E value
                  4.0e-72
Match length
                  448
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
```

MDC11, complete sequence

```
150949
Seq. No.
Seq. ID
                    LIB3175-050-P1-K1-F10
Method
                    BLASTX
NCBI GI
                    q1778141
BLAST score
                    220
                    4.0e-18
E value
Match length
                    55
% identity
                    80
                    (U66321) phosphate/phosphoenolpyruvate translocator
NCBI Description
                    precursor; PPT [Arabidopsis thaliana]
                    150950
Seq. No.
                    LIB3175-050-P1-K1-F3
Seq. ID
                    BLASTX
Method
NCBI GI
                    q553038
                    268
BLAST score
                    6.0e-24
E value
Match length
                    62
% identity
                    (M58464) beta-1,3-glucanase [Arabidopsis thaliana]
NCBI Description
                    150951
Seq. No.
                    LIB3175-050-P1-K1-F6
Seq. ID
Method
                    BLASTN
NCBI GI
                    g4757405
BLAST score
                    75
E value
                    3.0e - 34
                    245
Match length
% identity
                    96
                    Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                    MOJ10, complete sequence
Seq. No.
                    150952
Seq. ID
                    LIB3175-050-P1-K1-G11
Method
                    BLASTX
NCBI GI
                    q1175011
BLAST score
                    518
                    5.0e-53
E value
Match length
                    102
                    97
% identity
                    PLASMA MEMBRANE INTRINSIC PROTEIN 1B (TRANSMEMBRANE PROTEIN
NCBI Description
                    A) (TMP-A) >gi_296085_emb_CAA48356_ (X68293) transmembrane protein [Arabidopsis thaliana] >gi_3386599 (AC004665) plasma membrane intrinsic protein 1B [Arabidopsis thaliana]
Seq. No.
                    150953
                    LIB3175-050-P1-K1-G12
Seq. ID
Method
                    BLASTX
NCBI GI
                    q2618723
BLAST score
                    87
E value
                    5.0e-41
Match length
                    115
% identity
                    (U49073) IAA17 [Arabidopsis thaliana] >gi 2921756
NCBI Description
                    (AF040631) IAA17/AXR3 protein [Arabidopsis thaliana]
                    >gi 4389514 gb AAB70451 (AC000104) Identical to
```

Seq. No. Seq. ID

```
Arabidopsis gb_AF040632 and gb_U49073 IAA17/AXR3 gene. ESTs gb_H36782 and gb_F14074 come from this gene. [Arabidopsis thaliana]
```

```
150954
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-G2
Method
                  BLASTN
NCBI GI
                  g469109
BLAST score
                  154
                  3.0e-81
E value
Match length
                  241
% identity
                  94
NCBI Description A.thaliana (Columbia) Di19 mRNA
                  150955
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  g3402751
BLAST score
                  504
                  2.0e-62
E value
                  121
Match length
% identity
                  48
NCBI Description (AL031187) putative protein [Arabidopsis thaliana]
Seq. No.
                  150956
                 LIB3175-050-P1-K1-H12
Seq. ID
Method
                  BLASTX
                              . . .
NCBI GI
                  g3184281
BLAST score
                  418
E value
                  3.0e-41
Match length
                  101
% identity
                  86
NCBI Description (AC004136) putative cytochrome P450 [Arabidopsis thaliana]
                  150957
Seq. No.
Seq. ID
                  LIB3175-050-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g1495273
BLAST score
                  482
E value
                  7.0e-49
                  97
Match length
% identity
NCBI Description (Z50752) sugar transporter [Arabidopsis thaliana]
Seq. No.
                  150958
                  LIB3175-050-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4581146
BLAST score
                  632
E value
                  3.0e-66
                  125
Match length
% identity
NCBI Description
                  (AC006919) putative fructose-bisphosphate aldolase,
                  cytoplasmic [Arabidopsis thaliana]
```

150959

LIB3175-050-P1-K1-H6

BLAST score

```
Method
                  BLASTX
NCBI GI
                  g3522945
BLAST score
                  325
                  5.0e - 32
È value
Match length
                  114
                  71
% identity
NCBI Description
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
Seq. No.
                  150960
                  LIB3175-050-P1-K1-H8
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924730
BLAST score
                  49
                  1.0e-18
E value
                  65
Match length
                  73
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MPI7, complete sequence [Arabidopsis thaliana]
                  150961
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g3176874
BLAST score
                  480
E value
                  3.0e-63
Match length
                  148
                  89
% identity
                   (AF065639) cucumisin-like serine protease [Arabidopsis
NCBI Description
                  thaliana]
                  150962
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-A12
Method
                  BLASTN
NCBI GI
                  q3063438
BLAST score
                  424
                  0.0e + 00
E value
                  459
Match length
                  98
% identity
                  Complete sequence of Arabidopsis F22013, complete sequence
NCBI Description
                  [Arabidopsis thaliana]
                  150963
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-A2
Method
                  BLASTN
NCBI GI
                  g3128134
BLAST score
                  106
                  1.0e-52
E value
Match length
                  272
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K18G13, complete sequence [Arabidopsis thaliana]
                  150964
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  g2182285
```

```
0.0e + 00
E value
Match length
                  411
% identity
                  98
NCBI Description
                  Sequence of BAC F5I14 from Arabidopsis thaliana chromosome
                  1, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150965
                  LIB3175-051-P1-K1-A6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3702735
BLAST score
                  298
E value
                  1.0e-167
Match length
                  373
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150966
                  LIB3175-051-P1-K1-A7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3334659
BLAST score
                  232
E value
                  3.0e-19
Match length
                  100
% identity
                  50
NCBI Description. (Y10489) putative cytochrome P450 [Glycine max]
Seq. No.
                  150967
Seq. ID
                  LIB3175-051-P1-K1-A8
Method
                  BLASTN
NCBI GI
                  q3869067
BLAST score
                  146
E value
                  2.0e-76
Match length
                  405
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MCK7, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150968
Seq. ID
                  LIB3175-051-P1-K1-A9
Method
                  BLASTN
NCBI GI
                  q4589969
BLAST score
                  194
E value
                  1.0e-105
Match length
                  454
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F1P15 genomic
                  sequence, complete sequence
                  150969
Seq. No.
                  LIB3175-051-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2570223
BLAST score
                  43
E value
                  5.0e-15
Match length
                  107
% identity
                  90
```

```
NCBI Description Arabidopsis thaliana chromosome 1 BAC F20D22 sequence,
                  complete sequence [Arabidopsis thaliana]
                  150970
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-B11
Method
                  BLASTX
NCBI GI
                  g3925363
BLAST score
                  534
E value
                  1.0e-54
Match length
                  137
                  74
% identity
NCBI Description
                 (AF067961) homeodomain protein [Malus domestica]
                  150971
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g2088638
BLAST score
                  394
E value
                  0.0e + 00
Match length
                  414
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC T28M21 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  150972
Seq. ID
                  LIB3175-051-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g4689386
BLAST score
                  355
E value
                  1.0e-33
Match length
                  139
                  55
% identity
                  (AF139468) photosystem I reaction center subunit III [Vigna
NCBI Description
                  radiata]
                  150973
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g3157928
BLAST score
                  142
E value
                  4.0e-09
Match length
                  52
% identity
NCBI Description
                  (AC002131) Similar to fumarylacetoacetate hydrolase,
                  gb L41670 from Emericella nidulans. [Arabidopsis thaliana]
Seq. No.
                  150974
Seq. ID
                  LIB3175-051-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  g1171059
BLAST score
                  156
E value
                  2.0e-10
Match length
                  29
                  93
% identity
NCBI Description METALLOTHIONEIN-LIKE PROTEIN 1A (MT-1A) (MT-Q)
                  >gi_1361995_pir__S57858 metallothionein la - Arabidopsis
                  thaliana >gi_555978 (U15130) metallothionein-like protein
```

[Arabidopsis thaliana] >gi 1086457 (U11253) metallothionein [Arabidopsis thaliana] >gi\_1580893\_prf\_\_2116236B metallothionein 2 [Arabidopsis thaliana]

150975 Seq. No.

Seq. ID LIB3175-051-P1-K1-B7

Method BLASTX g2194132 NCBI GI BLAST score 246 7.0e-21 E value 80 Match length % identity 33

(AC002062) No definition line found [Arabidopsis thaliana] NCBI Description

150976 Seq. No.

Seq. ID LIB3175-051-P1-K1-B9

BLASTN Method NCBI GI g3128142 BLAST score 380 E value 0.0e + 00445 Match length 100 % identity

Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: NCBI Description

MQN23, complete sequence [Arabidopsis thaliana]

150977 Seq. No.

LIB3175-051-P1-K1-C12 Seq. ID

BLASTX Method NCBI GI g3329368 BLAST score 451 3.0e-47 E value Match length 106 % identity 92

NCBI Description (AF031244) nodulin-like protein [Arabidopsis thaliana]

150978 Seq. No.

LIB3175-051-P1-K1-C2 Seq. ID

Method BLASTX NCBI GI g3892050 BLAST score 393 E value 4.0e-38 Match length 112 % identity

NCBI Description (AC002330) hypothetical protein [Arabidopsis thaliana]

Seq. No. 150979

Seq. ID LIB3175-051-P1-K1-C4

Method BLASTN NCBI GI g2088638 BLAST score 156 E value 2.0e-82 280 Match length 89 % identity

Arabidopsis thaliana chromosome II BAC T28M21 genomic NCBI Description

sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 150980

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```
LIB3175-051-P1-K1-C5
Seq. ID
                   BLASTX
Method
                   g4585882
NCBI GI
                   110
BLAST score
                   2.0e-30
E value
Match length
                   88
% identity
NCBI Description
                   (AC005850) PSI type III chlorophyll a/b-binding protein
                   [Arabidopsis thaliana]
                   150981
Seq. No.
Seq. ID
                   LIB3175-051-P1-K1-C6
Method
                   BLASTN
NCBI GI
                   g3702735
BLAST score
                   346
                   0.0e+00
E value
                   434
Match length
                   99
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                   MQL5, complete sequence [Arabidopsis thaliana]
Seq. No.
                   150982
                   LIB3175-051-P1-K1-C7
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2129659
                   477
BLAST score
                   6.0e-48
E value
                   142
Match length
                   72
% identity
NCBI Description
                   oleosin, isoform 21K - Arabidopsis thaliana >gi_725260
                   (L40954) oleosin [Arabidopsis thaliana]
                   150983
Seq. No.
Seq. ID
                   LIB3175-051-P1-K1-C8
Method
                   BLASTX
NCBI GI
                   g510880
BLAST score
                   395
                   2.0e-38
E value
Match length
                   138
                   57
% identity
NCBI Description (X80067) putative aspartic protease [Brassica oleracea]
Seq. No.
                   150984
Seq. ID
                   LIB3175-051-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g135627
BLAST score
                   333
E value
                   4.0e-31
Match length
                   66
                   100
% identity
                   TRANSCRIPTION INITIATION FACTOR TFIID-2 (TATA-BOX FACTOR 2)
NCBI Description
                   (TATA SEQUENCE-BINDING PROTEIN 2) (TBP-2)
                   >gi_99764_pir__S10945 transcription initiation factor IID
(clone At-1) - Arabidopsis thaliana >gi_16546_emb_CAA38742_
                   (X54995) transcription initiation factor II [Arabidopsis
                   thaliana] >gi_4204264 (AC005223) 43453 [Arabidopsis
                   thaliana] >gi_227073 prf__1613452A transcription initiation
```

% identity

NCBI Description

thaliana]

## factor TFIID-1 [Arabidopsis thaliana]

Seq. No. 150985 Seq. ID LIB3175-051-P1-K1-D10 Method BLASTX NCBI GI q4033469 BLAST score 405 E value 1.0e-48 Match length 129 59 % identity NCBI Description ARGININE/SERINE-RICH SPLICING FACTOR RSP41 >gi 1707370 emb CAA67799 (X99436) splicing factor [Arabidopsis thaliana] 150986 Seq. No. Seq. ID LIB3175-051-P1-K1-D3 Method BLASTN NCBI GI q4455168 BLAST score 253 1.0e-140 E value Match length 455 % identity 99 Arabidopsis thaliana DNA chromosome 4, BAC clone F10M10 NCBI Description (ESSAII project) Seq. No. 150987 Seq. ID LIB3175-051-P1-K1-D4 Method BLASTN NCBI GI g4713943 BLAST score 427 E value 0.0e + 00Match length 443 % identity 99 NCBI Description Arabidopsis thaliana chromosome 1 BAC T8K14 sequence, complete sequence Seq. No. 150988 Seq. ID LIB3175-051-P1-K1-D5 Method BLASTN NCBI GI q4159701 BLAST score 348 E value 0.0e + 00Match length 453 % identity 98 NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22G18, complete sequence Seq. No. 150989 Seq. ID LIB3175-051-P1-K1-D7 Method BLASTX NCBI GI g4580394 BLAST score 254 E value 8.0e-22 Match length 107

19288

(AC007171) putative fatty acid elongase [Arabidopsis

```
150990
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q730526
BLAST score
                  644
                  2.0e-67
E value
                  132
Match length
                  95
% identity
NCBI Description
                  60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG)
                  >gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis
                  thaliana >gi 404166 emb CAA53005 (X75162) BBC1 protein
                  [Arabidopsis thaliana] .
Seq. No.
                  150991
                  LIB3175-051-P1-K1-E11
Seq. ID
Method
                  BLASTX
                  g2983997
NCBI GI
BLAST score
                  226
E value
                  1.0e-18
Match length
                  96
% identity
                  47
NCBI Description (AE000749) hypothetical protein [Aquifex aeolicus]
Seq. No.
                  150992
Seq. ID
                  LIB3175-051-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g4519192
BLAST score
                  223
E value
                  1.0e-122
Match length
                  400
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MBK21, complete sequence
                  150993
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-E2
Method
                  BLASTX
NCBI GI
                  g1931640
BLAST score
                  158
E value
                  1.0e-10
Match length
                  98
% identity
NCBI Description
                  (U95973) Serine carboxypeptidase isolog [Arabidopsis
                  thaliana]
                  150994
Seq. No.
                  LIB3175-051-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3639089
BLAST score
                  741
                  6.0e-79
E value
Match length
                  151
% identity
                  (AF090445) phospholipase D1 [Brassica oleracea]
NCBI Description
                  >gi 4324969 gb AAD17208 (AF113918) phospholipase D1 -
                  [Brassica oleracea var. capitata]
```

```
Seq. No.
                  150995
                  LIB3175-051-P1-K1-E6
Seq. ID
Method
                  BLASTN
NCBI GI
                  q972928
BLAST score
                  210
E value
                   1.0e-114
Match length
                   353
                   92
% identity
                  Arabidopsis thaliana IAA13 (IAA13) gene, complete cds
NCBI Description
                  150996
Seq. No.
                  LIB3175-051-P1-K1-E7
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4586109
BLAST score
                   423
                   9.0e-42
E value
                  79
Match length
                  100
% identity
                   (AL049638) putative protein [Arabidopsis thaliana]
NCBI Description
                  150997
Seq. No.
                  LIB3175-051-P1-K1-E8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2791834
BLAST score
                   455
                   2.0e-47
E value
Match length
                  104
% identity
                   95
                   (AF041463) elongation factor 1-alpha [Manihot esculenta]
NCBI Description
Seq. No.
                  150998
                  LIB3175-051-P1-K1-E9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4417280
BLAST score
                   689
E value
                  8.0e-73
Match length
                  143
% identity
                  97
NCBI Description
                  (AC007019) putative ATP synthase [Arabidopsis thaliana]
Seq. No.
                  150999
                  LIB3175-051-P1-K1-F10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1346520
BLAST score
                  372
E value
                  1.0e-42
Match length
                  101
% identity
                  90
NCBI Description
                  S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE
                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)
                  >gi 790978 emb CAA56590 (X80362) S-adenosyl-L-methionine
                  synthetase [Brassica juncea]
                  151000
Seq. No.
                  LIB3175-051-P1-K1-F11
Seq. ID
Method
                  BLASTN
```

```
NCBI GI
                  q4662640
BLAST score
                  406
                  0.0e + 00
E value
                  430
Match length
                  99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F15K19 genomic
                  sequence, complete sequence
                  151001
Seq. No.
                  LIB3175-051-P1-K1-F12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g131360
BLAST score
                  201
E value
                  2.0e-15
Match length
                  40
                  100
% identity
NCBI Description
                  PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR
                  >gi 81727 pir S02115 photosystem II protein psbK precursor
                  - white mustard chloroplast >gi 12209 emb CAA31909
                  (X13558) K preprotein (AA -24 to 37) [Sinapis alba]
                  151002
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-F2
Method
                  BLASTX
NCBI GI.
                  q3193316
BLAST score
                  119
E value
                  2.0e-59
Match length
                  149
                  85
% identity
NCBI Description
                  (AF069299) contains similarity to nucleotide sugar
                  epimerases [Arabidopsis thaliana]
Seq. No.
                  151003
Seq. ID
                  LIB3175-051-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g2341035
BLAST score
                  319
E value
                  2.0e-29
Match length
                 - 61
% identity
NCBI Description
                   (AC000104) Match to Arabidopsis photolysase (PHH1) gene
                   (gb_X99061) and cryptochrome 2 apoprotein (CRY2)
                   (gb_U43397). ESTs gb_W43661 and gb_Z25638 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  151004
                  LIB3175-051-P1-K1-F4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4519192
BLAST score
                  79
E value
                  2.0e-36
Match length
                  229
```

Seq. No. 151005

88

% identity

NCBI Description

MBK21, complete sequence

Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:

```
Seq. ID
                  LIB3175-051-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3449321
BLAST score
                  371
E value
                  0.0e+00
Match length
                  431
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MTG10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151006
Seq. ID
                  LIB3175-051-P1-K1-F6
Method
                  BLASTX
NCBI GI
                  g4580392
BLAST score
                  452
E value
                  3.0e-45
Match length
                  112
% identity
                  88
NCBI Description (AC007171) hypothetical protein [Arabidopsis thaliana]
                  151007
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g1076316
BLAST score
                  184
E value
                  1.0e-15
Match length
                  61
% identity
                  56
NCBI Description
                  drought-induced protein Di19 - Arabidopsis thaliana
                  >gi_469110_emb_CAA55321_ (X78584) Di19 [Arabidopsis
                  thaliana]
Seq. No.
                  151008
                  LIB3175-051-P1-K1-F9
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4159706
BLAST score
                  60
E value
                  5.0e-26
Match length
                  60
% identity
                  100
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MGL6, complete sequence
Seq. No.
                  151009
                  LIB3175-051-P1-K1-G1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4335711
BLAST score
                  277
E value
                  1.0e-154
Match length
                  289
% identity
                  99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F9013 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151010
                  LIB3175-051-P1-K1-G10
Seq. ID
Method
                  BLASTX
```

```
NCBI GI
                  g3193285
BLAST score
                  570
                  7.0e-59
E value
Match length
                  131
                  82
% identity
NCBI Description
                  (AF069298) T14P8.18 gene product [Arabidopsis thaliana]
Seq. No.
                  151011
Seq. ID
                  LIB3175-051-P1-K1-G11
                  BLASTX
Method
                  q2494112
NCBI GI
BLAST score
                  801
                  6.0e-86
E value
                  152
Match length
                  99
% identity
                  (AC002376) Match to Arabidopsis ATHKCP (gb L40948). ESTs
NCBI Description
                  gb_ATTS0764, gb_R90646, gb_AA389809, gb_ATTS2615 come from
                  this gene. [Arabidopsis thaliana] >gi_3126868 (AF061570)
                  potassium channel beta subunit homolog [Arabidopsis
                  thaliana]
                  151012
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-G12
Method
                  BLASTN
                  q4757409
NCBI GI
BLAST score
                  116
                  2.0e-58
E value
Match length
                  464
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MVC8, complete sequence
Seq. No.
                  151013
Seq. ID
                  LIB3175-051-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g1709804
BLAST score
                  458
                  9.0e-46
E value
Match length
                  136
                  63
% identity
                  26S PROTEASE REGULATORY SUBUNIT S10B (P44) (CONSERVED
NCBI Description
                  ATPASE DOMAIN PROTEIN 44) >gi_1045497 (U36395) conserved
                  ATPase domain protein 44 [Spermophilus tridecemlineatus]
                  >gi 2213932 (AF006305) 26S proteasome regulatory subunit
                  [Homo sapiens]
Seq. No.
                  151014
Seq. ID
                  LIB3175-051-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  q2924728
BLAST score
                  118
                  1.0e-59
E value
Match length
                  457
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXH1, complete sequence [Arabidopsis thaliana]
```

```
Seq. No.
Seq. ID
                  LIB3175-051-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  q2351073
BLAST score
                  213
E value
                  1.0e-116
Match length
                  431
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYJ24, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151016
                  LIB3175-051-P1-K1-G9
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4454447
BLAST score
                  379
                  0.0e+00
E value
Match length
                  439
% identity
                  97
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F5H14 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151017
Seq. ID
                  LIB3175-051-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  q2119846
BLAST score
                  729
E value
                  2.0e-77
Match length
                  141
% identity
                  98
NCBI Description
                  chlorophyll a/b-binding protein type I precursor Lhb1B2 -
                  Arabidopsis thaliana >qi 16364 emb CAA45790 (X64460)
                  photosystem II type I chlorophyll a /b binding protein
                  [Arabidopsis thaliana] >qi 3128230 (AC004077) photosystem
                  II type I chlorophyll a/b binding protein [Arabidopsis
                  thaliana] >qi 3337371 (AC004481) photosystem II type I
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  151018
Seq. ID
                  LIB3175-051-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g2760320
BLAST score
                  599
E value
                  3.0e-62
Match length
                  127
% identity
NCBI Description
                  (AC002130) F1N21.4 [Arabidopsis thaliana]
Seq. No.
                  151019
Seq. ID
                  LIB3175-051-P1-K1-H12
Method
                  BLASTN
NCBI GI
                  g2656029
BLAST score
                  180
E value
                  1.0e-96
Match length
                  421
% identity
                  75
NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
```

```
MQB2
Seq. No.
                  151020
Seq. ID
                  LIB3175-051-P1-K1-H2
Method
                  BLASTX
                  g2494113
NCBI GI
BLAST score
                   323
                   4.0e-30
E value
                  108
Match length
% identity
                   56
                   (AC002376) Strong similarity to Musa pectate lyase
NCBI Description
                   (gb X92943). ESTs gb AA042458, gb ATTS4502, gb N38552 come
                   from this gene. [Arabidopsis thaliana]
Seq. No.
                  151021
Seq. ID
                  LIB3175-051-P1-K1-H9
                  BLASTX
Method
NCBI GI
                  g4191783
BLAST score
                  206
E value
                   3.0e-16
Match length
                  131
% identity
NCBI Description
                   (AC005917) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  151022
Seq. ID
                  LIB3175-052-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  q3953465
BLAST score
                  450
E value
                  8.0e-45
Match length
                  110
% identity
NCBI Description
                   (AC002328) F20N2.10 [Arabidopsis thaliana]
Seq. No.
                  151023
Seq. ID
                  LIB3175-052-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  q511080
BLAST score
                  260
E value
                  1.0e-144
Match length
                  260
% identity
                  100
NCBI Description A.thaliana HEM15 mRNA for ferrochelatase
Seq. No.
                  151024
                  LIB3175-052-P1-K1-A11
Seq. ID
Method
                  BLASTX
NCBI GI
                  g282865
BLAST score
                  635
E value
                  2.0e-66
Match length
                  128
% identity
NCBI Description
                  chlorophyll a/b-binding protein - Arabidopsis thaliana
                  >qi 16207 emb CAA39534 (X56062) chlorophyll A/B-binding
```

protein [Arabidopsis thaliana] >gi\_166644 (M85150)
chlorophyll a/b-binding protein [Arabidopsis thaliana]
>gi 4678304 emb CAB41095.1 (AL049655) chlorophyll

## (

## a/b-binding protein [Arabidopsis thaliana]

```
Seq. No.
                  151025
                  LIB3175-052-P1-K1-A12
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4585993
BLAST score
                   162
                   5.0e-11
E value
                   40
Match length
                   75
% identity
                   (AC005287) Similar to serine/threonine kinases [Arabidopsis
NCBI Description
                  thaliana]
                   151026
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-A6
Method
                  BLASTN
NCBI GI
                  g431259
BLAST score
                   43
E value
                   5.0e-15
Match length
                  109
% identity
                   83
                  Arabidopsis thaliana 16kDa ubiquitin conjugating enzyme
NCBI Description
                   (UBC1) gene, complete cds
                  151027
Seq. No.
                  LIB3175-052-P1-K1-A8
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2335089
BLAST score
                   61
E value
                   2.0e-26
Match length
                   92
% identity
                  Arabidopsis thaliana chromosome II BAC T11A7 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
                  151028
Seq. No.
                  LIB3175-052-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                   g2281081
BLAST score
                   244
E value
                   1.0e-135
Match length
                   454
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F18019 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151029
Seq. ID
                  LIB3175-052-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4586265
BLAST score
                  549
                  2.0e-56
E value
                  126
Match length
```

% identity 80 NCBI Description (A)

scription (AL049640) putative protein [Arabidopsis thaliana]

Seq. No. 151030

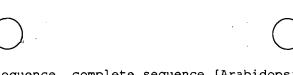
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LIB3175-052-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4039152
                  212
BLAST score
E value
                  6.0e-17
Match length
                  44
% identity
NCBI Description
                  (AF104221) low temperature and salt responsive protein
                  LTI6B [Arabidopsis thaliana] >gi 4325219 gb AAD17303
                  (AF122006) hydrophobic protein [Arabidopsis thaliana]
Seq. No.
                  151031
Seq. ID
                  LIB3175-052-P1-K1-B3
Method
                  BLASTN
                  g3985957
NCBI GI
BLAST score
                  44
E value
                  5.0e-16
                  82
Match length
                  96
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MYN8, complete sequence [Arabidopsis thaliana]
                  151032
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g4056506
BLAST score
                  610
E value
                  1.0e-63
                  124
Match length
                  98
% identity
NCBI Description (AC005896) nodulin-like protein [Arabidopsis thaliana]
Seq. No.
                  151033
Seq. ID
                  LIB3175-052-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  629
E value
                  8.0e-66
Match length
                  119
                  99
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi 16376 emb CAA27543 (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
                  151034
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-B9
Method
                  BLASTN
NCBI GI
                  g16174
                  51
BLAST score
E value
                  8.0e-20
Match length
                  212
% identity
                  76
NCBI Description A.thaliana ANT1 mRNA for adenylate translocator
Seq. No.
                  151035
                  LIB3175-052-P1-K1-C1
Seq. ID
```

```
Method
                  BLASTX
NCBI GI
                  g2894574
BLAST score
                  202
                  6.0e-16
E value
                  74
Match length
                  59
% identity
NCBI Description
                  (AL021890) peroxidase prxrl [Arabidopsis thaliana]
                  >gi_2961341_emb_CAA18099.1_ (AL022140) peroxidase prxr1
                  [Arabidopsis thaliana]
                  151036
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-C11
Method
                  BLASTX
NCBI GI
                  g2529682
BLAST score
                  300
E value
                  2.0e-27
Match length
                  113
                  57
% identity
                  (AC002535) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  151037
                  LIB3175-052-P1-K1-C7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1710780
BLAST score
                  377
E value
                  3.0e-36
Match length
                  111
                  68
% identity
NCBI Description
                  40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_
                  (X96613) cytoplasmic ribosomal protein S7 [Podospora
                  anserina]
Seq. No.
                  151038
Seq. ID
                  LIB3175-052-P1-K1-C8
Method
                  BLASTX
NCBI GI
                  q4415907
BLAST score
                  474
E value
                  1.0e-47
Match length
                  134
% identity
NCBI Description
                  (AC006282) 60S ribosomal protein L24 [Arabidopsis thaliana]
                  >gi_4581159 gb AAD24643.1 AC006919 21 (AC006919) putative
                  60S ribosomal protein L24 [Arabidopsis thaliana]
Seq. No.
                  151039
Seq. ID
                  LIB3175-052-P1-K1-D10
Method
                  BLASTX
NCBI GI
                  q3386565
BLAST score
                  408
E value
                  7.0e-40
Match length
                  148
% identity
                  (AF079588) 1-aminocyclopropane-1-carboxylate oxidase
NCBI Description
                  [Sorghum bicolor]
Seq. No.
                  151040
Seq. ID
                  LIB3175-052-P1-K1-D11
```

```
Method
                  BLASTN
NCBI GI
                  g3228389
BLAST score
                  156
                  3.0e-82
E value
                  470
Match length
                  86
% identity
                  Genomic sequence for Arabidopsis thaliana BAC F17L21,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  151041
Seq. No.
                  LIB3175-052-P1-K1-D12
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2827528
BLAST score
                  381
                  1.0e-36
E value
                  121
Match length
                  61
% identity
NCBI Description
                  (AL021633) predicted protein [Arabidopsis thaliana]
                  151042
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  q1483217
BLAST score
                  396
                  0.0e+00
E value
Match length
                  457
                  99
% identity
NCBI Description A.thaliana gene induced upon wounding stress
Seq. No.
                  151043
                  LIB3175-052-P1-K1-D3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q425194
BLAST score
                  687
E value
                  1.0e-72
Match length
                  146
                  92
% identity
NCBI Description
                   (L26243) heat shock protein [Spinacia oleracea] >gi 2660772
                   (AF034618) cytosolic heat shock 70 protein [Spinacia
                  oleracea]
                  151044
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g3914740
BLAST score
                  472
E value
                  2.0e-47
Match length
                  134
                  73
% identity
                  60S RIBOSOMAL PROTEIN L26 >gi 2160300 dbj BAA18941
NCBI Description
                  (D78495) ribosomal protein [Brassica rapa]
                  151045
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  g14342
BLAST score
                  78
```

```
E value
                   6.0e-36
Match length
                  164
% identity
                  84
                  A.thaliana mRNA for carbonic anhydrase
NCBI Description
Seq. No.
                  151046
                  LIB3175-052-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4567273
BLAST score
                  546
E value
                  3.0e-56
Match length
                  106
                  99
% identity
NCBI Description
                   (ACO06841) putative vacuolar proton ATPase subunit
                   [Arabidopsis thaliana]
                  151047
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  a99735
BLAST score
                  773
E value
                  1.0e-82
                  147
Match length
                  99
% identity
                  L-ascorbate peroxidase (EC 1.11.1.11) precursor -
NCBI Description
                  Arabidopsis thaliana (fragment)
                  151048
Seq. No.
                  LIB3175-052-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3540185
BLAST score
                  248
E value
                   4.0e-21
Match length
                  78
% identity
                   (AC004122) Highly Similar to branched-chain amino acid
NCBI Description
                  aminotransferase [Arabidopsis thaliana]
Seq. No.
                  151049
Seq. ID
                  LIB3175-052-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  q3831459
BLAST score
                  534
E value
                  1.0e-66
Match length
                  136
% identity
NCBI Description (AC005700) putative homeobox protein [Arabidopsis thaliana]
Seq. No.
                  151050
Seq. ID
                  LIB3175-052-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g3757512
BLAST score
                  242
E value
                  1.0e-133
Match length
                  444
                  100
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F12A24 genomic
```

% identity



sequence, complete sequence [Arabidopsis thaliana]

151051 Seq. No. Seq. ID LIB3175-052-P1-K1-E3 Method BLASTX q1172873 NCBI GI BLAST score 618 2.0e-64 E value 138 Match length 88 % identity NCBI Description CYSTEINE PROTEINASE RD21A PRECURSOR >qi 541857 pir JN0719 drought-inducible cysteine proteinase (EC 3.4.22.-) RD21A precursor - Arabidopsis thaliana >gi 435619 dbj BAA02374 (D13043) thiol protease [Arabidopsis thaliana] Seq. No. 151052 LIB3175-052-P1-K1-E7 Seq. ID BLASTX Method g2129659 NCBI GI BLAST score 303 1.0e-27 E value Match length 104 % identity 62 oleosin, isoform 21K - Arabidopsis thaliana >gi 725260 NCBI Description (L40954) oleosin [Arabidopsis thaliana] Seq. No. 151053 LIB3175-052-P1-K1-E8 Seq. ID Method BLASTX NCBI GI g4539405 BLAST score 631 E value 5.0e-66 Match length 127 % identity (AL049524) putative ribosomal protein L9, cytosolic NCBI Description [Arabidopsis thaliana] Seq. No. 151054 LIB3175-052-P1-K1-E9 Seq. ID Method BLASTX NCBI GI g3759184 BLAST score 257 E value 4.0e-22 Match length 107 % identity (AB018441) phi-1 [Nicotiana tabacum] NCBI Description Seq. No. 151055 Seq. ID LIB3175-052-P1-K1-F1 Method BLASTX q3979940 NCBI GI BLAST score 192 E value 1.0e-14 Match length 74

NCBI Description (AL034393) Y18D10A.3 [Caenorhabditis elegans]

```
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q4455180
BLAST score
                   655
E value
                   8.0e-69
Match length
                   150
% identity
                   88
NCBI Description
                  (AL035521) putative protein [Arabidopsis thaliana]
Seq. No.
                   151057
                   LIB3175-052-P1-K1-F12
Seq. ID
Method
                  BLASTN
NCBI GI
                   g3152602
BLAST score
                   58
E value
                   6.0e-24
Match length
                   181
% identity
                   86
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F27L4 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   151058
                   LIB3175-052-P1-K1-F2
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4586265
BLAST score
                   495
E value
                   4.0e-50
Match length
                   112
% identity
NCBI Description
                   (AL049640) putative protein [Arabidopsis thaliana]
Seq. No.
                   151059
                  LIB3175-052-P1-K1-F3
Seq. ID
Method
                  BLASTX
NCBI GI
                   g1363489
BLAST score
                   570
E value
                   7.0e-59
Match length
                   133
% identity
                   83
NCBI Description
                  thioglucosidase (EC 3.2.3.1) 3D precursor - Arabidopsis
                   thaliana >gi 984052 emb CAA61592 (X89413) thioglucoside
                   glucohydrolase [Arabidopsis thaliana]
Seq. No.
                   151060
Seq. ID
                  LIB3175-052-P1-K1-F4
Method
                  BLASTX
NCBI GI
                   q4220473
BLAST score
                   646
                  8.0e-68
E value
Match length
                  129
% identity
                   (AC006069) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  151061
                  LIB3175-052-P1-K1-F5
Seq. ID
Method
                  BLASTN
NCBI GI
                  q1154626
```

```
BLAST score
                   1.0e-31
E value
                   330
Match length
                   76
% identity
NCBI Description A.thaliana CHLH gene
                   151062
Seq. No.
Seq. ID
                   LIB3175-052-P1-K1-F9
Method
                   BLASTX
NCBI GI
                   g2129538
BLAST score
                   568
E value
                   1.0e-58
Match length
                   112
% identity
                   100
                  AT103 protein - Arabidopsis thaliana >gi 1033195 (U38232)
NCBI Description
                   AT103 [Arabidopsis thaliana]
Seq. No.
                   151063
Seq. ID
                   LIB3175-052-P1-K1-G1
Method
                   BLASTX
NCBI GI
                   g2160133
BLAST score
                   360
E value
                   3.0e-34
Match length
                   90
% identity
NCBI Description
                   (AC000375) Strong similarity to Arabidopsis
                   gb X91953,F19K23.3,F19K23.15. ESTs
                   gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this
                   gene. [Arabidopsis thaliana]
Seq. No.
                   151064
Seq. ID
                   LIB3175-052-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   q2264378
BLAST score
                   612
E value
                   7.0e-64
Match length
                   133
% identity
                   89
NCBI Description
                   (AC002354) putative bZIP-like transcription factor
                   [Arabidopsis thaliana]
Seq. No.
                   151065
Seq. ID
                   LIB3175-052-P1-K1-G12
Method
                   BLASTN
NCBI GI
                   q1041701
BLAST score
                   74
                   9.0e-34
E value
Match length
                   90
% identity
NCBI Description
                  Arabidopsis thaliana expansin At-EXP1 (At-EXP1) mRNA,
                  partial cds
Seq. No.
                   151066
Seq. ID
                   LIB3175-052-P1-K1-G5
Method
                  BLASTN
NCBI GI
                   g886427
BLAST score
                   54
```

```
E value
                   2.0e-21
Match length
                   322
% identity
                   76
                  A.thaliana mRNA for zeta-crystallin homologue
NCBI Description
Seq. No.
                   151067
                  LIB3175-052-P1-K1-G7
Seq. ID
Method
                  BLASTN
                  g3449313
NCBI GI
BLAST score
                   164
E value
                   3.0e-87
Match length
                   299
                   89
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K21P3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151068
Seq. ID
                  LIB3175-052-P1-K1-G8
Method
                  BLASTX
NCBI GI
                   q4455253
BLAST score
                   685
E value
                   2.0e-72
Match length
                  149
                  89
% identity
                   (AL035523) superoxide dismutase (EC 1.15.1.1)
NCBI Description
                   (Fe)(fragment) [Arabidopsis thaliana]
                  151069
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-G9
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score
                   600
E value
                   2.0e-62
Match length
                  125
% identity
NCBI Description
                   (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  151070
Seq. ID
                  LIB3175-052-P1-K1-H1
Method
                  BLASTX
NCBI GI
                  q2677828
BLAST score
                  324
E value
                   4.0e-30
Match length
                  84
% identity
NCBI Description
                  (U93166) cysteine protease [Prunus armeniaca]
Seq. No.
                  151071
Seq. ID
                  LIB3175-052-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g3873710
                                                                                 : 4
BLAST score
                  274
E value
                  2.0e-24
Match length
                  67
% identity
NCBI Description
                   (Z73102) predicted using Genefinder; similar to Zinc
```

19304

finger, C2H2 type; cDNA EST EMBL: M89161 comes from this

gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409 comes

Seq. No. 151072

Seq. ID LIB3175-052-P1-K1-H11

Method BLASTX
NCBI GI g3873710
BLAST score 246
E value 6.0e-21
Match length 82
% identity 54

% identity 54
NCBI Description (Z73102) predicted using Genefinder; similar to Zinc

finger, C2H2 type; cDNA EST EMBL:M89161 comes from this gene; cDNA EST EMBL:T01394 comes from this gene; cDNA EST EMBL:T02192 comes from this gene; cDNA EST EMBL:D71409

comes

 Seq. No.
 151073

 Seq. ID
 LIB3175-052-P1-K1-H12

 Method
 BLASTX

NCBI GI g3924603 BLAST score 506 E value 2.0e-51 Match length 149 % identity 70

NCBI Description (AF069442) putative WD-repeat protein [Arabidopsis

thaliana]

Seq. No. 151074

Seq. ID LIB3175-052-P1-K1-H2

Method BLASTX
NCBI GI g1514649
BLAST score 82
E value 3.0e-42
Match length 123

Match length 123 % identity 80

NCBI Description (X86021) potassium channel [Solanum tuberosum]

Seq. No. 151075

Seq. ID LIB3175-052-P1-K1-H5

Method BLASTN
NCBI GI g2828278
BLAST score 231

E value 1.0e-127 Match length 442 % identity 97

NCBI Description Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16

(ESSAII project)

Seq. No. 151076

Seq. ID LIB3175-052-P1-K1-H7

Method BLASTX
NCBI GI g115767
BLAST score 742
E value 5.0e-79
Match length 143

Seq. No.

Seq. ID

Method

151081

BLASTX

LIB3175-053-P1-K1-A12

```
% identity
NCBI Description
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-165/180) (LHCP) >gi_81603 pir A29280 chlorophyll
                  a/b-binding protein ab165 - Arabidopsis thaliana
                  >gi_16368_emb_CAA27540 (X03907) chlorophyll a/b binding
                  protein (LHCP AB 65) [Arabidopsis thaliana]
                  >gi_16372_emb_CAA27541_ (X03908) chlorophyll a/b binding
                  protein (LHCP AB 180) [Arabidopsis thaliana]
                  151077
Seq. No.
Seq. ID
                  LIB3175-052-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g1345595
BLAST score
                  687
E value
                  1.0e-72
Match length
                  138
% identity
                  100
NCBI Description
                  14-3-3-LIKE PROTEIN GF14 LAMBDA (14-3-3-LIKE PROTEIN AFT1)
                  >gi 1084332_pir__S53727 14-3-3-like protein (ATF1) -
                  Arabidopsis thaliana >gi_953221 (U02565) 14-3-3-like
                  protein 1 [Arabidopsis thaliana] >gi 1549404 (U68545) GF14
                  lambda [Arabidopsis thaliana]
Seq. No.
                  151078
Seq. ID
                  LIB3175-052-P1-K1-H9
Method
                  BLASTX
NCBI GI
                  g2160147
BLAST score
                  441
E value
                  8.0e-44
Match length
                  108
% identity
                  (AC000375) EST gb ATTS3706 comes from this gene.
NCBI Description
                  [Arabidopsis thalīana]
Seq. No.
                  151079
Seq. ID
                  LIB3175-053-P1-K1-A10
Method
                  BLASTX
NCBI GI
                  q70644
BLAST score
                  309
E value
                  3.0e-28
Match length
                  84
% identity
NCBI Description ubiquitin precursor - common sunflower (fragment)
Seq. No.
                  151080
Seq. ID
                  LIB3175-053-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  q2677828
BLAST score
                  435
E value
                  5.0e-43
Match length
                  114
% identity
NCBI Description (U93166) cysteine protease [Prunus armeniaca]
```

```
NCBI GI
                  g4544399
BLAST score
                  529
E value
                  4.0e-54
Match length
                  146
% identity
NCBI Description
                  (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
                  thaliana
                  151082
Seq. No.
Seq. ID
                  LIB3175-053-P1-K1-A2
Method
                  BLASTX
NCBI GI
                  g4741940
BLAST score
                  494
                  5.0e-50
E value
Match length
                  93
% identity
                  (AF134120) Lhca2 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  151083
                  LIB3175-053-P1-K1-A5
Seq. ID
Method
                  BLASTX
NCBI GI
                  q132110
BLAST score
                  103
                  2.0e-04
E value
                  83
Match length
% identity
                  28
NCBI Description
                  RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 3B PRECURSOR
                  (RUBISCO SMALL SUBUNIT 3B) >gi_68060_pir__RKMUB3
                  ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain
                  B3 precursor - Arabidopsis thaliana >gi_16195_emb_CAA32702_
                  (X14564) ribulose bisphosphate carboxylase [Arabidopsis
                  thaliana]
                  151084
Seq. No.
                  LIB3175-053-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1518540
BLAST score
                  581
E value
                  4.0e-60
Match length
                  120
% identity
NCBI Description
                  (U53418) UDP-glucose dehydrogenase [Glycine max]
Seq. No.
                  151085
Seq. ID
                  LIB3175-053-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  q4757394
BLAST score
                  179
                  4.0e-96
E value
Match length
                  229
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K1904, complete sequence
Seq. No.
                  151086
Seq. ID
                  LIB3175-053-P1-K1-B12
Method
                  BLASTX
```

Method

BLASTX

```
NCBI GI
                  g3522945
                  631
BLAST score
                  4.0e-66
E value
                  119
Match length
% identity
NCBI Description
                  (AC004411) putative cytochrome P450 [Arabidopsis thaliana]
                  151087
Seq. No.
                  LIB3175-053-P1-K1-B2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  421
E value
                  2.0e-41
Match length
                  108
                  58
% identity
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  151088
Seq. ID
                  LIB3175-053-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  q135467
BLAST score
                  708
E value
                  5.0e-75
Match length
                  152
                  88
% identity
                  TUBULIN BETA-4 CHAIN >gi_2129546_pir__$68122 beta-tubulin 4
NCBI Description
                  - Arabidopsis thaliana >gi_166640 (M21415) beta-tubulin
                  [Arabidopsis thaliana]
                  151089
Seq. No.
Seq. ID
                  LIB3175-053-P1-K1-B8
Method
                  BLASTX
NCBI GI
                  q3776558
BLAST score
                  598
E value
                  4.0e-62
Match length
                  136
                  93
% identity
                   (AC005388) Identical to gb L14814 DNA for tissue-specific
NCBI Description
                  acyl carrier protein isoform 2 from A. thaliana. ESTs
                  gb_AA597351, gb_T41805, gb_H36871, gb_R30210, gb_AA042549,
                  gb_Z47650, gb_H76304 and gb_AA597348 come from this gene.
                  [Arabidopsi
Seq. No.
                  151090
Seq. ID
                  LIB3175-053-P1-K1-B9
Method
                  BLASTX
NCBI GI
                  g2194139
BLAST score
                  295
E value
                  7.0e-27
Match length
                  98
% identity
NCBI Description
                   (AC002062) EST gb_ATTS0887 comes from this gene.
                  [Arabidopsis thaliana]
Seq. No.
                  151091
                  LIB3175-053-P1-K1-C2
Seq. ID
```

```
NCBI GI
                  g2651305
BLAST score
                  338
E value
                  1.0e-31
Match length
                  147
% identity
                  52
NCBI Description
                  (AC002336) hypothetical protein [Arabidopsis thaliana]
                  151092
Seq. No.
                  LIB3175-053-P1-K1-C3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q4006893
BLAST score
                  624
                  4.0e-65
E value
                  125
Match length
% identity
                  97
NCBI Description
                  (Z99708) aminopeptidase-like protein [Arabidopsis thaliana]
                  151093
Seq. No.
                  LIB3175-053-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  q3386612
BLAST score
                  217
                  2.0e-25
E value
Match length
                  121
% identity
                  53
NCBI Description
                 (AC004665) DNA-binding protein, dbp [Arabidopsis thaliana]
Seq. No.
                  151094
                  LIB3175-053-P1-K1-C5
Seq. ID
Method
                  BLASTN
NCBI GI
                  g2924732
BLAST score
                  279
                  1.0e-156
E value
Match length
                  310
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUA2, complete sequence [Arabidopsis thaliana]
                  151095
Seq. No.
Seq. ID
                  LIB3175-053-P1-K1-C6
Method
                  BLASTN
NCBI GI
                  g4220632
BLAST score
                  141
E value
                  2.0e-73
Match length
                  287
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K6M13, complete sequence [Arabidopsis thaliana]
                  151096
Seq. No.
Seq. ID
                  LIB3175-053-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g2511594
BLAST score
                  50
E value
                  1.0e-12
Match length
                  80
% identity
                  60
```

Method

BLASTX

```
NCBI Description (Y13694) multicatalytic endopeptidase complex, proteasome
                  precursor, beta subunit [Arabidopsis thaliana]
                  >gi 2827525 emb CAA16533_ (AL021633) multicatalytic
                  endopeptidase complex, proteasome precursor, beta subunit
                  [Arabidopsis thaliana] >gi 3421099 (AF043529) 20S
                  proteasome subunit PBA1 [Arabidopsis thaliana]
Seq. No.
                  151097
                  LIB3175-053-P1-K1-D4
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4589410
BLAST score
                  294
E value
                  1.0e-164
                  417
Match length
                  99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  F2015, complete sequence
Seq. No.
                  151098
                  LIB3175-053-P1-K1-D5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212869
BLAST score
                  591
                  2.0e-61
E value
                  121
Match length
                  88
% identity
NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]
Seq. No.
                  151099
                  LIB3175-053-P1-K1-D8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1706958
BLAST score
                  270
E value
                  9.0e-24
                  136
Match length
                  47
% identity
NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]
                  151100
Seq. No.
                  LIB3175-053-P1-K1-E10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g112743
BLAST score
                  286
E value
                  3.0e-26
Match length
                  66
% identity
                  2S SEED STORAGE PROTEIN 4 PRECURSOR (2S ALBUMIN STORAGE
NCBI Description
                  PROTEIN) >gi 68856 pir NWMU4 2S albumin 4 precursor -
                  Arabidopsis thaliana >gi 166617 (M22033) albumin 2S subunit
                  4 precursor [Arabidopsis thaliana] >gi 395202 emb CAA80869
                  (Z24744) 2S albumin isoform 4 [Arabidopsis thaliana]
                  >gi 4490713 emb CAB38847.1 (AL035680) NWMU4-2S albumin 4
                  precursor [Arabidopsis thaliana]
Seq. No.
                  151101
Seq. ID
                  LIB3175-053-P1-K1-E12
```

```
NCBI GI
                  q401169
BLAST score
                  277
E value
                  5.0e-25
Match length
                  53
                  100
% identity
NCBI Description
                 TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP)
                  151102
Seq. No.
                  LIB3175-053-P1-K1-E2
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2894598
BLAST score
                  154
                  2.0e-31
E value
Match length
                  121
% identity
NCBI Description (AL021889) putative protein [Arabidopsis thaliana]
Seq. No.
                  151103
Seq. ID
                  LIB3175-053-P1-K1-E3
Method
                  BLASTX
NCBI GI
                  g266829
BLAST score
                  682
E value
                  5.0e-72
Match length
                  131
                  100
% identity
NCBI Description
                  SERINE/THREONINE PROTEIN PHOSPHATASE PP1 ISOZYME 1
                  >gi_81655_pir__S20882 phosphoprotein phosphatase (EC
                  3.1.3.16) 1 catalytic chain (clone TOPP1) - Arabidopsis
                  thaliana >gi_16431_emb_CAA45611_ (X64328) protein
                  phosphatase-1 [Arabidopsis thaliana] >gi 166572 (M93408)
                  phosphoprotein phosphatase 1 [Arabidopsis thaliana]
                  >gi 3980395 (AC004561) phosphoprotein phosphatase-type 1
                  catalytic subunit [Arabidopsis thaliana]
Seq. No.
                  151104
Seq. ID
                  LIB3175-053-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g115385
BLAST score
                  681
E value
                  7.0e-72
Match length
                  130
                  100
% identity
NCBI Description
                 CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
                  (CAB-4) (LHCP) >gi_166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  151105
Seq. ID
                  LIB3175-053-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q2833627
BLAST score
                  72
E value
                  3.0e-32
Match length
                  233
                  88
% identity
NCBI Description Arabidopsis thaliana chromosome 1 BAC F1707 complete
```

sequence [Arabidopsis thaliana]

```
Seq. No.
                   151106
Seq. ID
                  LIB3175-053-P1-K1-F1
Method
                  BLASTN
NCBI GI
                  g3242970
BLAST score
                   46
E value
                   4.0e-17
Match length
                   90
                   88
% identity
                  Arabidopsis thaliana BAC T4I9, chromosome IV, near 17 cM,
NCBI Description
                  complete sequence [Arabidopsis thaliana]
                  151107
Seq. No.
Seq. ID
                  LIB3175-053-P1-K1-F10
Method
                  BLASTN
NCBI GI
                  g4406790
BLAST score
                  213
E value
                   1.0e-116
                  303
Match length
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T1016 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
                  151108
Seq. No.
Seq. ID
                  LIB3175-053-P1-K1-F2
Method
                  BLASTX
NCBI GI
                  g4585935
BLAST score
                  157
E value
                   4.0e-11
                  38
Match length
% identity
                   (AC007211) putative chlorophyll A/B binding protein
NCBI Description
                   [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1
                   (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  151109
Seq. ID
                  LIB3175-053-P1-K1-F3
Method
                  BLASTX
NCBI GI
                  g1353352
BLAST score
                  282
                   3.0e-46
E value
                  149
Match length
                   59
% identity
NCBI Description
                   (U31975) alanine aminotransferase [Chlamydomonas
                  reinhardtii]
Seq. No.
                  151110
Seq. ID
                  LIB3175-053-P1-K1-F4
Method
                  BLASTX
NCBI GI
                  g4538963
BLAST score
                  633
E value
                  1.0e-74
Match length
                  143
                  78
% identity
NCBI Description
                   (ALO49488) chlorophyll a/b-binding protein-like
                   [Arabidopsis thaliana] >gi 4741958 gb AAD28776.1 AF134129_1
```

(AF134129) Lhcb5 protein [Arabidopsis thaliana]

```
Seq. No.
                  151111
Seq. ID
                  LIB3175-053-P1-K1-F8
Method
                  BLASTX
NCBI GI
                  q1345592
BLAST score
                  161
E value
                  3.0e-11
Match length
                  59
                  63
% identity
                  14-3-3-LIKE PROTEIN GF14 EPSILON >qi 1022778 (U36446) GF14
NCBI Description
                  epsilon isoform [Arabidopsis thaliana]
Seq. No.
                  151112
                  LIB3175-053-P1-K1-G10
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2341034
BLAST score
                  396
E value
                  2.0e-38
Match length
                  86
% identity
NCBI Description
                  (AC000104) F19P19.13 [Arabidopsis thaliana]
Seq. No.
                  151113
Seq. ID
                  LIB3175-053-P1-K1-G11
Method
                  BLASTX
NCBI GI
                  g2129562
BLAST score
                  157
E value
                  7.0e-11
Match length
                  48
% identity
NCBI Description
                  class III ADH, glutathione-dependent formaldehyde
                  dehydrogenase. - Arabidopsis thaliana
                  >gi_1143388 emb CAA57973_ (X82647) class III ADH,
                  glutathione-dependent formaldehyde dehydrogenase.
                  [Arabidopsis thaliana]
Seq. No.
                  151114
Seq. ID
                  LIB3175-053-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  q2118220
BLAST score
                  296
E value
                  6.0e-27
Match length
                  77
% identity
NCBI Description
                  H+-transporting ATPase (EC 3.6.1.35), vacuolar, 16K chain
                  (clone AVA-P1) - Arabidopsis thaliana >gi 926929 (L44581)
                  vacuolar H+-pumping ATPase 16 kDa proteolipid [Arabidopsis
                  thaliana] >qi 926933 (L44583) vacuolar H+-pumping ATPase 16
                  kDa proteolipid [Arabidopsis thaliana]
                  >gi 3096941 emb CAA18851.1 (AL023094) vacuolar
                  H+-transporting ATPase 16K chain [Arabidopsis thaliana]
                  >gi 4539311 emb CAB38812.1 (AL035679) H+-transporting
                  ATPase 16K chain P2, vacuolar [Arabidopsis thaliana]
                  >gi 4589976 gb AAD26493.1 AC007195 7 (AC007195) vacuolar
                  H+-pumping ATPase 16 kDa proteolipid [Arabidopsis thaliana]
Seq. No.
                  151115
Seq. ID
                  LIB3175-053-P1-K1-G4
```

```
Method
                  BLASTX
NCBI GI
                  g4689382
BLAST score
                  282
                  2.0e-39
E value
                  147
Match length
                   60
% identity
NCBI Description
                   (AF139466) chlorophyll a/b binding protein CP29 [Vigna
                  151116
Seq. No.
Seq. ID
                  LIB3175-053-P1-K1-G5
Method
                  BLASTX
NCBI GI
                  g2760830
BLAST score
                  144
                  3.0e-09
E value
Match length
                  63
% identity
                   (AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  151117
Seq. ID
                  LIB3175-053-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q1076660
BLAST score
                  264
                  5.0e-23
E value
                  85
Match length
                  71
% identity
NCBI Description
                  D13F(MYBST1) protein - potato >gi_786426_bbs_159122
                   (S74753) MybSt1=Myb-related transcriptional activator
                   {DNA-binding domain repeats} [Solanum tuberosum=potatoes,
                  leaf, Peptide, 342 aa] [Solanum tuberosum]
Seq. No.
                  151118
Seq. ID
                  LIB3175-053-P1-K1-G7
Method
                  BLASTN
NCBI GI
                  q4263753
BLAST score
                  200
E value
                  1.0e-108
                  351
Match length
                  97
% identity
NCBI Description
                  Arabidopsis thaliana chromosome V map near 60.5 cM,
                  complete sequence [Arabidopsis thaliana]
                  151119
Seq. No.
Seq. ID
                  LIB3175-053-P1-K1-G8
                  BLASTN
Method
NCBI GI
                  g4115370
BLAST score
                  42
E value
                  1.0e-14
Match length
                  117
% identity
                  88
                  Arabidopsis thaliana chromosome II BAC F27D4 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151120
Seq. ID
                  LIB3175-053-P1-K1-G9
```

```
BLASTX
Method
NCBI GI
                   g4371282
                   257
BLAST score
E value
                   2.0e-22
Match length
                   70
                   76
% identity
                   (AC006260) putative 60S ribosomal protein L12 [Arabidopsis
NCBI Description
                   thaliana]
                   151121
Seq. No.
Seq. ID
                   LIB3175-053-P1-K1-H10
Method
                   BLASTX
NCBI GI
                   q4585997
BLAST score
                   286
E value
                   6.0e-26
Match length
                   91
                   67
% identity
NCBI Description
                   (AC005287) Hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   151122
Seq. ID
                   LIB3175-053-P1-K1-H2
Method
                   BLASTN
NCBI GI
                   q16202
BLAST score
                   103
E value
                   4.0e-51
Match length
                   147
                   93
% identity
NCBI Description A.thaliana of bcb gene encoding blue copper-binding protein
Seq. No.
                   151123
                   LIB3175-053-P1-K1-H3
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4589414
BLAST score
                   182
E value
                   7.0e-98
                   344
Match length
                   96
% identity
                   Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                   K14B15, complete sequence
Seq. No.
                   151124
                   LIB3175-053-P1-K1-H4
Seq. ID
Method
                   BLASTX
NCBI GI
                   g417103
BLAST score
                   46
E value
                   5.0e-63
Match length
                   136
% identity
                   92
                   HISTONE H3.2, MINOR >gi 282871 pir S24346 histone
NCBI Description
                   H3.3-like protein - Arabidopsis thaliana
                   >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein
[Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429)
                   histone H3.3 like protein [Arabidopsis thaliana] >gi_488563
```

(U09458) histone H3.2 [Medicago sativa] >gi\_488567 (U09460) histone H3.2 [Medicago sativa] >gi\_488569 (U09461) histone H3.2 [Medicago sativa] >gi\_488575 (U09464) histone H3.2 [Medicago sativa] >gi\_488577 (U09465) histone H3.2

[Medicago sativa] >gi\_510911\_emb\_CAA56153\_ (X79714) histone H3 [Lolium temulentum] >gi\_1435157\_emb\_CAA58445\_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi\_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi\_3273350\_dbj\_BAA31218\_ (AB015760) histone H3 [Nicotiana tabacum] >gi\_3885890 (AF093633) histone H3 [Oryza sativa] >gi\_4038469\_gb\_AAC97380\_ (AF109910) histone H3 [Porteresia coarctata] >gi\_4490754\_emb\_CAB38916.1\_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi\_4490755\_emb\_CAB38917.1\_ (AL035708) Histon H3 [Arabidopsis thaliana]

 Seq. No.
 151125

 Seq. ID
 LIB3175-053-P1-K1-H5

 Method
 BLASTX

 NCBI GI
 g3511285

 BLAST score
 150

E value 3.0e-10 Match length 46 % identity 63

NCBI Description (AF081534) cellulose synthase [Populus alba x Populus

tremula]

Seq. No.

151126

Seq. ID LIB3175-053-P1-K1-H6

Method BLASTX
NCBI GI g1706958
BLAST score 479
E value 2.0e-48
Match length 101
% identity 89

NCBI Description (U58284) cellulose synthase [Gossypium hirsutum]

Seq. No.

151127

Seq. ID LIB3175-054-P1-K1-A1

Method BLASTN
NCBI GI g1483219
BLAST score 33
E value 2.0e-09
Match length 65
% identity 88

NCBI Description A.thaliana mRNA for peroxidase ATPla, clone EST 103m21t7

Seq. No.

151128

Seq. ID LIB3175-054-P1-K1-A10

Method BLASTN
NCBI GI 94580744
BLAST score 266
E value 1.0e-148
Match length 401
% identity 96

NCBI Description Sequence of BAC F15I1 from Arabidopsis thaliana chromosome

1, complete sequence

Seq. No. 151129

Seq. ID LIB3175-054-P1-K1-A12

Method BLASTX NCBI GI g1362007

BLAST score 683 E value 4.0e-72 143 Match length 90 % identity

thioglucosidase (EC 3.2.3.1) - Arabidopsis thaliana NCBI Description >gi\_871992\_emb\_CAA55787\_ (X79195) thioglucosidase

[Arabidopsis thaliana]

151130 Seq. No.

LIB3175-054-P1-K1-A2 Seq. ID

Method BLASTX NCBI GI g1351271 BLAST score 343 3.0e-32 E value Match length 131 58 % identity

NCBI Description TRIOSEPHOSPHATE ISOMERASE CHLOROPLAST PRECURSOR (TIM) >gi 1084309 pir S52032 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - spinach >gi\_806312 (L36387) triosephosphate isomerase, chloroplast isozyme

[Spinacia oleracea]

151131 Seq. No.

Seq. ID LIB3175-054-P1-K1-A4

Method BLASTX NCBI GI g4835226 BLAST score 291 4.0e-26 E value 84 Match length

68 % identity

NCBI Description (ALO49862) putative protein [Arabidopsis thaliana]

Seq. No. 151132

Seq. ID LIB3175-054-P1-K1-A5

Method BLASTX NCBI GI q629602 BLAST score 267 2.0e-23 E value Match length 81 58 % identity

NCBI Description probable imbibition protein - wild cabbage

>gi 488787 emb CAA55893 (X79330) putative imbibition

protein [Brassica oleracea]

Seq. No. 151133

Seq. ID LIB3175-054-P1-K1-A6

Method BLASTX NCBI GI q416758 BLAST score 141 1.0e-69 E value 145 Match length % identity 91

SERINE CARBOXYPEPTIDASE PRECURSOR >gi\_166674 (M81130) NCBI Description

carboxypeptidase Y-like protein [Arabidopsis thaliana] >gi 445120 prf 1908426A carboxypeptidase Y [Arabidopsis

thaliana]

- 2

```
Seq. No.
                  151134
Seq. ID
                  LIB3175-054-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g4580365
BLAST score
                  181
                  3.0e-97
E value
Match length
                  361
% identity
                  95
                  Arabidopsis thaliana chromosome I BAC F3F20 genomic
NCBI Description
                  sequence, complete sequence
                  151135
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-B1
                  BLASTX
Method
                  g2894574
NCBI GI
BLAST score
                  626
                  2.0e-65
E value
Match length
                  121
% identity
                  98
                  (AL021890) peroxidase prxrl [Arabidopsis thaliana]
NCBI Description
                  >gi 2961341 emb CAA18099.1 (AL022140) peroxidase prxr1
                  [Arabidopsis thaliana]
                  151136
Seq. No.
                  LIB3175-054-P1-K1-B10
Seq. ID
                  BLASTX
Method
NCBI GI
                  g1402912
BLAST score
                  628
E value
                  9.0e-66
Match length
                  121
                  98
% identity
                  (X98317) peroxidase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  151137
Seq. ID
                  LIB3175-054-P1-K1-B11
Method
                  BLASTN
NCBI GI
                  g2264317
BLAST score
                  142
E value
                  4.0e-74
Match length
                  288
% identity 🐇
                  98
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MUG13, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151138
                  LIB3175-054-P1-K1-B12
Seq. ID
Method
                  BLASTX
NCBI GI
                  g133938
BLAST score
                  568
E value
                  1.0e-58
Match length
                  145
                  77
% identity
                  CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi 70866_pir__R3SP3
NCBI Description
                  ribosomal protein S3 - spinach chloroplast
                  >gi_12310_emb_CAA31715_ (X13336) ribosomal protein S3
                   [Spinacia oleracea]
```

```
Seq. No.
                  151139
Seq. ID
                  LIB3175-054-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  g4335711
                  159
BLAST score
E value
                  4.0e-84
Match length
                  407
                  99
% identity
                  Arabidopsis thaliana chromosome II BAC F9013 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  151140
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-B3
                  BLASTN
Method
NCBI GI
                  g3426063
BLAST score
                  386
E value
                  0.0e+00
Match length
                  411
                  99
% identity
NCBI Description Arabidopsis thaliana mRNA for monooxygenase
Seq. No.
                  151141
Seq. ID
                  LIB3175-054-P1-K1-B4
                  BLASTN
Method
NCBI GI
                  g4567300
BLAST score
                  219
E value
                  1.0e-120
Match length
                  422
% identity
                  99
                  Arabidopsis thaliana chromosome II P1 MHK10 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  151142
Seq. ID
                  LIB3175-054-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g4512656
BLAST score
                  164
                  4.0e-87
E value
Match length
                  359
% identity
                  85
NCBI Description Arabidopsis thaliana chromosome II BAC F7D19 genomic
                  sequence, complete sequence
                  151143
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-B7
Method
                  BLASTX
NCBI GI
                  g2501296
BLAST score
                  255
E value
                  6.0e-22
Match length
                  126
% identity
                  40
                  DNA GYRASE SUBUNIT B >gi 1652801 dbj BAA17720 (D90908) DNA
NCBI Description
                  gyrase B subunit [Synechocystis sp.]
Seq. No.
                  151144
Seq. ID
                  LIB3175-054-P1-K1-B8
Method
                  BLASTN
```

NCBI Description

```
NCBI GI
                     q3046847
 BLAST score
                     204
 E value
                     1.0e-111
Match length
                     348
 % identity
                     96
 NCBI Description
                     Arabidopsis thaliana genomic DNA, chromosome5, TAC clone:
                     K11J9, complete sequence [Arabidopsis thaliana]
 Seq. No.
                     151145
 Seq. ID
                     LIB3175-054-P1-K1-B9
 Method
                     BLASTX
 NCBI GI
                     q2384671
                     709
 BLAST score
 E value
                     3.0e-75
 Match length
                     143
 % identity
                     94
 NCBI Description
                     (AF012657) putative potassium transporter AtKT2p
                     [Arabidopsis thaliana]
 Seq. No.
                     151146
 Seq. ID
                     LIB3175-054-P1-K1-C10
 Method
                     BLASTN
 NCBI GI
                     g2980757
 BLAST score
                     341
 E value
                     0.0e + 00
 Match length
                     390
 % identity
                     96
                     Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18
 NCBI Description
                     (ESSAII project)
 Seq. No.
                     151147
 Seq. ID
                     LIB3175-054-P1-K1-C11
 Method
                     BLASTX
 NCBI GI
                     g1345973
 BLAST score
                     332
 E value
                     1.0e-53
 Match length
                     102
 % identity
                     100
                     OMEGA-3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
 NCBI Description
                     >gi_541882_pir__JQ2335 omega-3 fatty acid desaturase (EC
1.14.99.-) CF3 - Arabidopsis thaliana >gi_408483 (L22931)
                     omega-3 fatty acid desaturase [Arabidopsis thaliana]
                     >gi_471091_dbj_BAA04505_ (D17579) fatty acid desaturase
[Arabidopsis thaliana] >gi_1197795_dbj_BAA05514_ (D26508)
                     microsomal omega-3 fatty acid desaturase [Arabidopsis
                     thaliana] >gi 3420053 (AC004680) omega-3 fatty acid
                     desaturase [Arabidopsis thaliana]
 Seq. No.
                     151148
 Seq. ID
                     LIB3175-054-P1-K1-C12
 Method
                     BLASTX
 NCBI GI
                     g4204267
 BLAST score
                     617
 E value
                     2.0e-64
 Match length
                     148
 % identity
```

(AC005223) 55585 [Arabidopsis thaliana]

```
151149
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-C3
                  BLASTX
Method
NCBI GI
                  g116229
BLAST score
                  478
                  3.0e-48
E value
Match length
                  107
                  91
% identity
NCBI Description MITOCHONDRIAL CHAPERONIN HSP60 PRECURSOR
                  >qi 99676 pir S20876 chaperonin hsp60 precursor -
                  Arabidopsis thaliana >gi 16221 emb CAA77646 (Z11547)
                  chaperonin hsp60 [Arabidopsis thaliana]
                  151150
Seq. No.
                  LIB3175-054-P1-K1-C4
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1169598
BLAST score
                  484
                  8.0e-49
E value
Match length
                  100
% identity
                  88
                  OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM
NCBI Description
                   (DELTA-12 DESATURASE) >gi 438451 (L26296) delta-12
                  desaturase [Arabidopsis thaliana]
                  151151
Seq. No.
                  LIB3175-054-P1-K1-C5
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2245066
BLAST score
                  581
                  3.0e-60
E value
Match length
                  106
% identity
                  99
NCBI Description
                  (Z97342) Beta-Amylase [Arabidopsis thaliana]
                  151152
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2924520
                  620
BLAST score
                  9.0e-65
E value
Match length
                  124
% identity
NCBI Description
                   (AL022023) plasma membrane intrinsic protein (SIMIP)
                   [Arabidopsis thaliana]
                  151153
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-C9
Method
                  BLASTX
NCBI GI
                  q4164578
BLAST score
                  611
E value
                  1.0e-63
                  135
Match length
                  92
% identity
NCBI Description (AF098947) CTF2B [Arabidopsis thaliana]
```

```
Seq. No.
Seq. ID
                   LIB3175-054-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g2271477
BLAST score
                   469
                   5.0e-47
E value
                   108
Match length
% identity
                   84
NCBI Description (AF009631) AP47/50p [Arabidopsis thaliana]
                   151155
Seq. No.
                   LIB3175-054-P1-K1-D10
Seq. ID
                   BLASTX
Method
NCBI GI
                   q4539370
                   152
BLAST score
                   7.0e-10
E value
                   48
Match length
% identity
                   65
NCBI Description
                   (ALO49525) UDP-galactose 4-epimerase-like protein
                   [Arabidopsis thaliana]
Seq. No.
                   151156
                   LIB3175-054-P1-K1-D11
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4559321
BLAST score
                   537
E value
                   5.0e-55
Match length
                   135
% identity
                   80
NCBI Description
                   (AC007087) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                   151157
                   LIB3175-054-P1-K1-D12
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4539418
BLAST score
                   126
                   6.0e-66
E value
                   134
Match length
                   95
% identity
                   (AL049171) caffeoyl-CoA O-methyltransferase-like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   151158
                   LIB3175-054-P1-K1-D2
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4732169
                   397
BLAST score
                   0.0e + 00
E value
                   432
Match length
                   87
% identity
NCBI Description Arabidopsis thaliana BAC T3E15
                   151159
Seq. No.
                   LIB3175-054-P1-K1-D3
Seq. ID
                  BLASTX
Method
NCBI GI
                   g4467099
BLAST score
                   616
```

```
E value
                   2.0e-64
Match length
                   122
% identity
                   98
                   (AL035538) glycine hydroxymethyltransferase like protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   151160
Seq. ID
                  LIB3175-054-P1-K1-D4
Method
                  BLASTX
NCBI GI
                   q4539324
BLAST score
                   170
                   5.0e-12
E value
                   69
Match length
% identity
                   52
NCBI Description (AL035679) kinesin like protein [Arabidopsis thaliana]
Seq. No.
                   151161
                  LIB3175-054-P1-K1-D5
Seq. ID
Method
                   BLASTX
NCBI GI
                   g520478
BLAST score
                   372
                   2.0e-42
E value
                   95
Match length
                   94
% identity
NCBI Description
                   (U09137) pyruvate dehydrogenase E1 beta subunit
                   [Arabidopsis thaliana] >gi 1090498 prf 2019230A pyruvate
                   dehydrogenase [Arabidopsis thaliana]
Seq. No.
                   151162
Seq. ID
                   LIB3175-054-P1-K1-D6
Method
                   BLASTX
NCBI GI
                   g3915847
BLAST score
                   43
                   7.0e-51
E value
Match length
                   113
% identity
                   95
                   40S RIBOSOMAL PROTEIN S2 >gi 2335095 (AC002339) putative
NCBI Description
                   40S ribosomal protein S2 [Arabidopsis thaliana]
Seq. No.
                   151163
Seq. ID
                   LIB3175-054-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   g2739373
BLAST score
                   245
E value
                   8.0e-21
Match length
                   139
% identity
                   40
                   (AC002505) putative flavonol 3-o-glucosyltransferase
NCBI Description
                   [Arabidopsis thaliana]
                   151164
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-D8
Method
                   BLASTX
NCBI GI
                   g4678328
BLAST score
                   479
E value
                   3.0e-48
                   94
Match length
```

```
% identity
                  (AL049658) aldehyde dehydrogenase (NAD+)-like protein
NCBI Description
                  [Arabidopsis thaliana]
                  151165
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  g2739389
BLAST score
                  82
                  3.0e-45
E value
                126
Match length
% identity
                  73
NCBI Description (AC002505) Cf-2.2 like protein [Arabidopsis thaliana]
                  151166
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g166708.
BLAST score
                  106
E value
                  9.0e-45
                  98
Match length
                  95
% identity
                   (M64118) glyceraldehyde-3-phosphate dehydrogenase
NCBI Description
                  [Arabidopsis thaliana]
                  151167
Seq. No.
                  LIB3175-054-P1-K1-E11
Seq. ID
                  BLASTN
Method
                  g4803835
NCBI GI
BLAST score
                  275
E value
                  1.0e-153
Match length
                  295
                  98
% identity
NCBI Description
                  Arabidopsis thaliana mRNA for a dynamin-like protein ADL3,
                  complete cds
                  151168
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-E12
Method
                  BLASTX
NCBI GI
                  g4538912
BLAST score
                  236
                  1.0e-19
E value
Match length
                  89
% identity
NCBI Description (ALO49482) putative protein [Arabidopsis thaliana]
                  151169
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-E2
Method
                  BLASTN
                  g2642152
NCBI GI
BLAST score
                  231
E value
                  1.0e-127
Match length
                  399
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T517 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
```

```
151170
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  q115385
BLAST score
                  293
                  3.0e-29
E value
Match length
                  69
% identity
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-4) (LHCP) >gi 166646 (M63931) light-harvesting
                  chlorophyll a/b binding protein [Arabidopsis thaliana]
Seq. No.
                  151171
Seq. ID
                  LIB3175-054-P1-K1-E7
Method
                  BLASTN
NCBI GI
                  g1237123
BLAST score
                  363
                  0.0e + 00
E value
Match length
                  387
% identity
                  Arabidopsis thaliana photosystem I PSI-N mRNA, nuclear gene
NCBI Description
                  encoding chloroplast protein, complete cds
Seq. No.
                  151172
Seq. ID
                  LIB3175-054-P1-K1-E9
Method
                  BLASTN
NCBI GI
                  q4467131
BLAST score
                  108
E value
                  6.0e-54
Match length
                  192
% identity
                  97
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F20M13
NCBI Description
                   (ESSA project)
Seq. No.
                  151173
Seq. ID
                  LIB3175-054-P1-K1-F1
Method
                  BLASTX
NCBI GI
                  q4734009
BLAST score
                  125
E value
                   6.0e-10
Match length
                  90
% identity
                   (AC007178) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  151174
Seq. ID
                  LIB3175-054-P1-K1-F11
Method
                  BLASTN
NCBI GI
                  q3869066
BLAST score
                  186
E value
                  1.0e-100
Match length
                  358
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MBM17, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151175
Seq. ID
                  LIB3175-054-P1-K1-F12
```

```
Method
                      BLASTX
NCBI GI
                      g4204285
BLAST score
                      419
                      4.0e-41
E value
Match length
                      134
                      59
% identity
NCBI Description
                      (AC003027) lcl_prt_seq No definition line found
                      [Arabidopsis thaliana]
                      151176
Seq. No.
Seq. ID
                      LIB3175-054-P1-K1-F2
Method
                      BLASTX
NCBI GI
                      q4758946
BLAST score
                      186
                      7.0e-14
E value
                      71
Match length
                      55
% identity
NCBI Description
                      POP2 (yeast homolog) >gi 4106061 gb AAD02685 (AF053318)
                      CCR4-associated factor 1 [Homo sapiens]
                      151177
Seq. No.
Seq. ID
                      LIB3175-054-P1-K1-F3
Method
                      BLASTX
NCBI GI
                      g4206207
BLAST score
                      160
                      7.0e-11
E value
Match length
                      93
                      33
% identity
NCBI Description
                      (AF071527) putative reverse transcriptase [Arabidopsis
                      thaliana] >gi 4263040 gb AAD15309 (AC005142) putative
                      reverse transcriptase [Arabidopsis thaliana]
                      151178
Seq. No.
Seq. ID
                      LIB3175-054-P1-K1-F4
Method
                      BLASTX
NCBI GI
                      q1652892
BLAST score
                      247
                      5.0e-21
E value
                      148
Match length
% identity
                      26
NCBI Description (D90909) ABC transporter [Synechocystis sp.]
Seq. No.
                      151179
                      LIB3175-054-P1-K1-F5
Seq. ID
Method
                      BLASTX
NCBI GI
                      q1076708
BLAST score
                      602
E value
                      1.0e-62
Match length
                      123
                      25
% identity
NCBI Description
                      seed tetraubiquitin - common sunflower
                      >gi_303901_dbj_BAA03764_ (D16248) ubiquitin [Glycine max]
>gi_456714_dbj_BAA05670_ (D28123) Ubiquitin [Glycine max]
>gi_556688_emb_CAA84440_ (Z34988) seed tetraubiquitin
[Helianthus annuus] >gi_994785_dbj_BAA05085_ (D26092)
Ubiquitin [Glycine max] >gi_4263514_gb_AAD15340_ (AC004044)
                      putative polyubiquitin [Arabidopsis thaliana]
```

>gi\_1096513\_prf\_\_2111434A tetraubiquitin [Helianthus annuus]

Seq. No. 151180

Seq. ID LIB3175-054-P1-K1-F9

Method BLASTX
NCBI GI g3914826
BLAST score 461
E value 3.0e-46
Match length 110
% identity 85

NCBI Description DNA-DIRECTED RNA POLYMERASE CHLOROPLAST PRECURSOR

>gi\_2330560\_emb\_CAA69972\_ (Y08722) chloroplast

single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi\_2330564\_emb\_CAA69717\_ (Y08463) chloroplast single-subunit DNA-dependent RNA polymerase [Arabidopsis thaliana] >gi\_4115372 (AC005967) chloroplast single subunit

DNA-dependent RNA polymerase [Arabidopsis thaliana]

Seq. No. 151181

Seq. ID LIB3175-054-P1-K1-G10

Method BLASTX
NCBI GI g99735
BLAST score 789
E value 1.0e-84
Match length 149
% identity 99

NCBI Description L-ascorbate peroxidase (EC 1.11.1.11) precursor -

Arabidopsis thaliana (fragment)

Seq. No. 151182

Seq. ID LIB3175-054-P1-K1-G11

Method BLASTN
NCBI GI g4757392
BLAST score 224
E value 1.0e-123
Match length 421
% identity 100

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:

K14A17, complete sequence

Seq. No. 151183

Seq. ID LIB3175-054-P1-K1-G2

Method BLASTX
NCBI GI g1402904
BLAST score 657
E value 4.0e-69
Match length 130
% identity 97

NCBI Description (X98313) peroxidase [Arabidopsis thaliana]

Seq. No. 151184

Seq. ID LIB3175-054-P1-K1-G3

Method BLASTX
NCBI GI g4585882
BLAST score 625
E value 2.0e-65

Seq. No.

Seq. ID

151189

LIB3175-054-P1-K1-H10

```
Match length
                   126
% identity
                   98
                   (AC005850) PSI type III chlorophyll a/b-binding protein
NCBI Description
                   [Arabidopsis thaliana]
                   151185
Seq. No.
Seq. ID
                   LIB3175-054-P1-K1-G4
Method
                   BLASTX
                   g3157944
NCBI GI
                   748
BLAST score
                   9.0e-80
E value
Match length
                   148
                   98
% identity
                   (AC002131) Very strong similarity to aminomethyltransferase
NCBI Description
                   precursor gb_U79769 from Mesembryanthemum crystallinum.
                   ESTs gb_T43167, gb_T21076, gb_H36999, gb_T22773,
                   gb_N380\overline{3}8, gb_T137\overline{4}2, gb_Z265\overline{4}5, gb_T2075\overline{3} and gb_W43123
                   come from this ge
Seq. No.
                   151186
Seq. ID
                   LIB3175-054-P1-K1-G7
Method
                   BLASTX
NCBI GI
                   q267069
BLAST score
                   609
E value
                   2.0e-63
Match length
                   114
                   99
% identity
                   TUBULIN ALPHA-2/ALPHA-4 CHAIN >gi_320183_pir__JQ1594
NCBI Description
                   tubulin alpha chain - Arabidopsis thaliana >gi_166914
                   (M84696) apha-2 tubulin [Arabidopsis thaliana] >gi_166916
                   (M84697) alpha-4 tubulin [Arabidopsis thaliana]
Seq. No.
                   151187
Seq. ID
                   LIB3175-054-P1-K1-G8
Method
                   BLASTN
NCBI GI
                   g2245073
BLAST score
                   306
                   1.0e-172
E value
Match length
                   396
                   98
% identity
                   Arabidopsis thaliana DNA chromosome 4, ESSA I contig
NCBI Description
                   fragment No
                   151188
Seq. No.
Seq. ID
                   LIB3175-054-P1-K1-G9
                   BLASTX
Method
NCBI GI
                   g3914658
BLAST score
                   568
E value
                   1.0e-58
Match length
                   110
                   100
% identity
                   50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
                   >gi 1694974 emb CAA70851 (Y09635) plastid ribosomal
                   protein [Arabidopsis thaliana]
```

```
Method
                  BLASTN
NCBI GI
                  g3128143
BLAST score
                  42
                  2.0e-14
E value
                  126
Match length
                  84
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MTI20, complete sequence [Arabidopsis thaliana]
                  151190
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-H11
Method
                  BLASTX
NCBI GI
                  g4115364
BLAST score
                  528
                  5.0e-54
E value
                  109
Match length
                  94
% identity
                  (AC005957) putative fatty acid elongase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  151191
Seq. ID
                  LIB3175-054-P1-K1-H4
Method
                  BLASTX
                  g4586253
NCBI GI
BLAST score
                  567
                  2.0e-58
E value
                  150
Match length
                  66
% identity
NCBI Description (AL049640) auxilin-like protein [Arabidopsis thaliana]
Seq. No.
                  151192
Seq. ID
                  LIB3175-054-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g2129640
BLAST score
                  641
E value
                  4.0e-67
Match length
                  149
                  87
% identity
NCBI Description
                  magnesium chelatase chain - Arabidopsis thaliana
                  >gi_1154627_emb_CAA92802_ (Z68495) magnesium chelatase
                  subunit [Arabidopsis thaliana]
Seq. No.
                  151193
Seq. ID
                  LIB3175-054-P1-K1-H6
Method
                  BLASTX
NCBI GI
                  g4539460
BLAST score
                  99
E value
                  1.0e-03
Match length
                  136
% identity
                  (AL049500) putative protein [Arabidopsis thaliana]
NCBI Description
                  151194
Seq. No.
Seq. ID
                  LIB3175-054-P1-K1-H7
Method
                  BLASTX
NCBI GI
                  g2129672
                  222
BLAST score
```

```
E value
                   1.0e-18
Match length
                   57
% identity
                   84
NCBI Description
                  photosystem II reaction center protein, 6.1K - Arabidopsis
                   thaliana >gi_950023_emb_CAA62296_ (X90769) component of 6.1
                   kDa polypeptide of photosystem II reaction center
                   [Arabidopsis thaliana]
Seq. No.
                  151195
Seq. ID
                  LIB3175-054-P1-K1-H8
Method
                  BLASTN
NCBI GI
                   g4567259
BLAST score
                   354
E value
                   0.0e + 00
Match length
                   431
% identity
                   99
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F3K23 genomic
                   sequence, complete sequence
                  151196
Seq. No.
                  LIB3175-054-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4585935
BLAST score
                   646
E value
                   8.0e-68
Match length
                   123
% identity
NCBI Description
                   (AC007211) putative chlorophyll A/B binding protein
                   [Arabidopsis thaliana] >gi_4741946_gb_AAD28770.1_AF134123_1
                   (AF134123) Lhcb2 protein [Arabidopsis thaliana]
Seq. No.
                  151197
Seq. ID
                  LIB3175-055-P1-K1-A1
Method
                  BLASTX
NCBI GI
                  g4314378
BLAST score
                   512
E value
                   2.0e-52
Match length
                   98
% identity
NCBI Description
                   (AC006232) putative lipase [Arabidopsis thaliana]
Seq. No.
                  151198
Seq. ID
                  LIB3175-055-P1-K1-A10
Method
                  BLASTN
NCBI GI
                  q3702724
BLAST score
                  275
                  1.0e-153
E value
Match length
                  383
% identity
                   98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K17N15, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151199
Seq. ID
                  LIB3175-055-P1-K1-A4
Method
                  BLASTN
NCBI GI
                  g1732569
BLAST score
                  60
```

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```
9.0e-26
E value
Match length
                   84
% identity
                   93
                   Arabidopsis thaliana beta-glucosidase (psr3.1) mRNA,
NCBI Description
                   complete cds
                   151200
Seq. No.
                   LIB3175-055-P1-K1-A5
Seq. ID
Method
                   BLASTN
NCBI GI
                   q3985958
BLAST score
                   138
                   6.0e-72
E value
                   186
Match length
                   92
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MZN1, complete sequence [Arabidopsis thaliana]
                   151201
Seq. No.
                   LIB3175-055-P1-K1-A6
Seq. ID
Method
                   BLASTN
NCBI GI
                   g3335356
BLAST score
                   320
E value
                   1.0e-180
Match length
                   426
                   97
% identity
                  Arabidopsis thaliana chromosome II BAC F16M14 genomic
NCBI Description
                   sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   151202
Seq. ID
                  LIB3175-055-P1-K1-A8
Method
                   BLASTX
NCBI GI
                   g2146733
BLAST score
                   445
E value
                   3.0e-44
Match length
                   75
% identity
                   100
NCBI Description GAST1 protein homolog (clone GASA1) - Arabidopsis thaliana
Seq. No.
                   151203
                  LIB3175-055-P1-K1-A9
Seq. ID
Method
                  BLASTX
NCBI GI
                   g3819710
BLAST score
                   526
E value
                   1.0e-53
Match length
                   96
% identity
                   100
                   (AJ224161) delta-8 sphingolipid desaturase [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                   151204
                  LIB3175-055-P1-K1-B1
Seq. ID
Method
                  BLASTN
NCBI GI
                  g4063730
BLAST score
                   409
                  0.0e+00
E value
                   429
Match length
% identity
                  99
```

```
NCBI Description Arabidopsis thaliana BAC F21J6 from chromosome V,
                  containing KNAT3 and mapping near 60.5 cM, complete
                  sequence [Arabidopsis thaliana]
                  151205
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-B10
Method
                  BLASTN
NCBI GI
                  g633027
BLAST score
                  373
                  0.0e + 00
E value
                  393
Match length
% identity
                  99
NCBI Description Arabidopsis thaliana mRNA for protein phosphatase 2C
Seq. No.
                  151206
Seq. ID
                  LIB3175-055-P1-K1-B12
Method
                  BLASTN
NCBI GI
                  g4220645
BLAST score
                  217
                  1.0e-118
E value
Match length
                  443
                  91
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MYA6, complete sequence [Arabidopsis thaliana]
                  151207
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g267077
BLAST score
                  749
                  7.0e-80
E value
Match length
                  138
% identity
                  99
NCBI Description
                  TUBULIN BETA-5 CHAIN >gi_320186_pir__JQ1589 tubulin beta-5
                  chain - Arabidopsis thaliana >gi 166902 (M84702) beta-5
                  tubulin [Arabidopsis thaliana]
Seq. No.
                  151208
Seq. ID
                  LIB3175-055-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g2281093
BLAST score
                  687
E value
                  1.0e-72
Match length
                  137
% identity
                  96
NCBI Description
                  (ACO02333) beta transducin isolog [Arabidopsis thaliana]
Seq. No.
                  151209
Seq. ID
                  LIB3175-055-P1-K1-B4
Method
                  BLASTN
```

NCBI GI g3510339
BLAST score 178
E value 1.0e-95
Match length 210
% identity 96

NCBI Description Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:

K3K7, complete sequence [Arabidopsis thaliana]

```
Seq. No.
                  151210
Seq. ID
                  LIB3175-055-P1-K1-B6
Method
                  BLASTN
NCBI GI
                  g4662628
BLAST score
                  185
                  1.0e-99
E value
Match length
                  381
                  90
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F27010 genomic
                  sequence, complete sequence
                  151211
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-B7
Method
                  BLASTN
NCBI GI
                  g4262221
BLAST score
                  372
E value
                  0.0e + 00
Match length
                  418
                  98
% identity
                  Arabidopsis thaliana chromosome II BAC F10A8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  151212
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-B8
Method
                  BLASTN
NCBI GI
                  g2828188
BLAST score
                  242
E value
                  1.0e-133
Match length
                  455
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K3K3, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151213
Seq. ID
                  LIB3175-055-P1-K1-C1
Method
                  BLASTX
NCBI GI
                  q4580389
BLAST score
                  709
E value
                  4.0e-75
Match length
                  147
                  89
% identity
NCBI Description
                  (AC007171) unknown protein [Arabidopsis thaliana]
Seq. No.
                  151214
Seq. ID
                  LIB3175-055-P1-K1-C10
Method
                  BLASTN
NCBI GI
                  q2696018
BLAST score
                  208
E value
                  1.0e-113
Match length
                  381
                  97
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MXC9, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151215
Seq. ID
                  LIB3175-055-P1-K1-C2
```

```
Method
                   BLASTN
NCBI GI
                   g3688169
BLAST score
                   42
                   3.0e-15
E value
                   42
Match length
                   100
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21
                   (ESSAII project)
                  151216
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-C3
Method
                  BLASTX
                  q2529229
NCBI GI
BLAST score
                   383
E value
                   6.0e-37
                   106
Match length
% identity
                   70
                   (AB007907) 6-phosphogluconate dehydrogenase [Glycine max]
NCBI Description
Seq. No.
                  151217
Seq. ID
                  LIB3175-055-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g1931640
BLAST score
                  145
                   3.0e-09
E value
                   67
Match length
% identity
NCBI Description
                   (U95973) Serine carboxypeptidase isolog [Arabidopsis
                  thaliana]
Seq. No.
                  151218
Seq. ID
                  LIB3175-055-P1-K1-C7
Method
                  BLASTX
NCBI GI
                  g1351272
BLAST score
                   422
                  1.0e-41
E value
Match length
                  103
                  82
% identity
NCBI Description
                  TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi 414550
                   (U02949) cytosolic triose phosphate isomerase [Arabidopsis
                   thaliana] >gi 742408 prf 2009415A triose phosphate
                  isomerase [Arabidopsis thaliana]
Seq. No.
                  151219
Seq. ID
                  LIB3175-055-P1-K1-C8
Method
                  BLASTX
                  g1695717
NCBI GI
BLAST score
                  712
E value
                  2.0e-75
Match length
                  147
                  95
% identity
NCBI Description
                  (D89341) luminal binding protein [Arabidopsis thaliana]
                  151220
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-D11
Method
                  BLASTX
NCBI GI
                  g3402487
```

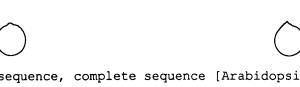
```
BLAST score
                   678
E value
                   1.0e-71
Match length
                   139
                   98
% identity
NCBI Description
                   (AB015138) Vacuolar proton pyrophosphatase [Arabidopsis
                   thaliana]
                   151221
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g2738248
BLAST score
                   569
E value
                   9.0e-59
Match length
                   109
                   100
% identity
NCBI Description
                   (U97200) cobalamin-independent methionine synthase
                   [Arabidopsis thaliana]
Seq. No.
                   151222
Seq. ID
                  LIB3175-055-P1-K1-D2
Method
                  BLASTN
NCBI GI
                  g4757405
BLAST score
                  319
E value
                   1.0e-179
Match length
                   378
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                  MOJ10, complete sequence
                  151223
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-D3
Method
                  BLASTX
NCBI GI
                   q3047125
BLAST score
                   591
E value
                   2.0e-61
Match length
                  124
% identity
NCBI Description
                  (AF058919) No definition line found [Arabidopsis thaliana]
                   151224
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-D4
Method
                  BLASTN
NCBI GI
                  g3510342
BLAST score
                  34
E value
                   6.0e-10
Match length
                   46
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MGN6, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151225
Seq. ID
                  LIB3175-055-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4371284
BLAST score
                  661
E value
                  1.0e-69
Match length
                  133
```

```
% identity
NCBI Description
                   (ACO06260) putative plasma membrane intrinsic protein 2B
                   [Arabidopsis thaliana]
                   151226
Seq. No.
Seq. ID
                   LIB3175-055-P1-K1-D7
Method
                   BLASTX
NCBI GI
                   q1931640
BLAST score
                   141
                   1.0e-08
E value
Match length
                   71
% identity
                   39
                   (U95973) Serine carboxypeptidase isolog [Arabidopsis
NCBI Description
                   thaliana]
                   151227
Seq. No.
Seq. ID
                   LIB3175-055-P1-K1-D8
Method
                   BLASTN
NCBI GI
                   g3650026
BLAST score
                   348
                   0.0e+00
E value
Match length
                   436
                   99
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T26I20 genomic
                   sequence, complete sequence [Arabidopsis thaliana]
                   151228
Seq. No.
Seq. ID
                   LIB3175-055-P1-K1-D9
Method
                   BLASTX
NCBI GI
                   g4185505
BLAST score
                   309
E value
                   3.0e-28
Match length
                   100
                   62
% identity
                   (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                   [Brassica napus]
Seq. No.
                   151229
Seq. ID
                  LIB3175-055-P1-K1-E1
Method
                  BLASTX
NCBI GI
                   g4490737
BLAST score
                   96
E value
                   3.0e-03
Match length
                   67
% identity
NCBI Description
                   (AL035708) putative protein [Arabidopsis thaliana]
Seq. No.
                  151230
Seq. ID
                  LIB3175-055-P1-K1-E2
Method
                  BLASTN
NCBI GI
                  g4544435
BLAST score
                  139
E value
                   4.0e-72
Match length
                   403
% identity
                   95
NCBI Description
                  Arabidopsis thaliana chromosome II BAC F14M13 genomic
                  sequence, complete sequence
```

```
Seq. No.
                  151231
                  LIB3175-055-P1-K1-E3
Seq. ID
                  BLASTN
Method
                  g2264314
NCBI GI
BLAST score
                  34
E value
                  2.0e-09
Match length
                  170
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MQK4, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151232
Seq. ID
                  LIB3175-055-P1-K1-E4
                  BLASTX
Method
NCBI GI
                  g4531442
BLAST score
                  200
E value
                  5.0e-16
                  77
Match length
% identity
                  56
NCBI Description (AC006224) hypothetical protein [Arabidopsis thaliana]
                  151233
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-E5
Method
                  BLASTX
NCBI GI
                  q4531442
BLAST score
                  500
E value
                  1.0e-50
Match length
                  136
                  79
% identity
NCBI Description (AC006224) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  151234
                  LIB3175-055-P1-K1-E7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4519184
BLAST score
                  215
E value
                  1.0e-117
                  425
Match length
% identity
                  94
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K16F13, complete sequence
Seq. No.
                  151235
Seq. ID
                  LIB3175-055-P1-K1-F2
                  BLASTN
Method
NCBI GI
                  g2642152
BLAST score
                  360
E value
                  0.0e + 00
                  381
Match length
% identity
                  99
                  Arabidopsis thaliana chromosome II BAC T5I7 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  151236
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-F3
Method
                  BLASTX
```

```
NCBI GI
                   q3341690
BLAST score
                   563
E value
                   4.0e-58
Match length
                   123
% identity
                   88
                   (AC003672) hypothetical protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   151237
                   LIB3175-055-P1-K1-F4
Seq. ID
                   BLASTN
Method
NCBI GI
                   g4531433
BLAST score
                   63
                   6.0e-27
E value
                   251
Match length
                   87
% identity
                   Arabidopsis thaliana chromosome II P1 MFL8 genomic
NCBI Description
                   sequence, complete sequence
Seq. No.
                   151238
Seq. ID
                   LIB3175-055-P1-K1-F5
Method
                   BLASTX
NCBI GI
                   g4531442
BLAST score
                   612
E value
                   7.0e-64
                   137
Match length
                   92
% identity
                   (AC006224) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   151239
Seq. No.
                   LIB3175-055-P1-K1-F7
Seq. ID
Method
                   BLASTN
NCBI GI
                   g4220640
BLAST score
                   64
E value
                   1.0e-27
                   200
Match length
% identity
                   83
                   Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
NCBI Description
                   MPE11, complete sequence [Arabidopsis thaliana]
                   151240
Seq. No.
                   LIB3175-055-P1-K1-F9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4185505
BLAST score
                   451
E value
                   6.0e-45
Match length
                   115
% identity
                   75
                   (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                   [Brassica napus]
                   151241
Seq. No.
Seq. ID
                   LIB3175-055-P1-K1-G10
Method
                   BLASTX
NCBI GI
                   g1170203
BLAST score
                   540
E value
                   2.0e-55
Match length
                   143
```

```
% identity
NCBI Description
                  GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) >gi 454359
                  (U03774) glutamyl-tRNA reductase [Arabidopsis thaliana]
                  151242
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-G11
Method
                  BLASTN
NCBI GI
                  q4531433
BLAST score
                  117
                  5.0e-59
E value
Match length
                  342
                  87
% identity
                  Arabidopsis thaliana chromosome II P1 MFL8 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  151243
Seq. ID
                  LIB3175-055-P1-K1-G2
Method
                  BLASTX
NCBI GI
                  g2129759
                  557
BLAST score
                  2.0e-57
E value
Match length
                  108
% identity
                  96
NCBI Description
                  UDPglucose 4-epimerase (EC 5.1.3.2) - Arabidopsis thaliana
                  >gi 1143392 emb CAA90941 (Z54214) uridine diphosphate
                  glucose epimerase [Arabidopsis thaliana]
                  151244
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-G3
Method
                  BLASTN
                  g4531433
NCBI GI
BLAST score
                  33
                  3.0e-09
E value
                  89
Match length
% identity
                  84
                  Arabidopsis thaliana chromosome II P1 MFL8 genomic
NCBI Description
                  sequence, complete sequence
Seq. No.
                  151245
Seq. ID
                  LIB3175-055-P1-K1-G6
Method
                  BLASTX
NCBI: GI
                  q4531442
BLAST score
                  225
E value
                  1.0e-31
                  142
Match length
% identity
NCBI Description (AC006224) hypothetical protein [Arabidopsis thaliana]
Seq. No.
                  151246
Seq. ID
                  LIB3175-055-P1-K1-G9
Method
                  BLASTN
NCBI GI
                  g4406752
BLAST score
                  40
E value
                  3.0e-13
Match length
                  60
                  92
% identity
NCBI Description Arabidopsis thaliana chromosome II BAC F19B11 genomic
```



```
sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                   151247
                   LIB3175-055-P1-K1-H10
Seq. ID
Method
                   BLASTX
NCBI GI
                   g4734010
BLAST score
                   325
E value
                   4.0e-30
                   144
Match length
% identity
                   44
                  (AC007178) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                   151248
Seq. No.
Seq. ID
                   LIB3175-055-P1-K1-H11
Method
                   BLASTX
NCBI GI
                   g1864017
BLAST score
                   541
E value
                   1.0e-55
                   104
Match length
                   98
% identity
                  (D63396) elongation factor-1 alpha [Nicotiana tabacum]
NCBI Description
Seq. No.
                   151249
Seq. ID
                   LIB3175-055-P1-K1-H12
Method
                   BLASTN
NCBI GI
                   q2058281
BLAST score
                   48
                   3.0e-18
E value
Match length
                   108
                   94
% identity
                  A.thaliana mRNA for AtRanBPla protein
NCBI Description
Seq. No.
                   151250
                   LIB3175-055-P1-K1-H3
Seq. ID
Method
                   BLASTX
NCBI GI
                   g2654440
BLAST score
                   266
E value
                   3.0e-23
Match length
                   124
% identity
                   52
NCBI Description (U70076) Lemir [Lycopersicon esculentum]
                   151251
Seq. No.
                  LIB3175-055-P1-K1-H4
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4734010
BLAST score
                  277
                   1.0e-24
E value
Match length
                  122
% identity
                  (AC007178) hypothetical protein [Arabidopsis thaliana]
NCBI Description
                  151252
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-H5
```

Method BLASTX NCBI GI g4734009 BLAST score 61

```
E value
                   1.0e-09
Match length
                  107
                   31
% identity
NCBI Description
                  (AC007178) hypothetical protein [Arabidopsis thaliana]
                  151253
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-H6
                  BLASTX
Method
NCBI GI
                  q3893822
BLAST score
                  501
E value
                   6.0e-51
                  116
Match length
% identity
                  (U96498) ATPase beta subunit [Nicotiana sylvestris]
NCBI Description
                  151254
Seq. No.
Seq. ID
                  LIB3175-055-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g3421102
BLAST score
                  652
E value
                  1.0e-68
Match length
                  133
% identity
                  (AF043530) 20S proteasome beta subunit PBB1 [Arabidopsis
NCBI Description
                  thaliana]
                  151255
Seq. No.
                  LIB3175-055-P1-K1-H9
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2191177
BLAST score
                  625
E value
                  2.0e-65
Match length
                  128
% identity
                  100
                  (AF007270) belongs to the SPOU family of rRNA methylases.
NCBI Description
                   [Arabidopsis thaliana]
                  151256
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-A1
Method
                  BLASTN
NCBI GI
                  g3449326
BLAST score
                  447
E value
                  0.0e + 00
Match length
                  463
% identity
                  99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K19M22, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151257
Seq. ID
                  LIB3175-056-P1-K1-A11
Method
                  BLASTX
NCBI GI
                  g4469003
BLAST score
                  179
E value
                  4.0e-13
Match length
                  120
% identity
                  (AL035602) putative protein [Arabidopsis thaliana]
NCBI Description
```

```
Seq. No.
                  151258
Seq. ID
                  LIB3175-056-P1-K1-A12
Method
                  BLASTN
NCBI GI
                   g4589418
BLAST score
                   192
E value
                   1.0e-104
                   449
Match length
                   99
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                  K21G20, complete sequence
                  151259
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-A3
                  BLASTX
Method
NCBI GI
                   g3286693
BLAST score
                   568
E value
                   1.0e-58
Match length
                   122
% identity
                   93
NCBI Description
                   (Y15433) 33 kDa polypeptide of oxygen-evolving complex
                   (OEC) in photosystem II [Arabidopsis thaliana]
Seq. No.
                   151260
Seq. ID
                  LIB3175-056-P1-K1-A4
Method
                  BLASTX
NCBI GI
                  g3043415
BLAST score
                  761
E value
                  3.0e-81
Match length
                  151
                   99
% identity
NCBI Description
                  (Y17053) At-hsc70-3 [Arabidopsis thaliana]
Seq. No.
                  151261
Seq. ID
                  LIB3175-056-P1-K1-A5
Method
                  BLASTN
NCBI GI
                  g2244991
BLAST score
                  268
E value
                   1.0e-149
Match length
                   456
                   97
% identity
NCBI Description
                  Arabidopsis thaliana DNA chromosome 4, ESSA I contig
                  fragment No
Seq. No.
                  151262
Seq. ID
                  LIB3175-056-P1-K1-A7
Method
                  BLASTX
NCBI GI
                  g4204260
BLAST score
                  225
                  2.0e-18
E value
                  57
Match length
% identity
NCBI Description (AC005223) 25568 [Arabidopsis thaliana]
Seq. No.
                  151263
Seq. ID
                  LIB3175-056-P1-K1-B10
Method
                  BLASTX
```

```
NCBI GI
                    g3928134
BLAST score
                    536
E value
                    7.0e-55
                    147
Match length
                    29
% identity
NCBI Description
                   (AJ130956) annexin P38 [Capsicum annuum]
Seq. No.
                    151264
Seq. ID
                    LIB3175-056-P1-K1-B11
Method
                    BLASTX
NCBI GI
                    q4099088
BLAST score
                    509
E value
                    1.0e-51
                    101
Match length
                    100
% identity
                   (U83177) SNF1 family protein kinase [Arabidopsis thaliana]
NCBI Description
Seq. No.
                    151265
Seq. ID
                    LIB3175-056-P1-K1-B12
Method
                    BLASTN
NCBI GI
                    g4049332
BLAST score
                    342
E value
                    0.0e + 00
Match length
                    454
                    99
% identity
                    Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4
NCBI Description
                    (ESSAII project)
Seq. No.
                    151266
Seq. ID
                    LIB3175-056-P1-K1-B2
Method
                    BLASTX
NCBI GI
                    g1931639
                    255
BLAST score
E value
                    6.0e-22
Match length
                    110
% identity
                    43
NCBI Description (U95973) lysophospholipase isolog [Arabidopsis thaliana]
Seq. No.
                    151267
Seq. ID
                    LIB3175-056-P1-K1-B3
Method
                    BLASTX
NCBI GI
                    g1703108
BLAST score
                    672
E value
                    8.0e-71
Match length
                    125
% identity
                    100
                    ACTIN 2/7 >gi 2129525 pir S71210 actin 2 - Arabidopsis thaliana >gi 2129528 pir S68107 actin 7 - Arabidopsis thaliana >gi 1049307 (U37281) actin-2 [Arabidopsis
NCBI Description
                    thaliana] >gi 1943863 (U27811) actin7 [Arabidopsis
                    thaliana]
Seq. No.
                    151268
Seq. ID
                    LIB3175-056-P1-K1-B4
Method
                    BLASTX
NCBI GI
                    g1705620
BLAST score
                    788
```

```
E value
                   2.0e-84
Match length
                   147
% identity
                   100
                  CATALASE 2 >gi 1246399 emb CAA64220 (X94447) catalase
NCBI Description
                   [Arabidopsis thaliana]
                   151269
Seq. No.
Seq. ID
                   LIB3175-056-P1-K1-B6
Method
                  BLASTX
NCBI GI
                   g3582340
                  189
BLAST score
                   3.0e-14
E value
                  88
Match length
                   49
% identity
NCBI Description (AC005496) unknown protein [Arabidopsis thaliana]
                   151270
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-C1
Method
                  BLASTX
NCBI GI
                   g3913648
BLAST score
                   376
                   4.0e-36
E value
Match length
                  122
                   60
% identity
NCBI Description FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR)
                  151271
Seq. No.
                  LIB3175-056-P1-K1-C4
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3241923
BLAST score
                  245
E value
                   1.0e-135
Match length
                   461
% identity
                   99
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MMN10, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151272
Seq. ID
                  LIB3175-056-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  g1531762
BLAST score
                  195
E value
                   6.0e-15
Match length
                  51
% identity
                  (Y07765) S-adenosylmethionine decarboxylase [Arabidopsis
NCBI Description
                  thaliana]
                  151273
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-C7
                  BLASTX
Method
NCBI GI
                  g4235093
BLAST score
                  143
E value
                  9.0e-09
Match length
                  102
% identity
NCBI Description (AF108944) beta-xylosidase [Aspergillus niger]
```

```
Seq. No.
                   151274
Seq. ID
                   LIB3175-056-P1-K1-C9
Method
                   BLASTX
NCBI GI
                   g927428
BLAST score
                   637
E value
                   1.0e-66
Match length
                   152
% identity
                   79
NCBI Description
                   (X86733) fis1 [Linum usitatissimum]
Seq. No.
                   151275
                   LIB3175-056-P1-K1-D10
Seq. ID
Method
                   BLASTX
NCBI GI
                   q3641837
BLAST score
                   620
E value
                   1.0e-64
Match length
                   125
% identity
                   99
NCBI Description
                   (AL023094) Nonclathrin coat protein gamma - like protein
                   [Arabidopsis thaliana]
Seq. No.
                   151276
                   LIB3175-056-P1-K1-D11
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4159707
                   273
BLAST score
                   1.0e-152
E value
                   454
Match length
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone:
                  MJK13, complete sequence
Seq. No.
                   151277
Seq. ID
                  LIB3175-056-P1-K1-D2
Method
                  BLASTX
NCBI GI
                   g1922937
BLAST score
                   644
E value
                   1.0e-67
Match length
                   126
% identity
                   100
                   (AC000106) Similar to Glycine SRC2 (gb AB000130). ESTs
NCBI Description
                   gb_H76869,gb_T21700,gb_ATTS5089 come from this gene.
                   [Arabidopsis thaliana]
Seq. No.
                   151278
Seq. ID
                  LIB3175-056-P1-K1-D3
Method
                  BLASTX
NCBI GI
                   g2160169
BLAST score
                   349
E value
                   6.0e-33
Match length
                   126
% identity
                   (AC000132) No definition line found [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   151279
Seq. ID
                  LIB3175-056-P1-K1-D4
```

```
Method
                  BLASTX
NCBI GI
                  q3292829
BLAST score
                  209
E value
                  2.0e-16
                  82
Match length
% identity
                  (AL031018) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  151280
Seq. ID
                  LIB3175-056-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  q112681
BLAST score
                  647
E value
                  7.0e-68
Match length
                  151
                  83
% identity
                  12S SEED STORAGE PROTEIN PRECURSOR >gi 81604 pir S08509
NCBI Description
                  cruciferin precursor (CRA1) - Arabidopsis thaliana
                  >gi 166676 (M37247) 12S storage protein CRA1 [Arabidopsis
                  thaliana] >gi 808936 emb CAA32493 (X14312) 12S seed
                  storage protein [Arabidopsis thaliana]
                  151281
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-D7
Method
                  BLASTN
NCBI GI
                  q3510343
BLAST score
                  428
E value
                  0.0e+00
Match length
                  428
% identity
                  100
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MJC20, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151282
Seq. ID
                  LIB3175-056-P1-K1-D9
Method
                  BLASTX
NCBI GI
                  q4678349
BLAST score
                  678
E value
                  2.0e-71
Match length
                  151
% identity
                  (AL049659) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  151283
Seq. ID
                  LIB3175-056-P1-K1-E1
Method
                  BLASTX
NCBI GI
                  g3668175
BLAST score
                  677
E value
                  2.0e-71
Match length
                  145
% identity
                  (AB006778) vegetative storage protein [Arabidopsis
NCBI Description
                  thaliana]
                  151284
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-E10
Method
                  BLASTX
```

```
NCBI GI
                   q4725950
BLAST score
                   274
                   4.0e-24
E value
Match length
                   129
                   50
% identity
NCBI Description
                   (AL049730) putative Phospholipase D [Arabidopsis thaliana]
                   >gi 4725951 emb CAB41722.1 (ALO49730) putative
                   proline-rich protein [Arabidopsis thaliana]
                   151285
Seq. No.
Seq. ID
                   LIB3175-056-P1-K1-E11
Method
                   BLASTX
NCBI GI
                   g2623962
BLAST score
                   668
E value
                   2.0e-70
                   144
Match length
% identity
                   86
NCBI Description
                   (Y12540) isocitrate dehydrogenase (NADP+) [Apium
                   graveolens]
Seq. No.
                   151286
Seq. ID
                   LIB3175-056-P1-K1-E12
Method
                   BLASTX
NCBI GI
                   q4033467
BLAST score
                   189
E value
                   3.0e-14
                   36
Match length
                   100
% identity
                   ARGININE/SERINE-RICH SPLICING FACTOR RSP31
NCBI Description
                   >gi_1707366_emb_CAA67798_ (X99435) splicing factor
                   [Arabidopsis thaliana]
                   151287
Seq. No.
Seq. ID
                   LIB3175-056-P1-K1-E4
Method
                   BLASTX
NCBI GI
                   g2979559
                   276
BLAST score
E value
                   2.0e-24
Match length
                   60
% identity
                   (AC003680) putative DNA binding protein [Arabidopsis
NCBI Description
                   thaliana]
Seq. No.
                   151288
                  LIB3175-056-P1-K1-E5
Seq. ID
Method
                  BLASTX
NCBI GI
                   g4567269
BLAST score
                   607
E value
                   3.0e-63
Match length
                  133
% identity
                   91
NCBI Description (AC006841) unknown protein [Arabidopsis thaliana]
Seq. No.
                  151289
Seq. ID
                  LIB3175-056-P1-K1-E6
Method
                  BLASTX
NCBI GI
                  g464986
```

BLAST score E value 6.0e-78 Match length 137 % identity 99 NCBI Description

UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN

LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi\_421857\_pir\_\_S32674 ubiquitin--protein ligase (EC
6.3.2.19) UBC9 - Arabidopsis thaliana

>gi\_297884\_emb\_CAA78714\_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi\_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana]

>gi 600391 emb CAA51201 (X72626) ubiquitin conjugating

enzyme E2 [Arabidopsis thaliana]

>gi 4455355\_emb\_CAB36765.1 (AL035524) ubiquitin-protein

ligase UBC9 [Arabidopsis thaliana]

Seq. No. Seq. ID

151290 LIB3175-056-P1-K1-E7

Method BLASTX NCBI GI q3947448 BLAST score 346 E value 1.0e-32 151 Match length % identity

NCBI Description (AL033535) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this

gene; cDNA EST yk499g5.5 comes from this gene

[Caenorhabdi... >gi\_3947543\_emb\_CAA88952\_ (Z49127) cDNA EST yk301f1.5 comes from this gene; cDNA EST yk475f6.3 comes from this gene; cDNA EST yk301f1.3 comes from this gene; cDNA EST yk475f6.5 comes from this gene; cDNA EST yk499g5.5

comes from this gene [Caenorhabditi

Seq. No. Seq. ID

151291

LIB3175-056-P1-K1-E9

Method BLASTX NCBI GI q2244981 BLAST score 262 E value 9.0e-23 113 Match length % identity

NCBI Description (Z97340) similarity to proline-rich protein APG -

Arabidopsis [Arabidopsis thaliana]

Seq. No. 151292

Seq. ID LIB3175-056-P1-K1-F1

Method BLASTN NCBI GI g3406034 BLAST score 213 1.0e-116 E value Match length 418

98 % identity NCBI Description BAC F18A17 from chromosome V containing TINY at 60.5 cM,

complete sequence [Arabidopsis thaliana]

Seq. No. 151293

19348 .

, A. . . .

```
Seq. ID
                   LIB3175-056-P1-K1-F10
Method
                   BLASTX
NCBI GI
                   q2505874
BLAST score
                   705
E value
                   9.0e-75
Match length
                   137
                   99
% identity
NCBI Description
                   (Y12776) putative kinase [Arabidopsis thaliana]
Seq. No.
                   151294
                  LIB3175-056-P1-K1-F11
Seq. ID
                   BLASTX
Method
NCBI GI
                   g3451077
BLAST score
                   146
                   2.0e-09
E value
Match length
                   36
% identity
                   69
                   (AL031326) cysteine proteinase - like protein [Arabidopsis
NCBI Description
                   thaliana]
                   151295
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-F12
Method
                   BLASTN
NCBI GI
                   g4220633
BLAST score
                   362
                   0.0e + 00
E value
Match length
                   398
                   98
% identity
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
NCBI Description
                   K7J8, complete sequence [Arabidopsis thaliana]
                   151296
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-F3
Method
                   BLASTX
NCBI GI
                   q3668086
                   223
BLAST score
E value
                   4.0e-18
Match length
                   64
% identity
NCBI Description
                   (AC004667) unknown protein [Arabidopsis thaliana]
Seq. No.
                   151297
Seq. ID
                  LIB3175-056-P1-K1-F4
Method
                  BLASTX
NCBI GI
                   q4503161
BLAST score
                   196
E value
                   5.0e-15
Match length
                  141
                   30
% identity
                  cullin 1 >gi 2493906 sp Q13616 CUL1 HUMAN CULLIN HOMOLOG 1
NCBI Description
                   (CUL-1) >gi 1381142 (U58087) Hs-CUL-1 [Homo sapiens]
Seq. No.
                  151298
Seq. ID
                  LIB3175-056-P1-K1-F5
Method
                  BLASTN
NCBI GI
                  g3193282
BLAST score
                  452
```

```
E value
                  0.0e + 00
Match length
                  460
% identity
                  100
                  Arabidopsis thaliana BAC T14P8
NCBI Description
                  151299
Seq. No.
                  LIB3175-056-P1-K1-F6
Seq. ID
Method
                  BLASTN
NCBI GI
                  g3702729
BLAST score
                  140
E value
                  9.0e-73
                  401
Match length
% identity
                  98
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K2A11, complete sequence [Arabidopsis thaliana]
                  151300
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-F7
Method
                  BLASTX
NCBI GI
                  g4539465
BLAST score
                  138
E value
                  1.0e-31
                  72
Match length
                  91
% identity
NCBI Description
                  (AL049500) putative protein [Arabidopsis thaliana]
Seq. No.
                  151301
                  LIB3175-056-P1-K1-F8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g1755162
BLAST score
                  640
E value
                  4.0e-67
Match length
                  138
% identity
                  90
NCBI Description
                  (U75192) germin-like protein [Arabidopsis thaliana]
Seq. No.
                  151302
Seq. ID
                  LIB3175-056-P1-K1-F9
Method
                  BLASTX
NCBI GI
                  g4741952
BLAST score
                  679
E value
                  1.0e-71
                  128
Match length
% identity
                  76
NCBI Description
                  (AF134126) Lhcb3 protein [Arabidopsis thaliana]
Seq. No.
                  151303
Seq. ID
                  LIB3175-056-P1-K1-G1
Method
                  BLASTX
NCBI GI
                  q3914658
BLAST score
                  645
E value
                  1.0e-67
Match length
                  146
                  87
% identity
                  50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR
NCBI Description
                  >gi 1694974 emb CAA70851 (Y09635) plastid ribosomal
                  protein [Arabidopsis thaliana]
```

Seq. No.

Seq. No. 151304 Seq. ID LIB3175-056-P1-K1-G11 Method BLASTX NCBI GI g4741952 BLAST score 709 E value 4.0e-75 Match length 136 % identity 75 NCBI Description (AF134126) Lhcb3 protein [Arabidopsis thaliana] Seq. No. 151305 Seq. ID LIB3175-056-P1-K1-G2 Method BLASTX NCBI GI q1706772 BLAST score 788 E value 2.0e-84 Match length 148 % identity 100 FARNESYL-DIPHOSPHATE FARNESYLTRANSFERASE (SQUALENE NCBI Description SYNTHETASE) (SQS) (SS) (FPP: FPP FARNESYLTRANSFERASE) >gi 1076324 pir S54251 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) - Arabidopsis thaliana >gi 798820 emb CAA60385 (X86692) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi\_806325\_dbj\_BAA06103\_ (D29017) squalene synthase
[Arabidopsis thaliana] >gi\_2232212 (AF004560) squalene synthase 1 [Arabidopsis thaliana] >gi 3096933 emb CAA18843.1 (AL023094) farnesyl-diphosphate farnesyltransferase [Arabidopsis thaliana] >gi 4098519 (U79159) squalene synthase [Arabidopsis thaliana] Seq. No. 151306 Seq. ID LIB3175-056-P1-K1-G3 Method BLASTX NCBI GI g2497886 BLAST score 289 E value 6.0e-26Match length 53 % identity METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B) NCBI Description >gi\_1361999\_pir\_\_S57862 metallothionein 2b - Arabidopsis thaliana >gi 1086463 (U11256) metallothionein [Arabidopsis thaliana] Seq. No. 151307 Seq. ID LIB3175-056-P1-K1-G4 Method BLASTX NCBI GI g2494275 BLAST score 250 E value 2.0e-21 Match length 75 % identity NCBI Description ELONGATION FACTOR P (EF-P) >gi 1399829 (U59235) elongation

19351

factor P [Synechococcus PCC7942]

```
LIB3175-056-P1-K1-G6
Seq. ID
                  BLASTN
Method
                  a3059018
NCBI GI
                  41
BLAST score
                  1.0e-13
E value
                  453
Match length
                  95
% identity
                  Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12
NCBI Description
                  (ESSAII project)
                  151309
Seq. No.
                  LIB3175-056-P1-K1-G8
Seq. ID
                  BLASTX
Method
NCBI GI
                  q2781394
                  239
BLAST score
                  5.0e-20
E value
                  108
Match length
                  52
% identity
NCBI Description (U70424) O-methyltransferase 1 [Arabidopsis thaliana]
                  151310
Seq. No.
                  LIB3175-056-P1-K1-H1
Seq. ID
Method
                  BLASTN
NCBI GI
                  q3985958
                  312
BLAST score
E value
                  1.0e-175
                  428
Match length
% identity
                  97
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
NCBI Description
                  MZN1, complete sequence [Arabidopsis thaliana]
                  151311
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-H10
Method
                  BLASTX
NCBI GI
                  g4544399
BLAST score
                  475
                  8.0e-48
E value
                  132
Match length
% identity
                   (AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis
NCBI Description
                   thaliana]
                   151312
Seq. No.
                  LIB3175-056-P1-K1-H11
Seq. ID
Method
                   BLASTX
                   q1107501
NCBI GI
BLAST score
                   402
                   4.0e-39
E value
                   99
Match length
% identity
                   (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
NCBI Description
                   Match to gb_X91954 orf gene product from A. thaliana. ESTs
                   gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                   this gene. [Arabidopsis thaliana]
                   151313
Seq. No.
                   LIB3175-056-P1-K1-H12
Seq. ID
```

```
Method
                  BLASTX
NCBI GI
                  g1363487
BLAST score
                  422
                  8.0e-42
E value
                  85
Match length
% identity
                  100
                  IAA7 protein - Arabidopsis thaliana >gi_972917 (U18409)
NCBI Description
                  IAA7 [Arabidopsis thaliana]
                  151314
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-H2
Method
                  BLASTX
NCBI GI
                  g2462749
BLAST score
                  147
                  3.0e-09
E value
Match length
                  107
% identity
                  32
NCBI Description
                   (AC002292) Putative Serine/Threonine protein kinase
                  [Arabidopsis thaliana]
                  151315
Seq. No.
Seq. ID
                  LIB3175-056-P1-K1-H3
Method
                  BLASTX
NCBI GI
                  g2911057
BLAST score
                  636
E value
                  1.0e-66
Match length
                  124
% identity
                  100
                   (AL021961) caffeoyl-CoA O-methyltransferase - like protein
NCBI Description
                  [Arabidopsis thaliana]
Seq. No.
                  151316
Seq. ID
                  LIB3175-056-P1-K1-H5
Method
                  BLASTX
NCBI GI
                  g1107501
BLAST score
                  199
E value
                  1.0e-15
Match length
                  84
% identity
NCBI Description
                  (X91954) orf [Arabidopsis thaliana] >gi_3367530 (AC004392)
                  Match to gb_X91954 orf gene product from A. thaliana. ESTs
                  gb_Z17604, gb_H76594, gb_AA597972 and gb_AA394824 come from
                  this gene. [Arabidopsis thaliana]
Seq. No.
                  151317
                  LIB3175-056-P1-K1-H7
Seq. ID
Method
                  BLASTX
NCBI GI
                  q481914
BLAST score
                  608
                  2.0e-63
E value
                  120
Match length
% identity
                  glutamate--ammonia ligase (EC 6.3.1.2) - rape
NCBI Description
                  >gi_436422_emb_CAA54151.1_ (X76736) glutamine [Brassica
                  napus]
Seq. No.
                  151318
```

19353

e, '

Seq. No.

151323

Seq. ID LIB3175-056-P1-K1-H9 Method BLASTX NCBI GI g4587549 BLAST score 320 E value 1.0e-29 Match length 59 % identity 100 (ACO06577) Similar to gb\_U55861 RNA binding protein NCBI Description nucleolysin (TIAR) from Mus musculus and contains several PF\_00076 RNA recognition motif domains. ESTs gb T21032 and gb T44127 come from this gene. [Arabidopsis t 151319 Seq. No. Seq. ID LIB3175-057-P1-K1-A1 Method BLASTX NCBI GI g2146727 BLAST score 515 2.0e-55 E value Match length 123 97 % identity NCBI Description cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 -Arabidopsis thaliana (fragment) >gi 598069 (L37884) cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana] Seq. No. 151320 Seq. ID LIB3175-057-P1-K1-A10 Method BLASTX NCBI GI g1871185 BLAST score 232 3.0e-19 E value Match length 62 % identity 77 (U90439) seven in absentia isolog [Arabidopsis thaliana] NCBI Description 151321 Seq. No. Seq. ID LIB3175-057-P1-K1-A11 Method BLASTN NCBI GI g4249393 BLAST score 266 E value 1.0e-148 Match length 274 99 % identity NCBI Description Arabidopsis thaliana chromosome II BAC T9J23 genomic sequence, complete sequence [Arabidopsis thaliana] Seq. No. 151322 Seq. ID LIB3175-057-P1-K1-A12 Method BLASTX NCBI GI g1707013 BLAST score 222 E value 4.0e-18 Match length 90 % identity NCBI Description (U78721) Brassica napus hypothetical protein 2 isolog [Arabidopsis thaliana]

```
Seq. ID
                   LIB3175-057-P1-K1-A2
Method
                   BLASTN
NCBI GI
                   q598070
BLAST score
                   51
E value
                   4.0e-20
Match length
                   83
                   90
% identity
NCBI Description
                  Arabidopsis thaliana cinnamyl alcohol dehydrogenase (CAD1)
                   gene, complete cds
                   151324
Seq. No.
                  LIB3175-057-P1-K1-A4
Seq. ID
                  BLASTX
Method
NCBI GI
                   g1001294
BLAST score
                   264
                   5.0e-23
E value
                   104
Match length
                   42
% identity
NCBI Description
                   (D64006) hypothetical protein [Synechocystis sp.]
Seq. No.
                   151325
Seq. ID
                  LIB3175-057-P1-K1-A6
Method
                  BLASTX
NCBI GI
                   g3269293
BLAST score
                   259
E value
                   2.0e-22
                   95
Match length
                   57
% identity
                   (AL030978) putative protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                   151326
                  LIB3175-057-P1-K1-A7
Seq. ID
Method
                   BLASTX
                   g2146727
NCBI GI
BLAST score
                   328
E value
                   7.0e-31
                   67
Match length
                   100
% identity
                   cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) CAD1 -
NCBI Description
                  Arabidopsis thaliana (fragment) >gi 598069 (L37884)
                  cinnamyl-alcohol dehydrogenase [Arabidopsis thaliana]
                   151327
Seq. No.
                  LIB3175-057-P1-K1-A8
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3033400
                   402
BLAST score
E value
                   3.0e-39
                  78
Match length
% identity
                   (AC004238) putative Ser/Thr protein kinase [Arabidopsis
NCBI Description
                  thaliana]
                  151328
Seq. No.
                  LIB3175-057-P1-K1-B1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3212879
```

```
BLAST score
                  593
E value
                  1.0e-61
Match length
                  142
% identity
                  85
NCBI Description
                  (AC004005) putative ribosomal protein L7 [Arabidopsis
                  thaliana]
                  151329
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g1168256
BLAST score
                  679
                  1.0e-71
E value
                  142
Match length
                  94
% identity
NCBI Description ASPARTATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR
                  (TRANSAMINASE A) >gi_693688 (U15026) aspartate
                  aminotransferase [Arabidopsis thaliana] >gi_3201622
                  (AC004669) aspartate aminotransferase [Arabidopsis
                  thaliana]
                  151330
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-B2
Method
                  BLASTN
NCBI GI
                  q472876
BLAST score
                  75
E value
                  2.0e-34
Match length
                  123
% identity
                  90
NCBI Description A.thaliana mRNA for plasma membrane intrinsic protein 2a
Seq. No.
                  151331
Seq. ID
                  LIB3175-057-P1-K1-B3
Method
                  BLASTX
NCBI GI
                  g115783
BLAST score
                  619
E value
                  1.0e-64
Match length
                  128
% identity
                  93
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                  (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                  chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                  thaliana]
Seq. No.
                  151332
Seq. ID
                  LIB3175-057-P1-K1-B4
Method
                  BLASTN
NCBI GI
```

Method BLASTN
NCBI GI g2462076
BLAST score 443
E value 0.0e+00
Match length 451
% identity 100

NCBI Description A.thaliana mRNA for oxal-like gene

Seq. No. 151333

Seq. ID LIB3175-057-P1-K1-B6

Method BLASTX

```
q1184075
NCBI GI
BLAST score
                   251
E value
                   2.0e-21
Match length
                   148
% identity
                   3
                    (U42444) Cf-2.1 [Lycopersicon pimpinellifolium]
NCBI Description
                   >gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon
                   esculentum]
                   151334
Seq. No.
                   LIB3175-057-P1-K1-B8
Seq. ID
                   BLASTX
Method
NCBI GI
                   g2499236
BLAST score
                   314
E value
                   2.0e-40
                   113
Match length
                   77
% identity
NCBI Description
                   NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST
                   >gi_1419474_emb_CAA66944_ (X98298) ndhA [Arabidopsis
                   thaliana]
                   151335
Seq. No.
Seq. ID
                   LIB3175-057-P1-K1-B9
Method
                   BLASTX
NCBI GI
                   q4505337
BLAST score
                   281
E value
                   3.0e-25
Match length
                   92
% identity
                   59
NCBI Description
                   nucleotide binding protein 1 (E.coli MinD like)
                   >gi_1709232_sp_P53384_NBP_HUMAN NUCLEOTIDE-BINDING PROTEIN
(NBP) >gi_1082661_pir__JC4010 nucleotide-binding protein -
                   human >gi_515644 (U01833) putative nucleotide-binding
                   protein [Homo sapiens]
                   151336
Seq. No.
Seq. ID
                   LIB3175-057-P1-K1-C1
Method
                   BLASTX
NCBI GI
                   g3273751
BLAST score
                   617
E value
                   2.0e-64
                   143
Match length
% identity
NCBI Description
                   (AF061518) manganese superoxide dismutase [Arabidopsis
                   thaliana]
                   151337
Seq. No.
Seq. ID
                   LIB3175-057-P1-K1-C10
Method
                   BLASTX
NCBI GI
                   q1170897
BLAST score
                   400
E value
                   7.0e-58
Match length
                   146
                   83
% identity
NCBI Description
                   MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR
                   >gi_1076276_pir S52039 NAD-malate dehydrogenase - cucumber
                   >gi 695311 (L31900) glyoxysomal malate dehydrogenase
```

Seq. No.

Seq. ID

151343

LIB3175-057-P1-K1-C7

```
[Cucumis sativus]
Seq. No.
                  151338
Seq. ID
                  LIB3175-057-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  g1762150
BLAST score
                  729
E value
                  2.0e-77
Match length
                  150
                  87
% identity
NCBI Description (U49919) lupeol synthase [Arabidopsis thaliana]
                  151339
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-C3
Method
                  BLASTX
NCBI GI
                  g4204285
BLAST score
                  408
E value
                  5.0e-40
Match length
                  98
                  73
% identity
                   (AC003027) 1cl prt seq No definition line found
NCBI Description
                   [Arabidopsis thaliana]
                  151340
Seq. No.
                  LIB3175-057-P1-K1-C4
Seq. ID
                  BLASTX
Method
NCBI GI
                  g3068713
BLAST score
                  632
E value
                   4.0e-66
Match length
                  145
% identity
                  90
NCBI Description (AF049236) unknown [Arabidopsis thaliana]
Seq. No.
                  151341
Seq. ID
                  LIB3175-057-P1-K1-C5
Method
                  BLASTX
NCBI GI
                  q4455223
BLAST score
                  381
E value
                  1.0e-36
Match length
                  73
% identity
                   (AL035440) putative DNA binding protein [Arabidopsis
NCBI Description
                  thaliana]
Seq. No.
                  151342
Seq. ID
                  LIB3175-057-P1-K1-C6
Method
                  BLASTX
NCBI GI
                  g2454182
BLAST score
                  537
E value
                  5.0e-55
Match length
                  146
                  75
% identity
                  (U80185) pyruvate dehydrogenase E1 alpha subunit
NCBI Description
                  [Arabidopsis thaliana]
```

```
Method
                   BLASTX
NCBI GI
                   g3859560
BLAST score
                   176
E value
                   1.0e-12
Match length
                   96
                   41
% identity
NCBI Description
                   (AF098668) acyl-protein thioesterase [Homo sapiens]
                   >gi_4581413_emb_CAB40158.1_ (AL031295) dJ886K2.4 (acyl-protein thioesterase) [Homo sapiens]
                   151344
Seq. No.
Seq. ID
                   LIB3175-057-P1-K1-D1
Method
                   BLASTX
NCBI GI
                   g3702321
BLAST score
                   727
                   3.0e-77
E value
Match length
                   139
% identity
                   56
                   (AC005397) putative TGF-beta receptor interacting protein
NCBI Description
                   [Arabidopsis thaliana]
Seq. No.
                   151345
Seq. ID
                   LIB3175-057-P1-K1-D10
Method
                   BLASTN
NCBI GI
                   q2160132
BLAST score
                   56
E value
                   6.0e-23
                   112
Match length
% identity
                   88
                   Sequence of BAC F19K23 from Arabidopsis thaliana chromosome
NCBI Description
                   1, complete sequence [Arabidopsis thaliana]
Seq. No.
                   151346
Seq. ID
                   LIB3175-057-P1-K1-D12
Method
                   BLASTX
NCBI GI
                   g2623962
BLAST score
                   379
                   1.0e-36
E value
                   81
Match length
% identity
                   90
                   (Y12540) isocitrate dehydrogenase (NADP+) [Apium
NCBI Description
                   graveolens]
Seq. No.
                   151347
Seq. ID
                   LIB3175-057-P1-K1-D3
Method
                   BLASTX
NCBI GI
                   q4063751
BLAST score
                   217
E value
                   2.0e-17
Match length
                   118
% identity
                   40
NCBI Description
                   (AC005851) putative white protein [Arabidopsis thaliana]
                   >gi_4510409 gb AAD21495.1 (AC006929) putative white
                   protein [Arabidopsis thaliana]
Seq. No.
                   151348
Seq. ID
                   LIB3175-057-P1-K1-D4
```

```
Method
                  BLASTX
NCBI GI
                  q4581156
BLAST score
                  702
E value
                  2.0e-74
                  148
Match length
                   95
% identity
NCBI Description
                  (AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.
                  151349
Seq. ID
                  LIB3175-057-P1-K1-D5
Method
                  BLASTX
NCBI GI
                  g3023848
BLAST score
                  529
E value
                  4.0e-54
Match length
                  116
                  33
% identity
                  GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE
NCBI Description
                  PROTEIN (WD-40 REPEAT AUXIN-DEPENDENT PROTEIN ARCA)
                  >gi 2289095 (U77381) WD-40 repeat protein [Arabidopsis
                  thaliana]
                  151350
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-D6
Method
                  BLASTX
NCBI GI
                  q4512675
BLAST score
                  591
E value
                  2.0e-61
Match length
                  135
% identity
                  81
NCBI Description
                  (AC006931) putative citrate synthase [Arabidopsis thaliana]
                  151351
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-D7
                  BLASTX
Method
NCBI GI
                  q4204274
BLAST score
                  631
E value
                  5.0e-66
                  120
Match length
% identity
                  95
NCBI Description
                   (AC004146) ribulose bisphosphate carboxylase, small subunit
                   [Arabidopsis thaliana]
Seq. No.
                  151352
Seq. ID
                  LIB3175-057-P1-K1-E11
Method
                  BLASTN
NCBI GI
                  g4159710
BLAST score
                  180
E value
                  1.0e-96
Match length
                  360
                  97
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MSD23, complete sequence
                  151353
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-E12
Method
                  BLASTN
NCBI GI
                  g4335744
```

BLAST score

```
BLAST score
                  262
E value
                   1.0e-145
Match length
                   399
% identity
                   99
                  Arabidopsis thaliana chromosome II BAC T4M8 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151354
                  LIB3175-057-P1-K1-E2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3337095
BLAST score
                  447
E value
                  2.0e-44
Match length
                  141
% identity
                   62
NCBI Description
                  (AB016206) polygalacturonase inhibitor (PGIP) [Citrus iyo]
Seq. No.
                  151355
Seq. ID
                  LIB3175-057-P1-K1-E3
Method
                  BLASTN
NCBI GI
                  g2656024
BLAST score
                  180
E value
                  1.0e-96
Match length
                  408
% identity
                  97
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone:
                  K15E6
Seq. No.
                  151356
Seq. ID
                  LIB3175-057-P1-K1-E4
Method
                  BLASTX
NCBI GI
                  g2129579
BLAST score
                  718
E value
                  3.0e-76
Match length
                  137
% identity
                  99
                  Dwarfl protein - Arabidopsis thaliana >gi 516043 (U12400)
NCBI Description
                  Dwarf1 [Arabidopsis thaliana]
Seq. No.
                  151357
Seq. ID
                  LIB3175-057-P1-K1-E7
Method
                  BLASTX
NCBI GI
                  g2160133
BLAST score
                  384
E value
                  5.0e-37
Match length
                  91
% identity
NCBI Description
                  (AC000375) Strong similarity to Arabidopsis
                  gb X91953, F19K23.3, F19K23.15. ESTs
                  gb_T21984,gb_ATTS0219,gb_ATTS0207,gb_T21984 come from this
                  gene. [Arabidopsis thaliana]
Seq. No.
                  151358
Seq. ID
                  LIB3175-057-P1-K1-E8
Method
                  BLASTX
NCBI GI
                  g3894183
```

```
E value
                   9.0e-46
Match length
                   130
% identity
                   74
NCBI Description
                   (AC005662) calmodulin-like protein [Arabidopsis thaliana]
Seq. No.
                   151359
                   LIB3175-057-P1-K1-E9
Seq. ID
Method
                   BLASTX
NCBI GI
                   g3511285
BLAST score
                   311
E value
                   2.0e-28
Match length
                   113
                   51
% identity
NCBI Description
                   (AF081534) cellulose synthase [Populus alba x Populus
                   tremula]
                   151360
Seq. No.
Seq. ID
                   LIB3175-057-P1-K1-F1
Method
                   BLASTX
NCBI GI
                   g120669
BLAST score
                   314
E value
                   3.0e-29
Match length
                   64
% identity
NCBI Description
                   GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
                   >gi_66014_pir__DEJMG glyceraldehyde-3-phosphate
dehydrogenase (EC 1.2.1.12) - Magnolia liliiflora
                   >gi_19566_emb_CAA42905_ (X60347) glyceraldehyde
                   3-phosphate dehydrogenase [Magnolia liliiflora]
Seq. No.
                   151361
                   LIB3175-057-P1-K1-F10
Seq. ID
Method
                   BLASTN
NCBI GI
                   q4510360
BLAST score
                   271
E value
                   1.0e-151
Match length
                   372
                   97
% identity
NCBI Description
                   Arabidopsis thaliana chromosome II BAC F11F19 genomic
                   sequence, complete sequence
Seq. No.
                   151362
Seq. ID
                   LIB3175-057-P1-K1-F11
Method
                   BLASTX
NCBI GI
                   q4538897
BLAST score
                   659
E value
                   3.0e-69
Match length
                   130
% identity
                   100
NCBI Description
                   (ALO49482) AX110P-like protein [Arabidopsis thaliana]
Seq. No.
                   151363
Seq. ID
                   LIB3175-057-P1-K1-F2
Method
                   BLASTX
NCBI GI
                   g115783
BLAST score
                   686
E value
                   2.0e-72
```

```
Match length
                   137
% identity
                   96
                  CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE I PRECURSOR
NCBI Description
                   (CAB-140) (LHCP) >gi_16376_emb_CAA27543_ (X03909)
                   chlorophyll a/b binding protein (LHCP AB 140) [Arabidopsis
                   thaliana]
                   151364
Seq. No.
Seq. ID
                   LIB3175-057-P1-K1-F4
Method
                   BLASTX
NCBI GI
                   q1666171
BLAST score
                   592
E value
                   2.0e-61
Match length
                   130
% identity
                   82
NCBI Description
                   (Y09105) unknown [Nicotiana plumbaginifolia]
Seq. No.
                  151365
Seq. ID
                  LIB3175-057-P1-K1-F5
Method
                   BLASTN
NCBI GI
                   q2351062
BLAST score
                   145
E value
                   6.0e-76
Match length
                   220
% identity
                   92
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  MAH20, complete sequence [Arabidopsis thaliana]
Seq. No.
                   151366
Seq. ID
                   LIB3175-057-P1-K1-F9
Method
                   BLASTN
NCBI GI
                   g4757392
BLAST score
                   159
E value
                   3.0e-84
Match length
                  187
% identity
                   97
                  Arabidopsis thaliana genomic DNA, chromosome 3, TAC clone:
NCBI Description
                   K14A17, complete sequence
Seq. No.
                   151367
Seq. ID
                   LIB3175-057-P1-K1-G1
Method
                  BLASTX
NCBI GI
                   g3395938
BLAST score
                   578
E value
                   8.0e-60
Match length
                  126
% identity
                   90
NCBI Description
                   (AF076924) polypyrimidine tract-binding protein homolog
                   [Arabidopsis thaliana]
Seq. No.
                   151368
                  LIB3175-057-P1-K1-G2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g2129609
BLAST score
                  372
E value
                   1.0e-35
Match length
                   123
```

```
% identity
NCBI Description
                  HD-ZIP protein - Arabidopsis thaliana
                  >qi 1212757 emb CAA91183 (Z54356) HD-ZIP [Arabidopsis
                  thaliana]
                  151369
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-G3
Method
                  BLASTX
NCBI GI
                  g1170505
                  547
BLAST score
E value
                  4.0e-56
                  105
Match length
% identity
                  100
                  EUKARYOTIC INITIATION FACTOR 4A-2 (EIF-4A-2)
NCBI Description
                  >gi 322504 pir JC1453 translation initiation factor
                  eIF-4A2 - Arabidopsis thaliana >gi 16556 emb CAA46189
                   (X65053) eukaryotic translation initiation factor 4A-2
                   [Arabidopsis thaliana] >gi 4585969 gb AAD25605.1 AC005287 7
                   (AC005287) Eukaryotic Initiation Factor 4A-2 [Arabidopsis
                  thaliana]
                  151370
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-G6
Method
                  BLASTX
NCBI GI
                  q542157
BLAST score
                  631
E value
                  5.0e-66
Match length
                  148
% identity
                  81
NCBI Description ribosomal 5S RNA-binding protein - Rice
Seq. No.
                  151371
                  LIB3175-057-P1-K1-G7
Seq. ID
Method
                  BLASTN
NCBI GI
                  q4589446
BLAST score
                  120
                  6.0e-61
E value
Match length
                  302
                  91
% identity
NCBI Description
                  Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                  T12B11, complete sequence
Seq. No.
                  151372
Seq. ID
                  LIB3175-057-P1-K1-G8
Method
                  BLASTN
NCBI GI
                  q3687221
BLAST score
                  382
E value
                  0.0e + 00
Match length
                  406
```

NCBI Description

% identity

ription Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq. No. 151373

Seq. ID LIB3175-057-P1-K1-G9

99

Method BLASTX NCBI GI g4432856

BLAST score

```
BLAST score
E value
                  1.0e-77
Match length
                  149
% identity
                  98
                  (AC006300) putative 2A6 protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  151374
Seq. ID
                  LIB3175-057-P1-K1-H11
                  BLASTN
Method
NCBI GI
                  g4589950
BLAST score
                  46
                  6.0e-17
E value
                  82
Match length
                  89
% identity
                  Arabidopsis thaliana chromosome II BAC T28P16 genomic
NCBI Description
                  sequence, complete sequence
                  151375
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-H12
Method
                  BLASTX
NCBI GI
                  g2981475
BLAST score
                  335
E value
                  2.0e-31
Match length
                  95
% identity
                   (AF053084) putative cinnamyl alcohol dehydrogenase [Malus
NCBI Description
                  domestica]
Seq. No.
                  151376
                  LIB3175-057-P1-K1-H2
Seq. ID
Method
                  BLASTX
                  g2497886
NCBI GI
BLAST score
                  300
                  3.0e-27
E value
                  54
Match length
                  100
% identity
                  METALLOTHIONEIN-LIKE PROTEIN 2B (MT-2B)
NCBI Description
                  >gi_1361999_pir__S57862 metallothionein 2b - Arabidopsis
                  thaliana >qi 1086463 (U11256) metallothionein [Arabidopsis
                  thaliana]
                  151377
Seq. No.
Seq. ID
                  LIB3175-057-P1-K1-H4
Method
                  BLASTX
NCBI GI
                  g4193388
BLAST score
                  503
E value
                  5.0e-51
Match length
                  134
% identity
NCBI Description
                  (AF091455) translationally controlled tumor protein [Hevea
                  brasiliensis]
Seq. No.
                  151378
Seq. ID
                  LIB3175-057-P1-K1-H8
Method
                  BLASTX
NCBI GI
                  g2335099
```

```
E value
                  3.0e-37
Match length
                  115
% identity
NCBI Description
                   (AC002339) unknown protein [Arabidopsis thaliana]
Seq. No.
                  151379
                  LIB3175-058-P1-K1-A1
Seq. ID
Method
                  BLASTX
NCBI GI
                  g4581109
BLAST score
                  444
                  2.0e-45
E value
Match length
                  111
                  86
% identity
NCBI Description
                  (AC005825) unknown protein [Arabidopsis thaliana]
Seq. No.
                  151380
                  LIB3175-058-P1-K1-A2
Seq. ID
Method
                  BLASTX
NCBI GI
                  g3386597
BLAST score
                  403
E value
                  2.0e-39
                  79
Match length
% identity
                   (AC004665) unknown protein [Arabidopsis thaliana]
NCBI Description
                  >gi 3702347 (AC005397) putative permease [Arabidopsis
                  thaliana]
                  151381
Seq. No.
Seq. ID
                  LIB3175-058-P1-K1-A3
Method
                  BLASTN
NCBI GI
                  g2342717
BLAST score
                  124
E value
                  2.0e-63
                  218
Match length
% identity
                  94
                  Arabidopsis thaliana chromosome II BAC T14G11 genomic
NCBI Description
                  sequence, complete sequence [Arabidopsis thaliana]
                  151382
Seq. No.
Seq. ID
                  LIB3175-058-P1-K1-A5
Method
                  BLASTX
NCBI GI
                  g4063751
BLAST score
                  214
E value
                  4.0e-17
Match length
                  131
% identity
                  42
                   (AC005851) putative white protein [Arabidopsis thaliana]
NCBI Description
                  >gi_4510409 gb_AAD21495.1_ (AC006929) putative white
                  protein [Arabidopsis thaliana]
Seq. No.
                  151383
Seq. ID
                  LIB3175-058-P1-K1-A7
Method
                  BLASTN
NCBI GI
                  g3461810
BLAST score
                  308
E value
                  1.0e-173
Match length
                  395
```

```
% identity
NCBI Description
                  Arabidopsis thaliana chromosome II BAC T17M13 genomic
                  sequence, complete sequence [Arabidopsis thaliana]
Seq. No.
                  151384
Seq. ID
                  LIB3175-058-P1-K1-A8
Method
                  BLASTX
NCBI GI
                  g529353
BLAST score
                  196
                  4.0e-15
E value
Match length
                  56
% identity
NCBI Description (U12757) diphenol oxidase [Acer pseudoplatanus]
                  151385
Seq. No.
Seq. ID
                  LIB3175-058-P1-K1-B1
Method
                  BLASTX
NCBI GI
                  g3851636
BLAST score
                  495
                  4.0e-50
E value
                  124
Match length
                  74
% identity
NCBI Description (AF098519) unknown [Avicennia marina] >gi 4128206
                  (AF056316) 40S ribosome protein S7 [Avicennia marina]
Seq. No.
                  151386
Seq. ID
                  LIB3175-058-P1-K1-B10
Method
                  BLASTX
NCBI GI
                  g4206206
BLAST score
                  657
E value
                  4.0e-69
Match length
                  139
                  91
% identity
NCBI Description
                  (AF071527) putative M-type thioredoxin [Arabidopsis
                  thaliana] >gi 4263039 gb AAD15308 (AC005142) putative
                  M-type thioredoxin [Arabidopsis thaliana]
Seq. No.
                  151387
Seq. ID
                  LIB3175-058-P1-K1-B11
                  BLASTX
Method
NCBI GI
                  g464662
BLAST score
                  213
E value
                  5.0e-17
Match length
                  105
% identity
                  48
NCBI Description
                  CHLOROPLAST 31 KD RIBONUCLEOPROTEIN PRECURSOR (RNA-BINDING
                  PROTEIN RNP-T) (RNA-BINDING PROTEIN 1)
                  >gi 282884 pir S28057 RNA-binding protein RNP-T -
                  Arabidopsis thaliana >gi 16490 emb CAA46347 (X65255)
                  RNA-binding protein [Arabidopsis thaliana] >gi 387569
                  (M94554) 31 kDa RNA binding protein [Arabidopsis thaliana]
                  >gi_475718 (U08467) RNA-binding protein 1 [Arabidopsis
                  thaliana] >gi_4220513_emb_CAA22986_ (AL035356) RNA-binding
                  protein RNP-T precursor [Arabidopsis thaliana]
                  >gi_737169_prf__1921382A RNA-binding protein [Arabidopsis
                  thaliana]
```

```
Seq. No.
                  151388
Seq. ID
                  LIB3175-058-P1-K1-B12
Method
                  BLASTX
NCBI GI
                  g99735
BLAST score
                  743
E value
                  3.0e-79
Match length
                  145
% identity
                  97
                  L-ascorbate peroxidase (EC 1.11.1.11) precursor -
NCBI Description
                  Arabidopsis thaliana (fragment)
                  151389
Seq. No.
Seq. ID
                  LIB3175-058-P1-K1-B2
Method
                  BLASTX
NCBI GI
                  g3212866
BLAST score
                  260
E value
                  1.0e-22
                  78
Match length
% identity
                   (AC004005) unknown protein [Arabidopsis thaliana]
NCBI Description
Seq. No.
                  151390
                  LIB3175-058-P1-K1-B3
Seq. ID
Method
                  BLASTX
NCBI GI
                  q1172872
BLAST score
                  455
E value
                  2.0e-45
Match length
                  88
% identity
                  100
NCBI Description
                  CYSTEINE PROTEINASE RD19A PRECURSOR >gi 541856 pir__JN0718
                  drought-inducible cysteine proteinase (EC 3.4.22.-) RD19A
                  precursor - Arabidopsis thaliana >gi 435618_dbj_BAA02373_
                   (D13042) thiol protease [Arabidopsis thaliana]
                  >gi_4539328_emb_CAB38829.1_ (AL035679) drought-inducible
                  cysteine proteinase RD19A precursor [Arabidopsis thaliana]
                  151391
Seq. No.
Seq. ID
                  LIB3175-058-P1-K1-B4
Method
                  BLASTX
NCBI GI
                  g2832359
BLAST score
                  306
                  7.0e-28
E value
                  79
Match length
                  82
% identity
NCBI Description (Y14072) HMG protein [Arabidopsis thaliana]
                  151392
Seq. No.
Seq. ID
                  LIB3175-058-P1-K1-B5
Method
                  BLASTX
NCBI GI
                  q4056469
BLAST score
                  608
                  3.0e-63
E value
Match length
                  119
                  99
% identity
NCBI Description
                   (AC005990) Strong similarity to gb_M95166 ADP-ribosylation
                  factor from Arabidopsis thaliana. ESTs gb Z25826,
                  gb_R90191, gb N65697, gb_AA713150, gb T46332, gb_AA040967,
```

E value

Match length

1.0e-51

```
gb AA712956, gb T46403, gb T46050, gb AI100391 and
                    gb Z25043 come from t
Seq. No.
                    151393
  Seq. ID
                    LIB3175-058-P1-K1-B6
  Method
                    BLASTX
  NCBI GI
                    q544425
  BLAST score
                    417
  E value
                    6.0e-41
                    82
 Match length
% identity
                    GLYCINE-RICH RNA-BINDING PROTEIN 8 (CCR1 PROTEIN)
  NCBI Description
                    >gi 419756 pir S30148 glycine-rich protein (clone AtGRP8)
                    - Arabidopsis thaliana >gi_16305_emb_CAA78712_ (Z14988)
                    glycine rich protein [Arabidopsis thaliana] >qi 166658
                    (L04171) ORF [Arabidopsis thaliana] >gi 166839 (L00649)
                    RNA-binding protein [Arabidopsis thaliana]
  Seq. No.
                    151394
  Seq. ID
                    LIB3175-058-P1-K1-B7
  Method
                    BLASTX
  NCBI GI
                    g3935156
  BLAST score
                    399
  E value
                    3.0e-43
                    110
  Match length
                    77
  % identity
                    (AC005106) T25N20.20 [Arabidopsis thaliana]
  NCBI Description
  Seq. No.
                    151395
  Seq. ID
                    LIB3175-058-P1-K1-B8
  Method
                    BLASTN
  NCBI GI
                    g3510343
  BLAST score
                    196
  E value
                    1.0e-106
                    460
  Match length
                    99
  % identity
  NCBI Description
                    Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:
                    MJC20, complete sequence [Arabidopsis thaliana]
  Seq. No.
                    151396
  Seq. ID
                    LIB3175-058-P1-K1-B9
  Method
                    BLASTX
  NCBI GI
                    g2827143
  BLAST score
                    274
  E value
                    2.0e-24
  Match length
                    79
  % identity
  NCBI Description
                    (AF027174) cellulose synthase catalytic subunit
                    [Arabidopsis thaliana]
                    151397
  Seq. No.
  Seq. ID
                    LIB3175-058-P1-K1-C1
 Method
                    BLASTX
  NCBI GI
                    g1709798
  BLAST score
                    508
```

```
% identity
                  26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG >gi 1155334
NCBI Description
                   (U43398) POTATP1 [Solanum tuberosum]
Seq. No.
                  151398
                  LIB3175-058-P1-K1-C10
Seq. ID
                  BLASTX
Method
NCBI GI
                  q4580460
                  280
BLAST score
                  8.0e-33
E value
                  111
Match length
                  77
% identity
                   (AC006081) putative 26S Protease Subunit 4 [Arabidopsis
NCBI Description
                  thaliana]
                  151399
Seq. No.
                  LIB3175-058-P1-K1-C11
Seq. ID
Method
                  BLASTX
                  g2342735
NCBI GI
                  372
BLAST score
                  7.0e-36
E value
                  90
Match length
% identity
                  (AC002341) unknown protein [Arabidopsis thaliana]
NCBI Description
                  151400
Seq. No.
Seq. ID
                  LIB3175-058-P1-K1-C12
Method
                  BLASTN
NCBI GI
                  q4587641
BLAST score
                  44
E value
                  1.0e-15
Match length
                  68
                  91
% identity
NCBI Description
                  Arabidopsis thaliana chromosome I BAC F20D21 genomic
                  sequence, complete sequence
                  151401
Seq. No.
Seq. ID
                  LIB3175-058-P1-K1-C2
Method
                  BLASTX
NCBI GI
                  q4185505
BLAST score
                  461
E value
                  4.0e-46
Match length
                  112
% identity
                   (AF101038) nonspecific lipid-transfer protein precursor
NCBI Description
                  [Brassica napus]
                  151402
Seq. No.
Seq. ID
                  LIB3175-058-P1-K1-C4
Method
                  BLASTX
NCBI GI
                  g2244749
BLAST score
                  671
E value
                  1.0e-70
Match length
                  132
% identity
NCBI Description (Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
```